

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
1 August 2002 (01.08.2002)

PCT

(10) International Publication Number
WO 02/059377 A2

- (51) International Patent Classification⁷: C12Q 1/68 (74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, 8th Floor, San Francisco, CA 94111-3834 (US).
- (21) International Application Number: PCT/US02/02242
- (22) International Filing Date: 24 January 2002 (24.01.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|------------|------------------------------|----|
| 60/263,965 | 24 January 2001 (24.01.2001) | US |
| 60/265,928 | 2 February 2001 (02.02.2001) | US |
| 09/829,472 | 9 April 2001 (09.04.2001) | US |
| 60/282,698 | 9 April 2001 (09.04.2001) | US |
| 60/288,590 | 4 May 2001 (04.05.2001) | US |
| 60/294,443 | 29 May 2001 (29.05.2001) | US |
- (71) Applicant: EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080-7019 (US).
- (72) Inventors: MACK, David, H.; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). GISH, Kurt, C.; 40 Perego Terrace #2, San Francisco, CA 94131 (US). AFAR, Daniel; 435 Visitacion Avenue, Brisbane, CA 94005 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: METHODS OF DIAGNOSIS OF BREAST CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BREAST CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in breast cancer. Related methods and compositions that can be used for diagnosis and treatment of breast cancer are disclosed. Also described herein are methods that can be used to identify modulators of breast cancer.

WO 02/059377 A2

METHODS OF DIAGNOSIS OF BREAST CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BREAST CANCER

5

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/263,965, filed January 24, 2001; USSN 60/265,928, filed February 2, 2001; USSN 09/829,472 filed April 9, 2001; USSN 60/282,698, filed April 9, 2001; USSN 60/288,590, filed May 4, 2001; and USSN
10 60/294,443, filed May 29, 2001, all of which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein
15 expression profiles and nucleic acids, products, and antibodies thereto that are involved in breast cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis and therapy of breast cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit breast cancer.

BACKGROUND OF THE INVENTION

Breast cancer is one of the most frequently diagnosed cancers and the second
leading cause of female cancer death in North America and northern Europe, with lung
cancer being the leading cause. Lifetime incidence of the disease in the United States is one-
in-eight, with a 1-in-29 lifetime risk of dying from breast cancer. Early detection of breast
25 cancer, using mammography, clinical breast examination, and self breast examination, has dramatically improved the treatment of the disease, although sensitivity is still major concern, as mammographic sensitivity has been estimated at only 60%–90%. Treatment of breast cancer consists largely of surgical lumpectomy or mastectomy, radiation therapy, anti-

hormone therapy, and/or chemotherapy. Although many breast cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons et al., 2000, Arch. Pathol. Lab. Med. 124:966-978; 5 Hamilton and Piccart, 2000, Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson, 2000, J. Clin. Oncol. 18:113sup-118sup).

Imaging of breast cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no 10 lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of breast cancers but not in normal tissues. Liefers et al., New England J. of Med. 15 339(4):223 (1998).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of breast cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens 20 suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer 25 (Ross and Fletcher, 1998, Stem Cells 16:413-428). Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma (Maloney et al., 1997, Blood 90:2188-2195; Leget and Czuczman, 1998, Curr. Opin. Oncol. 10:548-551).

Other potential immunotherapeutic targets have been identified for breast 30 cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane

protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in breast cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically distinct molecule, and is in early clinical trials as a vaccine target (Gilewski et al., 2000, Clin. Cancer Res. 6:1693-1701; Scholl et al., 2000, J. Immunother. 23:570-580).

5 The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3 (Bon et al., 1997, Clin. Chem. 43:585-593). However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease. Many other genes have been reported to be overexpressed in breast cancer, such as EGFR (Sainsbury et al., 1987, Lancet
10 1(8547):1398-1402), c-erbB3 (Naidu et al., 1988, Br. J. Cancer 78:1385-1390), FGFR2 (Penault-Llorca et al., 1991, Int. J. Cancer 61:170-176), PKW (Preiherr et al., 2000, Anticancer Res. 20:2255-2264), MTA1 (Nawa et al., 2000, J. Cell Biochem. 79:202-212), breast cancer associated gene 1 (Kurt et al., 2000, Breast Cancer Res. Treat. 59:41-48). Although monoclonal antibodies to the protein products of some of these overexpressed
15 genes have been reported (for review, see Green et al., 2000, Cancer Treat. Rev. 26:269-286), none are currently approved for breast cancer therapy in the US.

Disclosures of certain genes and ESTs described as being expressed in breast cancer are found in international patent applications WO-99/33869, WO-97/25426, WO-97/02280 and WO-00/55173, WO-98/45328 and WO-00/22130. Similarly, genes and ESTs
20 described as being expressed in breast cancer are disclosed in US Patent Nos. 5,759,776 and 5,693,522. The utility of such genes is described in each of these publications, and their disclosures are incorporated herein in their entirety.

While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The
25 elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of breast cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in breast and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of breast cancer. Further provided are methods that can
30 be used to screen candidate bioactive agents for the ability to modulate breast cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in breast cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate breast cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a breast cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25.

In one embodiment, the present invention provides a method of determining the level of a breast cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a breast cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-25.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat breast cancer. In another embodiment, the patient is suspected of having metastatic breast cancer.

In one embodiment, the patient is a human.

In one embodiment, the breast cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of breast cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a breast cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic breast cancer. In a further embodiment, the patient has a drug resistant form of breast cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the breast cancer-associated transcript to a level of the breast cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-25.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-25.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-25.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-25.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

5 In one aspect, the present invention provides a method of detecting a breast cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to breast cancer in a patient, the method comprising contacting a
10 biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-25.

In another aspect, the present invention provides a method for identifying a compound that modulates a breast cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a breast cancer-associated polypeptide, the
15 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

20 In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting
25 proliferation of a breast cancer-associated cell to treat breast cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay
30 comprising the steps of: (i) administering a test compound to a mammal having breast cancer

or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of breast cancer.

In one embodiment, the control is a mammal with breast cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-25 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having breast cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having breast cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a breast cancer. In one embodiment, a gene is selected from Tables 1-25. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of

expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

5 Also provided is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the breast cancer modulatory protein, or an animal lacking the breast cancer modulatory protein, for example as a result of a gene knockout.

10 Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-25, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

15 Furthermore, a method of diagnosing a disorder associated with breast cancer is provided. The method comprises determining the expression of a gene of Tables 1-25, preferably a gene of Table 25, in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with breast cancer.

20 In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in breast cancer.

25 In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a breast cancer modulating protein (breast cancer modulatory protein) or a fragment thereof and an antibody which binds to said breast cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a breast cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said breast cancer modulatory protein or fragment thereof. The method further includes determining the binding of said breast cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist.

30 Preferably, the agent inhibits breast cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a breast cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-25.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a breast cancer modulating protein, preferably encoded by a nucleic acid of Tables 1-25, more preferably of Table 25, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a breast cancer modulating protein, preferably selected from the nucleic acids of Tables 1-25, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a breast cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-25.

In another aspect of the invention, a method of treating an individual for breast cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a breast cancer modulating protein. In another embodiment, the method comprises administering to a patient having breast cancer an antibody to a breast cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for breast cancer (PC), including metastatic breast cancer, as well as methods for screening for compositions which modulate breast cancer. Also provided are methods for treating breast cancer.

Tables 1-24B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in breast cancer

samples. Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 18, 19, 20, 21, and 22 list those genes that are up-regulated in breast cancer cells. Table 14 lists those genes that are highly upregulated in breast cancer cells. Table 1, 2, 3, 15, and 23 list genes that are down-regulated in breast cancer cells and Table 16, lists genes that are highly down-regulated in breast cancer genes.

- 5 The Tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

- The term “breast cancer protein” or “breast cancer polynucleotide” or “breast cancer-associated transcript” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-25; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-25, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-25 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-25. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A “breast cancer polypeptide” and a “breast cancer polynucleotide,” include both naturally occurring or recombinant forms.

A “full length” breast cancer protein or nucleic acid refers to a breast cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type breast cancer polynucleotide or polypeptide sequences. The “full length” may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

“Biological sample” as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a breast cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

“Providing a biological sample” means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms “identical” or percent “identity,” in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.,* NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to

be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms,

which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the
5 National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial
10 neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid
15 sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the
20 sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of
25 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match
30 between two nucleotide or amino acid sequences would occur by chance. For example, a

nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

5 An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another
10 indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

 A "host cell" is a naturally occurring cell or a transformed cell that contains an
15 expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

20 The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a
25 preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and
30 most preferably at least 99% pure. "Purify" or "purification" in other embodiments means

removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino

acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell* (3rd ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that

often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together.

Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui & Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805

(1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp 169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is

relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the breast cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed

or not expressed at all. By the term “recombinant nucleic acid” herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear
5 form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced
10 recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic
15 acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two
20 or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type
25 promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers
30 to a functional linkage between a nucleic acid expression control sequence (such as a

promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

5 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

10 The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of
15 nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays"
20 (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at
25 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as
30 formamide. For selective or specific hybridization, a positive signal is at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a breast cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the breast cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease breast cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of breast cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a breast cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the breast cancer protein; measuring binding activity or binding assays, e.g. binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on breast cancer can also be performed using breast cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of breast cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for breast cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of breast cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of breast cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block

activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of breast cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate breast cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of breast cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the breast cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of breast cancer can also be identified by incubating breast cancer cells with the test compound and determining increases or decreases in the expression of 1 or more breast cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more breast cancer proteins, such as breast cancer proteins encoded by the sequences set out in Tables 1-25.

Samples or assays comprising breast cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a breast cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or

immortalization of the cell. *See, e.g., Freshney, Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

“Tumor cell” refers to precancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells or “transformation” in tissue culture, refers
5 to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of
new genetic material. Although transformation can arise from infection with a transforming
virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise
spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.
Transformation is associated with phenotypic changes, such as immortalization of cells,
10 aberrant growth control, nonmorphological changes, and/or malignancy (*see, Freshney, Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

“Antibody” refers to a polypeptide comprising a framework region from an
immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen.
The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta,
15 epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region
genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as
gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG,
IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or
its functional equivalent will be most critical in specificity and affinity of binding. *See Paul,*
20 *Fundamental Immunology.*

An exemplary immunoglobulin (antibody) structural unit comprises a
tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair
having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus
of each chain defines a variable region of about 100 to 110 or more amino acids primarily
25 responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy
chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-
characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin
digests an antibody below the disulfide linkages in the hinge region to produce F(ab)₂, a
30 dimer of Fab which itself is a light chain joined to V_H-C_{H1} by a disulfide bond. The F(ab)₂

may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)₂ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g., Kohler & Milstein, Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4:72 (1983); Cole *et al., pp. 77-96 in Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of breast cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal breast or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the breast, or breast cancer tissue or metastatic breast cancerous tissue can be compared with tissue samples of breast and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different breast cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in breast cancer versus non-breast cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate breast cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of breast cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the breast cancer expression profile. This may be done by making biochips comprising sets of the important breast cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the breast cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the breast cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the breast cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in breast cancer, herein termed "breast cancer sequences." As outlined below, breast cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in breast cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the breast cancer sequences are from humans; however, as will be appreciated by those in the art, breast cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other breast cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Breast cancer sequences from other organisms may be obtained using the techniques outlined below.

Breast cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, breast cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the breast cancer sequences can be generated.

A breast cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying breast cancer-associated sequences, the breast cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing breast cancer samples with metastatic cancer samples from other cancers, such as lung, breast, gastrointestinal cancers, ovarian, etc. Samples of different stages of breast cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art

for the preparation of mRNA. Suitable biochips are commercially available, e.g. from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between
5 normal and disease states are compared to genes expressed in other normal tissues, preferably normal breast, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, colon, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the breast cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some
10 embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, breast cancer sequences are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in the breast cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at
15 least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see*, e.g., Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and
20 <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). U.S. Patent Application N. 09/687,576, with the same assignee as the present application, further discloses related sequences, compositions, and methods of diagnosis and treatment of breast cancer is hereby expressly incorporated by reference.

25 In another preferred embodiment, breast cancer sequences are those that are down-regulated in the breast cancer; that is, the expression of these genes is lower in breast cancer tissue as compared to non-cancerous tissue (*see, e.g.*, Tables 1,2, 3, 15, 16 etc...). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

30

Informatics

The ability to identify genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with breast cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see Anderson, Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see U.S. Patent No. 5,811,231*). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing breast cancer, i.e., the identification of breast cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring,

gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

5 An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records
10 containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity
15 between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis
20 described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as
25 the merger of two or more such tree structures.

 See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxeavanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological*
30 *Science and Medicine* (1999); *Introduction to Computational Molecular Biology* (Setubal *et*

al., eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000);
Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach (Higgins &
Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the*
Internet (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and
5 Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer
and software for storing in computer-retrievable form assay data records cross-tabulated, e.g.,
with data specifying the source of the target-containing sample from which each sequence
specificity record was obtained.

10 In an exemplary embodiment, at least one of the sources of target-containing
sample is from a control tissue sample known to be free of pathological disorders. In a
variation, at least one of the sources is a known pathological tissue specimen, e.g., a
neoplastic lesion or another tissue specimen to be analyzed for breast cancer. In another
variation, the assay records cross-tabulate one or more of the following parameters for each
15 target species in a sample: (1) a unique identification code, which can include, e.g., a target
molecular structure and/or characteristic separation coordinate (e.g., electrophoretic
coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species
present in the sample.

The invention also provides for the storage and retrieval of a collection of
20 target data in a computer data storage apparatus, which can include magnetic disks, optical
disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM,
magnetic bubble memory devices, and other data storage devices, including CPU registers
and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern
in an array of magnetic domains on a magnetizable medium or as an array of charge states or
25 transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of
a transistor and a charge storage area, which may be on the transistor). In one embodiment,
the invention provides such storage devices, and computer systems built therewith,
comprising a bit pattern encoding a protein expression fingerprint record comprising unique
identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the

assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to
5 secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha,
10 PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem,
15 an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention,
20 which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of breast cancer-associated proteins

25 Breast cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the breast cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such
30 proteins often results in unregulated or dysregulated cellular processes (*see, e.g., Molecular*

Biology of the Cell (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or
5 targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly
10 conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a
15 few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.
20 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322-
25 (1998)).

In another embodiment, the breast cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular
30 domains of such proteins may have a number of functions including those already described

for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor,

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include

cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate
5 with the extracellular matrix and contribute to the maintenance of the cell structure.

Breast cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in*
10 *situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be
15 secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the breast cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature,
20 they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Breast cancer proteins that are secreted proteins are particularly
25 preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

Use of breast cancer nucleic acids

As described above, breast cancer sequence is initially identified by
30 substantial nucleic acid and/or amino acid sequence homology or linkage to the breast cancer

sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

5 The breast cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-25, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the breast cancer genes
10 can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

 Once the breast cancer nucleic acid is identified, it can be cloned and, if
15 necessary, its constituent parts recombined to form the entire breast cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant breast cancer nucleic acid can be further-used as a probe to identify and isolate other breast cancer nucleic acids, e.g., extended coding regions. It can also be
20 used as a "precursor" nucleic acid to make modified or variant breast cancer nucleic acids and proteins.

 The breast cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the breast cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below,
25 or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the breast cancer nucleic acids that include coding regions of breast cancer proteins can be put into expression vectors for the expression of breast cancer proteins, again for screening purposes or for administration to a patient.

 In a preferred embodiment, nucleic acid probes to breast cancer nucleic acids
30 (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are

made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the breast cancer nucleic acids, *i.e.* the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As
5 outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially
10 complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure,
15 composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

20 In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (*i.e.*, have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

25 As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By “immobilized” and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By “non-
30 covalent binding” and grammatical equivalents herein is meant one or more of electrostatic,

hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are
5 attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

10 In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to
15 contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and
20 copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low
25 Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize

sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g.,
5 the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g. using linkers as are known in the art; e.g.,
10 homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art,
15 and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which
20 bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described
25 in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of breast cancer-associated sequences. These assays are typically performed in
30 conjunction with reverse transcription. In such assays, a breast cancer-associated nucleic acid

sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of breast cancer-associated RNA. Methods of
5 quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent
10 dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of
15 amplification (*see*, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see* Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication
20 (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of breast cancer proteins from nucleic acids

In a preferred embodiment, breast cancer nucleic acids, e.g., encoding breast
25 cancer proteins are used to make a variety of expression vectors to express breast cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see*, e.g., Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating
30 extrachromosomal vectors or vectors which integrate into a host genome. Generally, these

expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the breast cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the breast cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g. in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression
5 vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating
10 vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The breast cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a breast
15 cancer protein, under the appropriate conditions to induce or cause expression of the breast cancer protein. Conditions appropriate for breast cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of
20 constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic
viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect
25 and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the breast cancer proteins are expressed in
30 mammalian cells. Mammalian expression systems are also known in the art, and include

retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.,* Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, breast cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the breast cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which

render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, breast cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, breast cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The breast cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the breast cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the breast cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the breast cancer protein is a breast cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the breast cancer protein is purified or isolated after expression. Breast cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the breast cancer protein may be purified using a standard anti-breast cancer protein antibody column. Ultrafiltration

and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the breast cancer protein. In some instances no purification will be necessary.

5 Once expressed and purified if necessary, the breast cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of breast cancer proteins

10 In one embodiment, the breast cancer proteins are derivative or variant breast cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative breast cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the breast cancer
15 peptide.

 Also included within one embodiment of breast cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the breast cancer
20 protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant breast cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation,
25 a feature that sets them apart from naturally occurring allelic or interspecies variation of the breast cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

 While the site or region for introducing an amino acid sequence variation is
30 predetermined, the mutation per se need not be predetermined. For example, in order to

optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed breast cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer
5 mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of breast cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in
10 some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the breast cancer protein are
15 desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the breast cancer proteins as needed. Alternatively,
20 the variant may be designed such that the biological activity of the breast cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide
25 backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or
30 alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue

having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

Covalent modifications of breast cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a breast cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a breast cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking breast cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-breast cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the breast cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence breast cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence breast cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express breast cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to breast cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence breast cancer polypeptide (for O-linked glycosylation sites). The breast cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the breast cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the breast cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the breast cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of breast cancer comprises linking the breast cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Breast cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a breast cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a breast cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the breast cancer polypeptide. The presence of such epitope-tagged forms of a breast cancer polypeptide can be detected using

an antibody against the tag polypeptide. Also, provision of the epitope tag enables the breast cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a breast cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky *et al.*, *Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp *et al.*, *BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al.*, *Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al.*, *J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other breast cancer proteins of the breast cancer family, and breast cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related breast cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the breast cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to breast cancer proteins

In a preferred embodiment, when the breast cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the breast cancer protein

should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller breast cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-25 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene

glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

10 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1-25 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

 In a preferred embodiment, the antibodies to breast cancer protein are capable of reducing or eliminating a biological function of a breast cancer protein, as is described below. That is, the addition of anti-breast cancer protein antibodies (either polyclonal or preferably monoclonal) to breast cancer tissue (or cells containing breast cancer) may reduce or eliminate the breast cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

25 In a preferred embodiment the antibodies to the breast cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include

human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all

respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of breast cancer with an antibody raised against breast cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the breast cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted breast cancer protein.

In another preferred embodiment, the breast cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the breast cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane breast cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the breast cancer protein. The antibody is also an antagonist of the breast cancer protein. Further, the antibody prevents activation of the transmembrane breast cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the breast cancer

protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that
5 activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, breast cancer is treated by administering to a patient antibodies directed against the transmembrane breast cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

10 In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the breast cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules
15 associated with or in close proximity to the breast cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with breast cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to breast cancer tissue or cells, results in
20 a reduction in the number of afflicted cells, thereby reducing symptoms associated with breast cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, croton, phenomycin, enomycin and the like. Cytotoxic agents also include
25 radiochemicals made by conjugating radioisotopes to antibodies raised against breast cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane breast cancer proteins not only serves to increase the local concentration of therapeutic moiety in the breast cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with
30 the therapeutic moiety.

In another preferred embodiment, the breast cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the breast cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The breast cancer antibodies of the invention specifically bind to breast cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of breast cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the breast cancer phenotype. Expression levels of genes in normal tissue (i.e., not undergoing breast cancer) and in breast cancer tissue (and in some cases, for varying severities of breast cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can

qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus breast cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is

5 detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via

10 standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is at least

15 about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the

20 final gene product itself (protein) can be monitored, e.g., with antibodies to the breast cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to breast cancer genes, i.e., those identified as being important in a breast cancer phenotype, can be evaluated in a breast cancer diagnostic test.

25 In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in

a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the breast cancer protein are detected. Although DNA or RNA encoding the breast cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a breast cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a breast cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, breast cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of breast cancer. Detection of these proteins in putative breast cancer tissue allows for detection or diagnosis

of breast cancer. In one embodiment, antibodies are used to detect breast cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the breast cancer protein is detected, e.g., by immunoblotting with antibodies raised against the breast cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the breast cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the breast cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the breast cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of breast cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing breast cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of breast cancer proteins.

Antibodies can be used to detect a breast cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous breast cancer protein.

In a preferred embodiment, *in situ* hybridization of labeled breast cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including

breast cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g.,* Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to breast cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, breast cancer probes may be attached to biochips for the detection and quantification of breast cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al., Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified breast cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the breast cancer phenotype or an identified physiological function of a breast cancer protein. As above, this can be done on an individual gene level or

by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

5 Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in breast cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the breast cancer protein. “Modulation” thus includes both an increase and a decrease in gene
10 expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing breast cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in breast cancer tissue compared to normal
15 tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in breast cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the breast cancer protein and standard
20 immunoassays. Proteomics and separation techniques may also allow quantification of expression.

 In a preferred embodiment, gene expression or protein monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

25 In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more breast cancer-associated sequences, e.g., a polynucleotide sequence set out in Table 17. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that

5 modulate breast cancer, modulate breast cancer proteins, bind to a breast cancer protein, or interfere with the binding of a breast cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or

10 indirectly alter the breast cancer phenotype or the expression of a breast cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a breast cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a breast cancer phenotype.

15 Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they

20 are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group,

25 preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred

30 are peptides.

In one aspect, a modulator will neutralize the effect of a breast cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a breast cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as

hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses
5 of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). *See, generally*, Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature*
10 *Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds,
15 U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

20 A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual
25 synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis,

MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, *etc.*).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of breast cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially

preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, *e.g.*, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of breast cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to,

temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, *etc.* which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the breast cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, *e.g.*, for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a breast cancer expression pattern leading to a normal expression pattern, or to modulate a single breast cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically

modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated breast cancer tissue reveals genes that are not expressed in normal tissue or breast cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for breast cancer genes or proteins.

5 In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated breast cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of breast cancer cells, that have an associated breast cancer expression profile. By
10 “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of
15 the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is
20 generated, as outlined herein.

Thus, e.g., breast cancer tissue may be screened for agents that modulate, e.g., induce or suppress the breast cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on breast cancer activity. By defining such a signature for the breast cancer phenotype, screens for new drugs that alter
25 the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular
30 differentially expressed gene as important in a particular state, screening of modulators of

either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins" or a "breast cancer modulatory protein". The breast cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the breast cancer modulatory protein is a fragment. In a preferred embodiment, the breast cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Table 25. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Table 25. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the breast cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, i.e., to cysteine.

In one embodiment the breast cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the breast cancer protein is conjugated to BSA.

Measurements of breast cancer polypeptide activity, or of breast cancer or the breast cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the breast cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of breast cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second

messengers such as cGMP. In the assays of the invention, mammalian breast cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a breast cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the breast cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the breast cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the breast cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins." The breast cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate

differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially
5 expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the breast cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a breast cancer protein and a candidate compound, and determining the binding of the compound to
10 the breast cancer protein. Preferred embodiments utilize the human breast cancer protein, although other mammalian proteins may also be used, e.g. for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative breast cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the breast cancer
15 protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of
20 suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible
25 with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of
30 the protein or agent, excess unbound material is removed by washing. The sample receiving

areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the breast cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the breast cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the breast cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the breast cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a breast cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput

screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the breast cancer protein and thus is capable of binding to, and potentially modulating, the activity of the breast cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the breast cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the breast cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the breast cancer proteins. In this embodiment, the methods comprise combining a breast cancer protein and a competitor in a first sample. A second sample comprises a test compound, a breast cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the breast cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the breast cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native breast cancer protein, but cannot bind to modified breast cancer proteins. The structure of the breast cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a

breast cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a breast cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising breast cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a breast cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate breast cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the breast cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting breast cancer cell division is provided. The method comprises administration of a breast cancer inhibitor. In another embodiment, a method of inhibiting breast cancer is provided. The method comprises administration of a breast cancer inhibitor. In a further embodiment, methods of treating cells or individuals with breast cancer are provided. The method comprises administration of a breast cancer inhibitor.

In one embodiment, a breast cancer inhibitor is an antibody as discussed above. In another embodiment, the breast cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of breast cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994), herein incorporated by reference. See also, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a

higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994),
5 *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a breast cancer-associated sequence and are grown for 24 hours at saturation
10 density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal
15 counterparts (*see, e.g.,* Temin, *J. Natl. Cancer Inst.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

20 *Tumor specific markers levels*

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.,* Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.*
25 *in Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.,* Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see*, Unkless *et al.*, *J. Biol. Chem.* 249:4295-4305 (1974);
30 Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-

312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth*. in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

5 *Invasiveness into Matrigel*

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate breast cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this
10 assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of
15 the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

20 Effects of breast cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the breast cancer gene is disrupted or in which a breast cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous breast cancer gene site in the mouse genome via homologous recombination.
25 Such mice can also be made by substituting the endogenous breast cancer gene with a mutated version of the breast cancer gene, or by mutating the endogenous breast cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which
30 is re-implanted into a recipient female. Some of these embryos develop into chimeric mice

that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi *et al.*, *Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al.*, *Manipulating the Mouse Embryo: A Laboratory Manual*,
5 Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella *et al.*, *J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated
10 mouse (see, e.g., Bradley *et al.*, *Br. J. Cancer* 38:263 (1978); Selby *et al.*, *Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a breast cancer-associated sequences are injected subcutaneously. After a suitable
15 length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of breast cancer

20 Antisense Polynucleotides

In certain embodiments, the activity of a breast cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e.*, a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a breast cancer protein mRNA, or a subsequence thereof.
25 Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar
30 moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other

sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the breast cancer protein mRNA. *See, e.g.,* Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant
5 means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense
oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by
10 binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for breast cancer molecules. A preferred antisense molecule is for a breast cancer sequences in Tables 1-25, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment
15 generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (*Cancer Res.* 48:2659 (1988) and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

20 *Ribozymes*

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of breast cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin
25 ribozymes, RNase P, and axhead ribozymes (*see, e.g.,* Castanotto *et al., Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al., Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent
30 No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g.,*

WO 94/26877; Ojwang *et al.*, *Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al.*, *Human Gene Therapy* 1:39-45 (1994); Leavitt *et al.*, *Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al.*, *Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al.*, *Virology* 205: 121-126 (1994)).

5 Polynucleotide modulators of breast cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does
10 not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of breast cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is
15 understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating breast cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-breast cancer antibody that reduces or eliminates the biological activity of an endogenous
20 breast cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a breast cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g. when the breast cancer sequence is down-regulated in breast cancer, such state may be reversed by increasing the amount of breast cancer gene product in the cell. This can be accomplished, e.g., by
25 overexpressing the endogenous breast cancer gene or administering a gene encoding the breast cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g. as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g. when the breast cancer

sequence is up-regulated in breast cancer, the activity of the endogenous breast cancer gene is decreased, e.g. by the administration of a breast cancer antisense nucleic acid.

In one embodiment, the breast cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to breast cancer proteins. Similarly,
5 the breast cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify breast cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a breast cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The breast cancer
10 antibodies may be coupled to standard affinity chromatography columns and used to purify breast cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the breast cancer protein.

Methods of identifying variant breast cancer-associated sequences

15 Without being bound by theory, expression of various breast cancer sequences is correlated with breast cancer. Accordingly, disorders based on mutant or variant breast cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant breast cancer genes, e.g., determining all or part of the sequence of at least one endogenous breast cancer genes in a cell. This may be accomplished
20 using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the breast cancer genotype of an individual, e.g., determining all or part of the sequence of at least one breast cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include
25 comparing the sequence of the sequenced breast cancer gene to a known breast cancer gene, i.e., a wild-type gene.

The sequence of all or part of the breast cancer gene can then be compared to the sequence of a known breast cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred
30 embodiment, the presence of a difference in the sequence between the breast cancer gene of

the patient and the known breast cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the breast cancer genes are used as probes to determine the number of copies of the breast cancer gene in the genome.

5 In another preferred embodiment, the breast cancer genes are used as probes to determine the chromosomal localization of the breast cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the breast cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a breast cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend
15 on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is
20 known in the art, adjustments for breast cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application N. 09/687,576, further discloses the use of compositions and
25 methods of diagnosis and treatment in breast cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal,
30 preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the breast cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the breast cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a breast cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that breast cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, *etc.*) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a breast cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacological Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ.

Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The*

Pharmacological Basis of Therapeutics, supra.

The compositions containing modulators of breast cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, *etc.* Such prophylactic treatments may be used, *e.g.*, in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present breast cancer protein-modulating compounds can be administered alone or in combination with additional breast cancer modulating compounds or with other therapeutic agent, *e.g.*, other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, *e.g.*, polynucleotides comprising nucleic acid sequences set forth in Tables 1-25, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of breast cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use

of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

In a preferred embodiment, breast cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, breast cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the breast cancer coding regions) can be administered in a gene therapy application. These breast cancer genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Breast cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (*see, e.g.,* Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.,* Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, (1991); Alonso *et al.*, *Vaccine* 12:299-306 (1994); Jones *et al.*, *Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.,* Takahashi *et al.*, *Nature* 344:873-875 (1990); Hu *et al.*, *Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g.,* Tam, *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, *et al.*, In: *Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al.*, *Nature* 320:535 (1986); Hu *et al.*, *Nature* 320:537 (1986); Kieny, *et al.*, *AIDS Bio/Technology* 4:790 (1986); Top *et al.*, *J. Infect. Dis.* 124:148 (1971); Chanda *et al.*, *Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g.,* Kofler *et al.*, *J. Immunol. Methods.* 192:25 (1996); Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993); Falo *et al.*, *Nature Med.* 7:649 (1995)), adjuvants (Warren *et al.*, *Annu. Rev. Immunol.* 4:369 (1986);

Gupta *et al.*, *Vaccine* 11:293 (1993)), liposomes (Reddy *et al.*, *J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al.*, *Science* 259:1745 (1993); Robinson *et al.*, *Vaccine* 11:957 (1993); Shiver *et al.*, In: *Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev.*

5 *Immunol.* 12:923 (1994) and Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide
10 or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or
15 aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

20 Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies
25 include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors
30 include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of

vaccinia virus, e.g., as a vector to express nucleotide sequences that encode breast cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization e.g. adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.,* Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a breast cancer gene or portion of a breast cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a breast cancer patient. The breast cancer gene used for DNA vaccines can encode full-length breast cancer proteins, but more preferably encodes portions of the breast cancer proteins including peptides derived from the breast cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a breast cancer gene. For example, breast cancer-associated genes or sequence encoding subfragments of a breast cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the breast cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment breast cancer genes find use in generating animal models of breast cancer. When the breast cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed

to the breast cancer gene will also diminish or repress expression of the gene. Animal models of breast cancer find use in screening for modulators of a breast cancer-associated sequence or modulators of breast cancer. Similarly, transgenic animal technology including gene knockout technology, e.g. as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the breast cancer protein. When desired, tissue-specific expression or knockout of the breast cancer protein may be necessary.

It is also possible that the breast cancer protein is overexpressed in breast cancer. As such, transgenic animals can be generated that overexpress the breast cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of breast cancer and are additionally useful in screening for modulators to treat breast cancer.

15

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, breast cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative breast cancer polypeptides or polynucleotides, small molecules inhibitors of breast cancer-associated sequences *etc.* A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the

like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of breast cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a breast cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing breast cancer-associated activity. Optionally, the kit contains biologically active breast cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

Purifying total RNA from tissue sample using TRIzol Reagent

The sample weight is first estimated. The tissue samples are homogenized in 1 ml of TRIzol per 50 mg of tissue using a homogenizer (e.g., Polytron 3100). The size of the generator/probe used depends upon the sample amount. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. A larger generator (e.g., 20 mm) is suitable for tissue samples weighing more than 0.6 g. Fill tubes should not be overfilled. If the working volume is greater than 2 ml and no greater than 10 ml, a 15 ml polypropylene tube (Falcon 2059) is suitable for homogenization.

Tissues should be kept frozen until homogenized. The TRIzol is added directly to the frozen tissue before homogenization. Following homogenization, the insoluble material is removed from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The cleared

homogenate is then transferred to a new tube(s). Samples may be frozen and stored at -60 to -70°C for at least one month or else continue with the purification.

The next process is phase separation. The homogenized samples are incubated for 5 minutes at room temperature. Then, 0.2 ml of chloroform per 1ml of TRIzol reagent is added to the homogenization mixture. The tubes are securely capped and shaken vigorously by hand (do not vortex) for 15 seconds. The samples are then incubated at room temp. for 2-3 minutes and next centrifuged at 6500 rpm in a Sorvall superspeed for 30 min. at 4°C.

The next process is RNA Precipitation. The aqueous phase is transferred to a fresh tube. The organic phase can be saved if isolation of DNA or protein is desired. Then 0.5 ml of isopropyl alcohol is added per 1ml of TRIzol reagent used in the original homogenization. Then, the tubes are securely capped and inverted to mix. The samples are then incubated at room temp. for 10 minutes and centrifuged at 6500 rpm in Sorvall for 20 min. at 4°C.

The RNA is then washed. The supernatant is poured off and the pellet washed with cold 75% ethanol. 1 ml of 75% ethanol is used per 1 ml of the TRIzol reagent used in the initial homogenization. The tubes are capped securely and inverted several times to loosen pellet without vortexing. They are next centrifuged at <8000 rpm (<7500 x g) for 5 minutes at 4°C.

The RNA wash is decanted. The pellet is carefully transferred to an Eppendorf tube (sliding down the tube into the new tube by use of a pipet tip to help guide it in if necessary). Tube(s) sizes for precipitating the RNA depending on the working volumes. Larger tubes may take too long to dry. Dry pellet. The RNA is then resuspended in an appropriate volume (e.g., 2 -5 ug/ul) of DEPC H₂O. The absorbance is then measured.

The poly A⁺ mRNA may next be purified from total RNA by other methods such as Qiagen's RNeasy kit. The poly A⁺ mRNA is purified from total RNA by adding the oligotex suspension which has been heated to 37°C and mixing prior to adding to RNA. The Elution Buffer is incubated at 70°C. If there is precipitate in the buffer, warm up the 2 x Binding Buffer at 65°C. The the total RNA is mixed with DEPC-treated water, 2 x Binding

Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook and next incubated for 3 minutes at 65°C and 10 minutes at room temperature.

The preparation is centrifuged for 2 minutes at 14,000 to 18,000 g, preferably, at a "soft setting," The supernatant is removed without disturbing Oligotex pellet. A little bit
5 of solution can be left behind to reduce the loss of Oligotex. The supernatant is saved until satisfactory binding and elution of poly A⁺ mRNA has been found.

Then, the preparation is gently resuspended in Wash Buffer OW2 and pipetted onto the spin column and centrifuged at full speed (soft setting if possible) for 1 minute.

Next, the spin column is transferred to a new collection tube and gently
10 resuspended in Wash Buffer OW2 and centrifuged as described herein.

Then, the spin column is transferred to a new tube and eluted with 20 to 100 ul of preheated (70°C) Elution Buffer. The Oligotex resin is gently resuspended by pipetting up and down. The centrifugation is repeated as above and the elution repeated with fresh elution buffer or first eluate to keep the elution volume low.

15 The absorbance is next read to determine the yield, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA is precipitated before proceeding with cDNA synthesis, as components leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.
20 0.4 vol. of 7.5 M NH₄OAc + 2.5 vol. of cold 100% ethanol is added and the preparation precipitated at -20°C 1 hour to overnight (or 20-30 min. at -70°C), and centrifuged at 14,000-16,000 x g for 30 minutes at 4°C. Next, the pellet is washed with 0.5 ml of 80% ethanol (-20°C) and then centrifuged at 14,000-16,000 x g for 5 minutes at room temperature. The 80% ethanol wash is then repeated. The last bit of ethanol from the pellet is then dried
25 without use of a speed vacuum and the pellet is then resuspended in DEPC H₂O at 1ug/ul concentration.

Alternatively the RNA may be purified using other methods (e.g., Qiagen's RNeasy kit).

No more than 100 ug is added to the RNeasy column. The sample volume is adjusted to 100 ul with RNase-free water. 350 ul Buffer RLT and then 250 ul ethanol (100%) are added to the sample. The preparation is then mixed by pipetting and applied to an RNeasy mini spin column for centrifugation (15 sec at >10,000 rpm). If yield is low, reapply the flowthrough to the column and centrifuge again.

Then, transfer column to a new 2 ml collection tube and add 500 ul Buffer RPE and centrifuge for 15 sec at >10,000 rpm. The flowthrough is discarded. 500 ul Buffer RPE and is then added and the preparation is centrifuged for 15 sec at >10,000 rpm. The flowthrough is discarded. and the column membrane dried by centrifuging for 2 min at maximum speed. The column is transferred to a new 1.5-ml collection tube. 30-50 ul of RNase-free water is applied directly onto column membrane. The column is then centrifuged for 1 min at >10,000 rpm and the elution step repeated.

The absorbance is then read to determine yield. If necessary, the material may be ethanol precipitated with ammonium acetate and 2.5X volume 100% ethanol.

First Strand cDNA Synthesis

The first strand can be make using using Gibco's "SuperScript Choice System for cDNA Synthesis" kit. The starting material is 5 ug of total RNA or 1 ug of polyA+ mRNA. For total RNA, 2 ul of SuperScript RT is used; for polyA+ mRNA, 1 ul of SuperScript RT is used. The final volume of first strand synthesis mix is 20 ul. The RNA should be in a volume no greater than 10 ul. The RNA is incubated with 1 ul of 100 pmol T7-T24 oligo for 10 min at 70°C followed by addition on ice of 7 ul of: 4ul 5X 1st Strand Buffer, 2 ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. The preparation is then incubated at 37°C for 2 min before addition of the SuperScript RT followed by incubation at 37°C for 1 hour.

Second Strand Synthesis

For the second strand synthesis, place 1st strand reactions on ice and add: 91 ul DEPC H₂O; 30 ul 5X 2nd Strand Buffer; 3 ul 10mM dNTP mix; 1 ul 10 U/ul E.coli DNA Ligase; 4 ul 10 U/ul E.coli DNA Polymerase; and 1 ul 2 U/ul RNase H. Mix and incubate 2

hours at 16°C. Add 2 ul T4 DNA Polymerase. Incubate 5 min at 16°C. Add 10 ul of 0.5M EDTA.

Cleaning up cDNA

5 The cDNA is purified using Phenol:Chloroform:Isoamyl Alcohol (25:24:1) and Phase-Lock gel tubes. The PLG tubes are centrifuged for 30 sec at maximum speed. The cDNA mix is then transferred to PLG tube. An equal volume of phenol:chloroform:isamyl alcohol is then added, the preparation shaken vigorously (no vortexing), and centrifuged for 5 minutes at maximum speed. The top aqueous solution is
10 transferred to a new tube and ethanol precipitated by adding 7.5X 5M NH₄OAc and 2.5X volume of 100% ethanol. Next, it is centrifuged immediately at room temperature for 20 min, maximum speed. The supernatant is removed, and the pellet washed with 2X with cold 80% ethanol. As much ethanol wash as possible should be removed before air drying the pellet; and resuspending it in 3 ul RNase-free water.

15

In vitro Transcription (IVT) and labeling with biotin

In vitro Transcription (IVT) and labeling with biotin is performed as follows: Pipet 1.5 ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2 ul T7 10xATP (75 mM) (Ambion); 2 ul T7 10xGTP (75 mM) (Ambion); 1.5 ul T7 10xCTP (75
20 mM) (Ambion); 1.5 ul T7 10xUTP (75 mM) (Ambion); 3.75 ul 10 mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75 ul 10 mM Bio-16-CTP (Enzo); 2 ul 10x T7 transcription buffer (Ambion); and 2 ul 10x T7 enzyme mix (Ambion). The final volume is 20 ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be furthered cleaned. Clean-up follows the previous instructions for RNeasy columns or Qiagen's RNeasy protocol
25 handbook. The cRNA often needs to be ethanol precipitated by resuspension in a volume compatible with the fragmentation step.

Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in
30 the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment

RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea
 5 of the transcript size range

For hybridization, 200 ul (10 ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made. The hybridization mix is: fragment labeled RNA (50 ng/ul final conc.); 50 pM 948-b control
 10 oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1 mg/ml herring sperm DNA; 0.5 mg/ml acetylated BSA; and 300 ul with 1xMES hyb buffer.

The hybridization reaction is conducted with non-biotinylated IVT (purified by RNeasy columns) (see example 1 for steps from tissue to IVT): The following mixture is prepared:

| | | |
|----|----------------------------|-------------------|
| 15 | IVT antisense RNA; 4 µg: | µl |
| | Random Hexamers (1 µg/µl): | 4 µl |
| | H ₂ O: | <u> µl </u> |
| | | 14 µl |

Incubate the above 14 µl mixture at 70°C for 10 min.; then put on ice.

20 The Reverse transcription procedure uses the following mixture:

| | | |
|----|------------------------|-------------------|
| | 0.1 M DTT: | 3 µl |
| | 50X dNTP mix: | 0.6 µl |
| | H ₂ O: | 2.4 µl |
| | Cy3 or Cy5 dUTP (1mM): | 3 µl |
| 25 | SS RT II (BRL): | 1 µl |
| | | <u> </u> |
| | | 16 µl |

The above solution is added to the hybridization reaction and incubated for 30 min., 42°C. Then, 1 µl SSII is added and incubated for another hour before being placed on ice.

The 50X dNTP mix contains 25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP and is made by adding 25 μ l each of 100mM dATP, dCTP, and dGTP; 10 μ l of 100mM dTTP to 15 μ l H₂O.]

RNA degradation is performed as follows. Add 86 μ l H₂O, 1.5 μ l 1M NaOH/
5 2 mM EDTA and incubate at 65°C, 10 min.. For U-Con 30, 500 μ l TE/sample spin at 7000 g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500 μ l buffer PB and proceed using Qiagen protocol. For DNase digestion, add 1 μ l of 1/100 dilution of DNase/30 μ l Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNase.

10

Sample preparation

For sample preparation, add Cot-1 DNA, 10 μ l; 50X dNTPs, 1 μ l; 20X SSC, 2.3 μ l; Na pyrophosphate, 7.5 μ l; 10 mg/ml Herring sperm DNA; 1 μ l of 1/10 dilution to 21.8 final vol. Dry
15 in speed vac. Resuspend in 15 μ l H₂O. Add 0.38 μ l 10% SDS. Heat 95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 ml 20X SSC+0.75ml 10% SDS in 250ml H₂O; 1X SSC: 5 min., 12.5 ml 20X SSC in 250ml H₂O; 0.2X SSC: 5 min., 2.5 ml 20X SSC in 250ml H₂O. Dry slides and scan at appropriate PMT's and channels.

TABLE 1: Figure 1 from BRCA 001 US

5 **Table 1** shows genes, (incorporated in their entirety here and throughout the application where primekeys are provided), downregulated in tumor tissue compared to normal breast tissue.

10

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 15 R1: Ratio of normal breast tissue to tumor

| | Pkey | ExAccn | UnigeneID | UnigeneTitle | R1 |
|----|--------|-----------|-----------|--|----|
| 20 | 100472 | D90084 | Hs.1023 | pyruvate dehydrogenase (lipoamide) alpha | 5 |
| | 100499 | T51986 | Hs.283108 | hemoglobin, gamma G | 10 |
| | 100545 | M55405 | | gb:Homo sapiens mucin (MUC-3) mRNA, part | 5 |
| | 100549 | BE142019 | Hs.222056 | Homo sapiens cDNA FLJ11572 fis, clone HE | 10 |
| | 100613 | X52078 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 5 |
| 25 | 100635 | BE259039 | Hs.129953 | Ewing sarcoma breakpoint region 1 | 5 |
| | 100645 | X16841 | Hs.167988 | neural cell adhesion molecule 1 | 5 |
| | 100654 | A03758 | | NM_000477*:Homo sapiens albumin (ALB), m | 10 |
| | 100702 | L27065 | | gb:Human neurofibromatosis 2 (NF2) mRNA, | 5 |
| | 100915 | M60832 | Hs.249239 | collagen, type VIII, alpha 2 | 5 |
| 30 | 100971 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 10 |
| | 101125 | AJ250562 | Hs.82749 | transmembrane 4 superfamily member 2 | 5 |
| | 101166 | M90424 | Hs.2099 | lipocalin 1 (protein migrating faster th | 5 |
| | 101184 | NM_001674 | Hs.460 | activating transcription factor 3 | 10 |
| | 101336 | NM_006732 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 10 |
| 35 | 101367 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 10 |
| | 101447 | M21305 | | gb:Human alpha satellite and satellite 3 | 10 |
| | 101461 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 10 |
| | 101511 | M27826 | Hs.267319 | endogenous retroviral protease | 10 |
| | 101634 | AV650262 | Hs.75765 | GRO2 oncogene | 5 |
| 40 | 101736 | M74447 | Hs.502 | transporter 2, ATP-binding cassette, sub | 10 |
| | 102208 | U22961 | | gb:Human mRNA clone with similarity to L | 10 |
| | 102297 | NM_001504 | Hs.198252 | G protein-coupled receptor 9 | 5 |
| | 102450 | U48251 | Hs.75871 | protein kinase C binding protein 1 | 10 |
| | 102515 | U89337 | Hs.169886 | tenascin XB | 10 |
| 45 | 102571 | U60115 | Hs.239069 | four and a half LIM domains 1 | 5 |
| | 102800 | AA313538 | | gb:EST185419 Colon carcinoma (HCC) oell | 10 |
| | 102857 | NM_006744 | Hs.76461 | retinol-binding protein 4, interstitial | 10 |
| | 102990 | AA829286 | Hs.332053 | serum amyloid A1 | 10 |
| | 103434 | X98085 | Hs.54433 | tenascin R (restriclin, janusin) | 5 |
| 50 | 103747 | AA081995 | | gb:zn26d06.r1 Stratagene neuroepithelium | 10 |
| | 103750 | AA126129 | | gb:zn78c07.r1 Stratagene neuroepithelium | 5 |
| | 103812 | AA137107 | Hs.326391 | Homo sapiens, clone MGC:16638, mRNA, com | 10 |
| | 103851 | AA326216 | Hs.8719 | hypothetical protein MGC1136 | 5 |
| | 104080 | AB041036 | Hs.57771 | kallikrein 11 (KLK11; TLSP; PRSS20; hipp | 5 |
| 55 | 104093 | R50727 | Hs.336970 | ESTs | 10 |
| | 104106 | AA422123 | | gb:zv26h12.r1 Soares_NhHMPu_S1 Homo sapi | 5 |
| | 104109 | AL353957 | Hs.284181 | hypothetical protein DKFZp434P0531 | 10 |
| | 104250 | F06638 | Hs.12440 | Homo sapiens clone 24734 mRNA sequence | 10 |
| | 104340 | AA426189 | | gb:zw11e09.r1 Soares_NhHMPu_S1 Homo sapi | 5 |
| 60 | 104492 | N73185 | Hs.94285 | EST | 10 |
| | 104506 | N91071 | Hs.109650 | ESTs | 10 |
| | 104511 | N99542 | Hs.572 | orosomucoid 1 | 5 |
| | 104532 | AA98763 | Hs.203013 | hypothetical protein FLJ12748 | 10 |

| | | | | | |
|----|--------|-----------|-----------|--|----|
| | 104536 | R24024 | Hs.158101 | Homo sapiens cDNA FLJ14673 fis, clone NT | 5 |
| | 104572 | Y11312 | Hs.132463 | phosphoinositide-3-kinase, class 2, beta | 5 |
| | 104659 | AW969769 | Hs.105201 | ESTs | 5 |
| 5 | 104677 | AA009764 | Hs.190380 | ESTs | 10 |
| | 104711 | AA017245 | Hs.32794 | ESTs | 10 |
| | 104731 | AA019300 | Hs.125070 | ESTs, Moderately similar to I54374 gene | 10 |
| | 104764 | AI039243 | Hs.278585 | ESTs | 5 |
| | 105005 | AI298208 | Hs.28805 | ESTs | 10 |
| 10 | 105036 | AA130390 | Hs.25549 | hypothetical protein FLJ20898 | 10 |
| | 105105 | R61532 | Hs.87016 | hypothetical protein FLJ22938 | 5 |
| | 105231 | AW970043 | Hs.238039 | hypothetical protein FLJ11090 | 5 |
| | 105239 | AA221036 | | gb:zr03f12.r1 Stratagene NT2 neuronal pr | 10 |
| | 105921 | AA421973 | Hs.169119 | ESTs, Weakly similar to T25731 hypotheti | 5 |
| | 105957 | BE242857 | Hs.27021 | hypothetical protein FLJ11159 | 5 |
| 15 | 106052 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 10 |
| | 106119 | AL359624 | Hs.11387 | KIAA1453 protein | 5 |
| | 106181 | AI803651 | Hs.191608 | ESTs | 10 |
| | 106194 | AW976171 | Hs.286194 | hypothetical protein FLJ22233 | 5 |
| | 106283 | AI085846 | Hs.25522 | KIAA1808 protein | 10 |
| 20 | 106379 | AL042069 | Hs.119021 | DKFZP434N061 protein | 10 |
| | 106451 | AW235928 | Hs.313182 | ESTs | 10 |
| | 106491 | AA135688 | Hs.10083 | Homo sapiens, clone IMAGE:4139786, mRNA, | 10 |
| | 106700 | AA906434 | Hs.3776 | zinc finger protein 216 | 5 |
| 25 | 106782 | AW054886 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 10 |
| | 106851 | AI458623 | | gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens | 5 |
| | 106870 | AI983730 | Hs.26530 | serum deprivation response (phosphatidyl | 5 |
| | 106892 | AI347578 | Hs.124015 | hypothetical protein MGC2605 | 5 |
| | 106954 | AF128847 | Hs.204038 | indolethylamine N-methyltransferase | 5 |
| 30 | 106991 | AJ223811 | Hs.30127 | hypothetical protein | 5 |
| | 107103 | AI446183 | Hs.9572 | ESTs, Highly similar to CYA5_HUMAN ADENY | 5 |
| | 107124 | AB006532 | Hs.31442 | RecQ protein-like 4 | 10 |
| | 107148 | AI005036 | Hs.334305 | GS1999full | 10 |
| | 107214 | AF127026 | Hs.5394 | myosin IA | 10 |
| 35 | 107242 | AB020672 | Hs.175411 | KIAA0865 protein | 10 |
| | 107331 | AI905985 | Hs.111805 | ESTs | 10 |
| | 107351 | U51704 | Hs.323428 | ESTs, Moderately similar to ALU8_HUMAN A | 5 |
| | 107423 | W26652 | Hs.6163 | PTEN induced putative kinase 1 | 5 |
| | 107447 | W28516 | Hs.19210 | hypothetical protein MGC11308 | 10 |
| 40 | 107451 | AL042425 | Hs.283976 | hypothetical protein PRO2389 | 10 |
| | 107453 | AI092790 | Hs.334703 | hypothetical protein FLJ14529 | 5 |
| | 107459 | W38002 | | Empirically selected from AFFX single pr | 10 |
| | 107683 | N53167 | Hs.47623 | ESTs | 10 |
| | 107711 | W96141 | Hs.220687 | ESTs | 10 |
| 45 | 107754 | AA017462 | Hs.269244 | ESTs | 10 |
| | 107757 | BE621721 | Hs.280792 | hypothetical protein FLJ12387 similar to | 10 |
| | 107864 | AA025060 | Hs.61246 | ESTs | 10 |
| | 107872 | BE271708 | Hs.95110 | ESTs, Weakly similar to A55943 1-phospha | 10 |
| | 107888 | AA025836 | Hs.191637 | ESTs | 5 |
| 50 | 107997 | AL049176 | Hs.82223 | chordin-like | 10 |
| | 108056 | AA043675 | Hs.62633 | ESTs | 10 |
| | 108081 | AA093668 | Hs.28578 | muscleblind (Drosophila)-like | 5 |
| | 108113 | AA012881 | Hs.72531 | hypothetical protein FLJ11838 | 10 |
| | 108238 | AA059473 | Hs.66783 | EST | 10 |
| 55 | 108257 | AA677927 | Hs.144269 | ESTs | 5 |
| | 108335 | AA070500 | | gb:zm70h03.s1 Stratagene neuroepithelium | 5 |
| | 108351 | AA071193 | | gb:zf79b12.s1 Soares_pineal_gland_N3HPG | 10 |
| | 108382 | NM_006770 | Hs.67726 | macrophage receptor with collagenous str | 5 |
| | 108392 | AA075124 | | gb:zm86a01.s1 Stratagene ovarian cancer | 10 |
| 60 | 108441 | AA079079 | | gb:zm97c09.s1 Stratagene colon HT29 (937 | 10 |
| | 108446 | AA085383 | | gb:zn13g03.s1 Stratagene hNT neuron (937 | 10 |
| | 108497 | AA074897 | | gb:zm85a05.r1 Stratagene ovarian cancer | 10 |
| | 108604 | AA934589 | Hs.49696 | ESTs | 5 |
| | 108662 | AF117646 | Hs.156637 | Cas-Br-M (murine) ectropic retroviral tr | 5 |
| 65 | 108706 | AA121820 | Hs.74569 | KIAA0842 protein | 10 |
| | 108738 | AA126583 | Hs.158725 | ESTs | 10 |
| | 108827 | AI273692 | Hs.110470 | ESTs | 10 |
| | 109123 | AI028376 | Hs.73232 | ESTs | 10 |

| | | | | | |
|----|--------|-----------|-----------|--|----|
| | 109389 | AA101325 | Hs.86154 | hypothetical protein FLJ12457 | 10 |
| | 109546 | F01449 | Hs.26954 | Homo sapiens mRNA; cDNA DKFZp762G123 (fr | 5 |
| | 109919 | R40604 | Hs.129539 | ESTs, Weakly similar to MCAT_HUMAN MITOC | 10 |
| | 110006 | A1094674 | Hs.30524 | ring finger protein 24 | 10 |
| 5 | 110141 | H46749 | Hs.31540 | ESTs | 10 |
| | 110354 | W22165 | Hs.22586 | ESTs | 5 |
| | 110433 | AW294162 | Hs.301062 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 10 |
| | 110448 | H51276 | Hs.13526 | hypothetical protein FLJ12688 | 10 |
| | 110455 | H52576 | | gb:y185e08.r1 Soares_pineal_gland_N3HPG | 5 |
| 10 | 110540 | H72639 | Hs.167608 | ESTs | 5 |
| | 110553 | H60593 | Hs.124990 | ESTs | 10 |
| | 110976 | AL044174 | Hs.159526 | patched (Drosophila) homolog | 10 |
| | 110987 | A1753316 | Hs.26034 | ESTs | 5 |
| | 111158 | N66616 | Hs.138629 | H.sapiens mRNA for subtelomeric repeat s | 5 |
| 15 | 111168 | A1798376 | | gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens | 10 |
| | 111187 | AJ224864 | Hs.9688 | leukocyte membrane antigen | 5 |
| | 111307 | AA641636 | Hs.37477 | ESTs, Weakly similar to T46908 hypothe | 5 |
| | 111400 | R00144 | Hs.189771 | ESTs | 10 |
| | 111498 | A1168511 | | gb:ow90h09.s1 Soares_fetal_liver_spleen_ | 10 |
| 20 | 111651 | R16733 | Hs.20499 | ESTs | 10 |
| | 111738 | R26065 | | gb:yh39d03.s1 Soares placenta Nb2HP Homo | 5 |
| | 111803 | AA593731 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 10 |
| | 111995 | R42333 | Hs.302292 | ESTs | 10 |
| | 112071 | AL117490 | Hs.47225 | Ras-associated protein Rap1 | 10 |
| 25 | 112204 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 10 |
| | 112258 | R51889 | Hs.24990 | ESTs | 5 |
| | 112490 | R31094 | Hs.24378 | ESTs | 10 |
| | 112588 | R77302 | | gb:y175h08.s1 Soares placenta Nb2HP Homo | 10 |
| | 112654 | BE618629 | Hs.268809 | ESTs | 5 |
| 30 | 112784 | T98628 | Hs.191290 | ESTs | 5 |
| | 112817 | A1057205 | Hs.14584 | ESTs | 5 |
| | 112885 | AA581428 | Hs.5021 | EST | 10 |
| | 112913 | T16837 | Hs.4241 | ESTs | 5 |
| | 113149 | T51588 | | gb:yb27e06.s1 Stratagene fetal spleen (9 | 10 |
| 35 | 113174 | T54659 | Hs.301755 | Homo sapiens cDNA FLJ11465 fis, clone HE | 5 |
| | 113203 | AA743563 | Hs.10305 | ESTs | 5 |
| | 113299 | AW207424 | Hs.332594 | ESTs | 10 |
| | 113367 | N92359 | Hs.14518 | ESTs, Moderately similar to A48752 B-cel | 10 |
| | 113457 | R16763 | Hs.268679 | ESTs | 5 |
| 40 | 113563 | AA913635 | Hs.326413 | Homo sapiens cDNA FLJ20812 fis, clone AD | 10 |
| | 113574 | R06874 | Hs.268628 | ESTs, Moderately similar to ALU1_HUMAN A | 5 |
| | 113776 | A1791905 | Hs.95549 | hypothetical protein | 10 |
| | 113790 | A1244311 | Hs.26912 | ESTs | 10 |
| | 113807 | W07586 | Hs.8045 | ESTs | 3 |
| 45 | 113958 | W86195 | | gb:zh54e05.s1 Soares_fetal_liver_spleen_ | 10 |
| | 114211 | Z39319 | Hs.27347 | EST | 10 |
| | 114254 | AB018263 | Hs.180338 | tumor necrosis factor receptor superfam | 5 |
| | 114349 | AA745978 | Hs.28273 | ESTs | 5 |
| | 114449 | AA020736 | | gb:ze63b11.s1 Soares retina N2b4HR Homo | 5 |
| 50 | 114484 | AA034378 | Hs.267319 | endogenous retroviral protease | 5 |
| | 114576 | AA065096 | | gb:zm60a02.s1 Stratagene fibroblast (937 | 5 |
| | 114624 | AA081507 | | gb:zn05b10.r1 Stratagene hNT neuron (937 | 5 |
| | 114844 | AA234826 | Hs.87386 | EST | 5 |
| | 114906 | AA234462 | Hs.87350 | ESTs | 5 |
| 55 | 115624 | AK000725 | Hs.50579 | hypothetical protein FLJ20718 | 3 |
| | 115666 | AF173081 | Hs.178215 | Vertebrate LIN7 homolog 1, Tax interact | 5 |
| | 115712 | AB020649 | Hs.74569 | KIAA0842 protein | 5 |
| | 115889 | AA398841 | Hs.39850 | hypothetical protein FLJ20517 | 10 |
| | 115949 | A1478427 | Hs.43125 | esophageal cancer related gene 4 protein | 10 |
| 60 | 116107 | AL133916 | Hs.172572 | hypothetical protein FLJ20093 | 10 |
| | 116180 | AA463902 | Hs.13522 | ESTs, Weakly similar to I38022 hypothe | 5 |
| | 116267 | AW968703 | Hs.30085 | hypothetical protein FLJ23186 | 5 |
| | 116291 | AW410377 | Hs.41502 | hypothetical protein FLJ21276 | 5 |
| | 116527 | AW194253 | Hs.68607 | ESTs | 10 |
| 65 | 116659 | BE314852 | Hs.168694 | Homo sapiens clone 23763 unknown mRNA, p | 5 |
| | 116708 | F10528 | Hs.70001 | ESTs, Moderately similar to JC6169 nucle | 5 |
| | 117058 | AW801806 | | gb:IL5-UM0070-110400-062-g07 UM0070 Homo | 5 |

| | | | | | |
|----|--------|-----------|-----------|--|----|
| | 117151 | AI803656 | Hs.42373 | ESTs | 5 |
| | 117226 | N20468 | | gb:yx39b10.s1 Soares melanocyte 2NbHM Ho | 10 |
| | 117323 | AI472863 | Hs.43387 | ESTs | 5 |
| | 117571 | N34417 | Hs.44584 | ESTs | 3 |
| 5 | 117624 | N26627 | Hs.82364 | ESTs, Weakly similar to JC4124 pregnancy | 5 |
| | 117673 | N40551 | Hs.184043 | Homo sapiens Ets-1 binding protein (E1B) | 10 |
| | 117847 | N49285 | Hs.182391 | ESTs | 10 |
| | 117877 | AW263476 | Hs.44268 | myelin gene expression factor 2 | 10 |
| | 117919 | BE222341 | Hs.279472 | ESTs | 5 |
| 10 | 118049 | N53145 | | gb:yv55f09.s1 Soares fetal liver spleen | 3 |
| | 118413 | AW955696 | Hs.90960 | ESTs | 10 |
| | 118613 | AI078236 | Hs.49688 | ESTs | 5 |
| | 118664 | N70907 | Hs.230619 | EST | 10 |
| | 118858 | AL122040 | Hs.102981 | Homo sapiens mRNA; cDNA DKFZp434G1972 (f | 3 |
| 15 | 118902 | AA993527 | Hs.293907 | hypothetical protein FLJ23403 | 5 |
| | 119039 | AI160570 | Hs.252097 | pregnancy specific beta-1-glycoprotein 6 | 3 |
| | 119159 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 5 |
| | 119216 | AA514422 | Hs.221849 | ESTs | 5 |
| | 119317 | AK002001 | Hs.51305 | v-maf musculoaponeurotic fibrosarcoma (a | 10 |
| 20 | 119366 | T77892 | | gb:yd20f04.s1 Soares fetal liver spleen | 5 |
| | 119378 | T81824 | Hs.90949 | EST | 5 |
| | 119528 | W38051 | | Empirically selected from AFFX single pr | 10 |
| | 119792 | AL049798 | Hs.80552 | dermatopontin | 3 |
| | 119800 | AF086332 | Hs.58314 | ESTs | 10 |
| 25 | 119817 | AF088061 | Hs.159690 | ESTs | 5 |
| | 119835 | AF086429 | Hs.58429 | ESTs | 5 |
| | 119923 | AW803308 | Hs.62954 | fem1in, heavy polypeptide 1 | 5 |
| | 119961 | U34249 | Hs.337461 | Human putative zinc finger protein (ZNFB | 5 |
| | 120379 | AL042725 | | gb:DKFZp434B1822_r1 434 (synonym: htes3) | 10 |
| 30 | 120931 | AW136934 | Hs.97162 | ESTs | 5 |
| | 121037 | AA907743 | Hs.142373 | ESTs | 5 |
| | 121282 | AA401695 | Hs.97334 | ESTs | 5 |
| | 121382 | AA405763 | Hs.111939 | Homo sapiens cDNA FLJ20470 fls, clone KA | 5 |
| | 121764 | AA421452 | Hs.164851 | ESTs, Weakly similar to KIAA0926 protein | 5 |
| 35 | 122034 | AK000229 | Hs.98017 | Homo sapiens cDNA FLJ20222 fls, clone CO | 10 |
| | 122441 | AA447555 | Hs.99116 | EST | 10 |
| | 122756 | AA458945 | Hs.95898 | ESTs | 10 |
| | 122771 | AW135093 | Hs.97282 | ESTs, Highly similar to G100_HUMAN 110 K | 5 |
| | 123601 | AA609122 | Hs.112645 | Homo sapiens mRNA; cDNA DKFZp434D2472 (f | 5 |
| 40 | 123623 | AI024595 | Hs.97508 | a disintegrin and metalloproteinase doma | 5 |
| | 123941 | AA621529 | | gb:af47a02.s1 Soares_totat_fetus_Nb2HF8_ | 10 |
| | 124215 | H62570 | | gb:yr44a01.r1 Soares fetal liver spleen | 5 |
| | 124276 | H83465 | | gb:ys91a11.s1 Soares retina N2b5HR Homo | 5 |
| | 124680 | AK001527 | Hs.163953 | hypothetical protein FLJ10665 | 5 |
| 45 | 125099 | NM_014312 | Hs.112377 | cortic al thymocyte receptor (X. laevis | 10 |
| | 125121 | T98199 | Hs.48403 | hypothetical protein FLJ10847 | 10 |
| | 125188 | BE299567 | Hs.271749 | ESTs, Moderately similar to ALU8_HUMAN A | 5 |
| | 125284 | NM_002666 | Hs.103253 | perilipin | 10 |
| | 125906 | BE256206 | Hs.17775 | p75NTR-associated cell death executor; o | 5 |
| 50 | 128484 | AA485421 | Hs.270503 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 10 |
| | 128511 | NM_002250 | Hs.10082 | potassium intermediate/small conductance | 10 |
| | 128538 | R44214 | Hs.101189 | ESTs | 5 |
| | 128606 | C16161 | Hs.283040 | hypothetical protein PRO2543 | 5 |
| | 128850 | AA193106 | Hs.180817 | chromosome 11 open reading frame 23 | 10 |
| 55 | 128870 | H39537 | Hs.75309 | eukaryotic translation elongation factor | 10 |
| | 128903 | AW150717 | Hs.296176 | STAT induced STAT inhibitor 3 | 10 |
| | 128931 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fls, clone NT | 10 |
| | 129001 | AA443323 | Hs.107812 | BPOZ protein | 5 |
| | 129091 | AA056483 | Hs.301463 | Human Chromosome 16 BAC clone CIT987SK-A | 5 |
| 60 | 129101 | NM_013403 | Hs.108665 | zinedin | 10 |
| | 129146 | AL117472 | Hs.108924 | SH3-domain protein 5 (ponsin) | 5 |
| | 129213 | AI146494 | Hs.109525 | ESTs, Weakly similar to IRX2_HUMAN IROQU | 3 |
| | 129228 | U40714 | Hs.239307 | tyrosyl-tRNA synthetase | 5 |
| | 129265 | AA530892 | Hs.171695 | dual specificity phosphatase 1 | 5 |
| 65 | 129285 | BE17015 | Hs.11006 | ESTs, Moderately similar to T17372 plasm | 10 |
| | 129346 | AF110141 | Hs.288908 | WAS protein family, member 2 | 10 |
| | 129368 | NM_003877 | Hs.110776 | STAT induced STAT inhibitor-2 | 5 |

| | | | | | |
|----|--------|-----------|--|--|----|
| | 129371 | X06828 | Hs.110802 | von Willebrand factor | 5 |
| | 129381 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 10 |
| | 129440 | W37944 | Hs.4007 | Sarcolemmal-associated protein | 5 |
| 5 | 129441 | BE061069 | Hs.301943 | KIAA0467 protein | 10 |
| | 129516 | AF020038 | Hs.11223 | isocitrate dehydrogenase 1 (NADP+), solu | 10 |
| | 129554 | BE222078 | Hs.113069 | ESTs | 10 |
| | 129684 | BE622468 | Hs.11924 | ESTs, Weakly similar to I38022 hypotheti | 5 |
| | 129702 | AI304966 | Hs.12035 | ESTs, Weakly similar to I38022 hypotheti | 5 |
| 10 | 129778 | AK001676 | Hs.12457 | hypothetical protein FLJ10814 | 10 |
| | 129893 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 5 |
| | 129928 | AI338993 | Hs.134535 | ESTs | 5 |
| | 129973 | AJ251760 | Hs.273385 | guanine nucleotide binding protein (G pr | 5 |
| | 129977 | NM_000399 | Hs.1395 | early growth response 2 (Krox-20 (Drosop | 5 |
| 15 | 130014 | NM_001158 | Hs.143102 | amine oxidase, copper containing 2 (reti | 5 |
| | 130085 | M62402 | Hs.274313 | Insulin-like growth factor binding prote | 10 |
| | 130089 | AA452006 | Hs.333199 | ESTs | 5 |
| | 130162 | W80711 | Hs.319946 | Homo sapiens mRNA for KIAA1727 protein, | 5 |
| | 130243 | D88435 | Hs.153227 | cyclin G associated kinase | 10 |
| 20 | 130315 | AI241084 | Hs.154353 | nonselective sodium potassium/proton exc | 5 |
| | 130339 | AA435746 | gb:zt79e03.s1 Soares_testis_NHT Homo sap | 5 | |
| | 130400 | V00517 | Hs.283108 | hemoglobin, gamma G | 10 |
| | 130436 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 10 |
| | 130478 | X72308 | Hs.251526 | small inducible cytokine A7 (monocyte ch | 5 |
| 25 | 130480 | BE222978 | Hs.15760 | MYG1 protein | 10 |
| | 130494 | AW390834 | Hs.75874 | pregnancy-associated plasma protein A | 5 |
| | 130563 | BE270472 | Hs.279900 | HSPC015 protein | 10 |
| | 130589 | AL110226 | Hs.16441 | DKFZP434H204 protein | 10 |
| | 130606 | AI652143 | Hs.288382 | hypothetical protein FLJ13111 | 5 |
| 30 | 130634 | AI769067 | Hs.127824 | ESTs, Weakly similar to T28770 hypotheti | 3 |
| | 130683 | AA993269 | Hs.17872 | Homo sapiens, clone IMAGE:3875012, mRNA | 10 |
| | 130689 | NM_006691 | Hs.17917 | extracellular link domain-containing 1 | 10 |
| | 130716 | AA232075 | Hs.18259 | XPA binding protein 1; putative ATP(GTP) | 5 |
| | 130718 | AF263462 | Hs.18376 | KIAA1319 protein | 10 |
| 35 | 130722 | N41322 | Hs.18441 | ESTs | 5 |
| | 130798 | M81349 | Hs.1955 | serum amyloid A4, constitutive | 10 |
| | 130840 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 10 |
| | 131184 | AB040935 | Hs.23954 | cerebral cell adhesion molecule | 10 |
| | 131261 | AA360419 | Hs.171776 | inositol(myo)-1(or 4)-monophosphatase 1 | 10 |
| 40 | 131282 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 10 |
| | 131328 | AW939251 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 10 |
| | 131340 | AK000393 | Hs.25817 | BTB (POZ) domain containing 2 | 5 |
| | 131341 | AF110908 | Hs.297660 | TNF receptor-associated factor 3 | 5 |
| | 131406 | H83294 | Hs.284122 | Wnt inhibitory factor-1 | 5 |
| 45 | 131489 | BE394648 | Hs.27414 | hypothetical protein | 5 |
| | 131543 | AW966881 | Hs.41639 | programmed cell death 2 | 10 |
| | 131692 | BE559681 | Hs.30736 | KIAA0124 protein | 5 |
| | 131753 | AA829286 | Hs.332053 | serum amyloid A1 | 10 |
| | 131756 | AA443966 | Hs.31595 | ESTs | 10 |
| 50 | 131785 | H69342 | Hs.26320 | TRABID protein | 10 |
| | 131815 | AA021258 | Hs.32753 | ESTs | 5 |
| | 131819 | BE244961 | Hs.173103 | FE65-LIKE 2 | 5 |
| | 131828 | AJ000263 | Hs.278658 | keratin, hair, basic, 6 (monilethrix) | 10 |
| | 131888 | AW294659 | Hs.34054 | Homo sapiens cDNA: FLJ22488 fis, clone H | 5 |
| 55 | 131927 | AJ003112 | Hs.34780 | doublecortin; lissencephaly, X-linked (d | 5 |
| | 131949 | AK000010 | Hs.258798 | hypothetical protein FLJ20003 | 10 |
| | 132115 | H81604 | Hs.178471 | KIAA0798 gene product | 5 |
| | 132177 | X80818 | Hs.178078 | glutamate receptor, metabotropic 4 | 5 |
| | 132296 | AA467752 | Hs.195161 | ESTs | 5 |
| 60 | 132426 | AW118072 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 10 |
| | 132477 | S68874 | Hs.170917 | prostaglandin E receptor 3 (subtype EP3) | 5 |
| | 132675 | AI291496 | Hs.5476 | Homo sapiens, clone IMAGE:3530123, mRNA, | 10 |
| | 132796 | NM_006283 | Hs.173159 | transforming, acidic coiled-coil contain | 10 |
| | 132898 | W28548 | Hs.224829 | ESTs | 10 |
| 65 | 132905 | NM_004235 | Hs.7934 | Kruppel-like factor 4 (gut) | 10 |
| | 132953 | BE175645 | Hs.321264 | LBP protein 32 | 5 |
| | 133116 | BE563966 | Hs.6529 | ESTs, Weakly similar to I78885 serine/th | 5 |
| | 133120 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 10 |

| | | | | | |
|----|--------|--------------|-----------|---|----|
| | 133139 | AF052138 | Hs.6580 | Homo sapiens cDNA: FLJ23227 fis, clone C | 5 |
| | 133163 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 5 |
| | 133268 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKH | 5 |
| | 133272 | NM_002776 | Hs.69423 | kalikrein 10 (KLK10) (PRSSL1) (nes1) | 5 |
| 5 | 133379 | AA207059 | | gb:zq80h09.s1 Stratagene hNT neuron (937 | 5 |
| | 133407 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 5 |
| | 133552 | H21497 | Hs.7471 | BBP-like protein 1 | 5 |
| | 133702 | L02321 | Hs.75652 | glutathione S-transferase M5 | 5 |
| | 133719 | H26904 | Hs.75736 | apolipoprotein D | 5 |
| 10 | 133731 | N71725 | Hs.272572 | hemoglobin, alpha 2 | 10 |
| | 133789 | T85626 | Hs.76239 | hypothetical protein FLJ20608 | 5 |
| | 134007 | AF072441 | Hs.7840 | calcineurin binding protein 1 | 10 |
| | 134055 | D86062 | Hs.182423 | ES1 (zebrafish) protein, human homolog o | 10 |
| | 134111 | AI372588 | Hs.8022 | TU3A protein | 10 |
| 15 | 134117 | AA081846 | Hs.7921 | Homo sapiens mRNA; cDNA DKFZp566E183 (fr | 10 |
| | 134177 | BE243319 | Hs.79672 | KIAA0652 gene product | 5 |
| | 134308 | AW905827 | Hs.81454 | ketohexokinase (fructokinase) | 10 |
| | 134361 | BE549343 | Hs.82208 | acyl-Coenzyme A dehydrogenase, very long | 5 |
| | 134369 | AF207664 | Hs.8230 | a disintegrin-like and metalloprotease (| 5 |
| 20 | 134449 | L34155 | Hs.83450 | laminln, alpha 3 (nicein (150kD), kalini | 5 |
| | 134467 | AI190413 | Hs.8373 | ESTs | 10 |
| | 134496 | M64936 | | gb:Homo sapiens retinoic acid-inducible | 10 |
| | 134510 | NM_002757 | Hs.250870 | mitogen-activated protein kinase kinase | 10 |
| | 134550 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 10 |
| 25 | 134577 | BE244323 | Hs.85951 | exportin, tRNA (nuclear export receptor | 5 |
| | 134591 | U73394 | Hs.166085 | killer cell immunoglobulin-like receptor | 5 |
| | 134678 | AL008583 | Hs.182595 | dynein, axonemal, light polypeptide 4 | 5 |
| | 134728 | D10216 | Hs.89394 | POU domain, class 1, transcription facto | 5 |
| | 134758 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 10 |
| 30 | 134786 | T29618 | Hs.89640 | TEK tyrosine kinase, endothelial (venous | 10 |
| | 134912 | T87521 | Hs.261457 | ESTs | 5 |
| | 134963 | NM_003394 | Hs.91985 | wingless-type MMTV integration site fami | 10 |
| | 134969 | H22570 | Hs.172572 | hypothetical protein FLJ20093 | 5 |
| | 135001 | AA302517 | Hs.92732 | KIAA1444 protein | 5 |
| 35 | 135066 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 10 |
| | 135173 | AL036557 | Hs.95910 | putative lymphocyte G0/G1 switch gene | 10 |
| | 135197 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 5 |
| | 135219 | AB002361 | Hs.96633 | KIAA0363 protein | 5 |
| | 135250 | U83171 | Hs.97203 | small inducible cytokine subfamily A (Cy | 5 |
| 40 | 135304 | AA416829 | Hs.191597 | ESTs | 5 |
| | 135337 | AA905406 | Hs.9905 | ESTs, Weakly similar to unnamed protein | 3 |
| | 135417 | X55019 | Hs.99975 | cholinergic receptor, nicotinic, delta p | 10 |
| | 101367 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 5 |
| | 128870 | H39537 | Hs.75309 | eukaryotic translation elongation factor | 5 |
| 45 | 129381 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 5 |
| | 130085 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 5 |
| | 130689 | NM_006691 | Hs.17917 | extracellular link domain-containing 1 | 10 |
| | 133120 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 3 |
| | 133407 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 5 |
| 50 | 133731 | N71725 | Hs.272572 | hemoglobin, alpha 2 | 5 |
| | 134369 | AF207664 | Hs.8230 | a disintegrin-like and metalloprotease (| 5 |
| | 135066 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 10 |
| | 135173 | AL036557 | Hs.95910 | putative lymphocyte G0/G1 switch gene | 5 |
| | 322580 | AK001852 | Hs.274151 | ligatin | 5 |
| 55 | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, type 2 | 10 |
| | 418043 | AW377752 | Hs.83341 | AXL receptor tyrosine kinase | 5 |
| | 427458 | BE208364 | Hs.29283 | ESTs, Weakly similar to LKHU proteoglycan link | 5 |
| | 446674 | AA563892 | Hs.306000 | solute carrier family 4 (anion exchanger), memb | 10 |
| | 449826 | U85642 | Hs.138506 | ESTs | 5 |
| 60 | | RC_H15814_s | | Human apM1 mRNA for GS3109 (novel adipose specific collagen | 10 |
| | | YEL024w/RIP1 | | EST - YEL024w/RIP1 | 3 |

TABLE 1A

Table 1 A shows the accession numbers for those pkeys lacking unigeneID's for Table 1. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15

| Pkey | CAT Number | Accessions |
|----------|-------------|--|
| 108446 | 112224_1 | AA085383 AA126091 AA074174 AA075373 AA079120 AA070831 AA075978 AA075372 AA128503 |
| 108497 | 110079_2 | AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929 |
| 124215 | 1597154_1 | H62570 H59063 |
| 117058 | 1219924_1 | AW801806 H90434 BE086530 |
| 110455 | 46874_1 | H52576 AF085971 H52172 |
| 111168 | 38585_1 | AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 |
| 111498 | 411008_1 | AI168511 AI022712 AA700366 R07371 R07324 |
| 104340 | 46289_10 | AA426189 F15201 |
| 103747 | 117944_1 | AA081995 AA101099 |
| 134496 | 46501_1 | M64936 AI025512 AI382987 BE061777 AA089966 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 |
| AI684569 | AA257011 | AI079277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514 |
| 103750 | 118365_1 | AA126129 AA126033 AA082561 |
| 105239 | 34624_1 | AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 |
| 120379 | 34624_3 | AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849 AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757 AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045 |
| 114624 | 111686_1 | AA081507 AA070071 AA070840 AA084362 |
| 106851 | 322947_1 | AI458623 AA639708 AA485409 R22065 AA485570 |
| 108392 | 113549_1 | AA075124 AA075208 |
| 100545 | 22955_11 | M55405 AW752552 |
| 100654 | tigr_HT2969 | A03758 A06977 A15293 D17029 D17107 D17171 L00132 L00133 M12523 M13075 M13076 M92816 U22961 V00494 V00495 X51363 X51364 X51365 |
| 100702 | tigr_HT3413 | L27065 |
| 102208 | 6735_9 | U22961 AA203623 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195 AI209170 AI186653 AI127795 AI183846 H77389 AI589465 AA629390 H94306 AI018388 R68584 AA027196 AI745413 AI685092 AI093426 AI623873 AI074570 N50096 AA047486 N25060 AA327614 AI042512 AI383957 AI156873 AI333101 |

5 N70806 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265
 AA877103 W84464 AA625146 R68379 AI133207 AI132980 AI133214 AI064826 AI061615 AI133473 AI174852 AI133404
 AI133272 V00494 M12523 M12523 AI207526 AI133120 AI064802 AI174993 AI114729 AI061645 AI064716 AI064959 H77388
 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248416 AI207432 AI133684 AI133345 AI174710
 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF063516 AI110642 AI114559 AI114498 AI114759
 AI207568 AI064960 AI174753 AI114666 R69184 R00011 AI064997 T60501 AI207701 T71735 AA385318 H73569 T60496
 H94399 AI133158 T74675 AA484750 T73413 T55909 R50261 T72061 N80533 T51189 T74936 AI207490 AI132925 AI064701
 AI174748 AI114663 AI133104 AI132999 AI133100 AI064925 AI064979 AI133063 AA343347 T69091 AA233989 T39772
 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091136 AA334608 T57411 Z20979
 10 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468
 AA332728 T51362 AI114589 R06691 AI110629 AF063503 AI140543 AA334661 AA332720 AA343262 T73513 T86549
 AI114840 T57284 T39981 T61407 T72757 T51749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174786
 AI132926 R09237 AI064838 AI133660 T60398 T88753 T55930 T92126 AI444602 T60996 AI114792 H93911 AI133106
 R10779 AI065020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI064857 AI110730 AF074637 AI207567
 15 H71080 T73217 AA343950 AI174743 AA334224 AA334281 R06692 T64739 T40163 T60628 T81661 T73179 R01842
 AA501730 T39931 T39662 T40136 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951
 AA005016 T60361 T69176 T73356 T58795 T61233 T39955 T60612 AI114676 AI064778 AA035710 W52763 AI114786
 T83564 AA341859 T81684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305675
 20 AA343592 T53836 T46869 T64721 T55508 W05241 T54019 T57945 T60513 T48364 AF075308 W86731 T82851 T48269
 H54053 T73211 AI114590 T48317 T55965 T74857 R84226 T56552 T52231 T74946 T76976 R02576 T95666 AI203974
 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI064737 AW051713 AA936693 AI133117 AI766232 A913646
 T83962 AI065112 AI207689 AI174684 AI207702 T81475 AI133325 AI032512 AA701169 AI936354 AI114720 AI433289
 AA046980 AI823482 AI114536 AA860651 AW242644 R07469 AW300438 AI133416 AW271670 AI991363 T78943 AI823481
 25 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T62890 T71374 T68294 AI174774 T67411 T68318
 AI064689 T56624 T69010 T68982 T68302 AI332829 T72908 AI064819 AI205880 T62895 T69430 T95111 AA025050 T73330
 W52657 T71984 T69118 W92684 AI114860 T62093 T61797 AI522333 T73322 H92981 T56018 T61811 T57232 AI336158
 T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R94581 T71311 T61819 T89358 T67708 T70918
 T59166 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T67908 R16809 T69394
 30 AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890
 T67751 AI174983 T51679 T54851 H69880 N73734 AA443453 T73466 H69672 N53869 T68447 D11809 D12412 T64300
 T28321 T55864
 35 123941 genbank_AA621529 AA621529
 118049 genbank_N53145 N53145
 102800 14782_20 AA313538 U88895 U88902
 104106 AA422123_i_atAA422123_j
 111738 genbank_R26065 R26065
 113149 genbank_T51588 T51588
 113958 genbank_W86195 W86195
 108335 genbank_AA070500 AA070500
 40 108351 genbank_AA071193 AA071193
 108441 genbank_AA079079 AA079079
 124276 genbank_H83465 H83465
 101447 entrez_M21305 M21305
 117226 genbank_N20468 N20468
 45 133379 genbank_AA207059 AA207059,AA207241
 119366 genbank_T77892 T77892
 119528 NOT_FOUND_entrez_W38051 W38051
 112588 genbank_R77302 R77302
 114449 genbank_AA020736 AA020736
 50 114576 genbank_AA065096 AA065096
 107459 W38002_s_at W38002_s
 130339 genbank_AA435746 AA435746

TABLE 2: Figure 2 from BRCA 001 US

5 **Table 2** shows genes downregulated in tumor tissue compared to normal breast tissue.

| | | | | | |
|----|----------------|---|-----------|--|----|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of normal breast tissue to tumor | | | |
| 15 | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
| 20 | 100499 | T51986 | Hs.283108 | hemoglobin, gamma G | 10 |
| | 100549 | BE142019 | Hs.222056 | Homo sapiens cDNA FLJ11572 fls, clone HE | 10 |
| | 100654 | A03758 | | NM_000477*:Homo sapiens albumin (ALB), m | 10 |
| | 100971 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 10 |
| | 101184 | NM_001674 | Hs.460 | activating transcription factor 3 | 10 |
| 25 | 101336 | NM_006732 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 10 |
| | 101367 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 10 |
| | 101447 | M21305 | | gbHuman alpha satellite and satellite 3 | 10 |
| | 101461 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 10 |
| | 101511 | M27826 | Hs.267319 | endogenous retroviral protease | 10 |
| 30 | 101736 | M74447 | Hs.502 | transporter 2, ATP-binding cassette, sub-famil | 10 |
| | 102208 | U22961 | | gbHuman mRNA clone with similarity to L | 10 |
| | 102450 | U48251 | Hs.75871 | protein kinase C binding protein 1 | 10 |
| | 102800 | AA313538 | | gb:EST185419 Colon carcinoma (HCC) cell | 10 |
| | 102857 | NM_006744 | Hs.76461 | retinol-binding protein 4, interstitial | 10 |
| 35 | 102990 | AA829286 | Hs.332053 | serum amyloid A1 | 10 |
| | 103747 | AA081995 | | gb:zn26d06.r1 Stratagene neuroepithelium | 10 |
| | 103812 | AA137107 | Hs.326391 | Homo sapiens, clone MGC:16638, mRNA, com | 10 |
| | 104093 | R50727 | Hs.336970 | ESTs | 10 |
| | 104109 | AL353957 | Hs.284181 | hypothetical protein DKFZp434P0531 | 10 |
| 40 | 104250 | F06638 | Hs.12440 | Homo sapiens clone 24734 mRNA sequence | 10 |
| | 104492 | N73185 | Hs.94285 | EST | 10 |
| | 104506 | N91071 | Hs.109650 | ESTs | 10 |
| | 104532 | AI498763 | Hs.203013 | hypothetical protein FLJ12748 | 10 |
| | 104677 | AA009764 | Hs.190380 | ESTs | 10 |
| 45 | 104711 | AA017245 | Hs.32794 | ESTs | 10 |
| | 104731 | AA019300 | Hs.125070 | ESTs, Moderately similar to I54374 gene | 10 |
| | 105005 | AI298208 | Hs.28805 | ESTs | 10 |
| | 105036 | AA130390 | Hs.25549 | hypothetical protein FLJ20898 | 10 |
| | 105239 | AA221036 | | gb:zn03f12.r1 Stratagene NT2 neuronal pr | 10 |
| 50 | 106052 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypothet | 10 |
| | 106181 | AI803651 | Hs.191608 | ESTs | 10 |
| | 106283 | AI085846 | Hs.25522 | KIAA1808 protein | 10 |
| | 106379 | AL042069 | Hs.119021 | DKFZP434N061 protein | 10 |
| | 106451 | AW235928 | Hs.313182 | ESTs | 10 |
| 55 | 106491 | AA135688 | Hs.10083 | Homo sapiens, clone IMAGE:4139786, mRNA, | 10 |
| | 106782 | AW054886 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 10 |
| | 107124 | AB006532 | Hs.31442 | RecQ protein-like 4 | 10 |
| | 107148 | AI005036 | Hs.334305 | GS1999full | 10 |
| | 107214 | AF127026 | Hs.5394 | myosin IA | 10 |
| 60 | 107242 | AB020672 | Hs.175411 | KIAA0865 protein | 10 |
| | 107331 | AI905985 | Hs.111805 | ESTs | 10 |
| | 107447 | W28516 | Hs.19210 | hypothetical protein MGC11308 | 10 |
| | 107451 | AL042425 | Hs.283976 | hypthetical protein PRO2389 | 10 |
| | 107872 | BE271708 | Hs.95110 | ESTs, Weakly similar to A55943 1-phospha | 10 |
| 65 | 108351 | AA071193 | | gb:zf79b12.s1 Soares_pineal_gland_N3HPG | 10 |
| | 109546 | F01449 | Hs.26954 | Homo sapiens mRNA; cDNA DKFZp762G123 (fr | 10 |
| | 110433 | AW294162 | Hs.301062 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 10 |
| | 110976 | AL044174 | Hs.159526 | patched (Drosophila) homolog | 5 |

| | | | | | |
|----|--------|-----------|-----------|---|----|
| | 111168 | AI798376 | | gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens | 10 |
| | 111651 | R16733 | Hs.20499 | ESTs | 10 |
| | 111803 | AA593731 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 10 |
| | 114484 | AA034378 | Hs.267319 | endogenous retroviral protease | 10 |
| 5 | 125284 | NM_002666 | Hs.103253 | perilipin | 10 |
| | 128850 | AA193106 | Hs.180817 | chromosome 11 open reading frame 23 | 5 |
| | 128903 | AW150717 | Hs.296176 | STAT induced STAT inhibitor 3 | 10 |
| | 129346 | AF110141 | Hs.288908 | WAS protein family, member 2 | 10 |
| | 129381 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 10 |
| 10 | 129516 | AF020038 | Hs.11223 | isocitrate dehydrogenase 1 (NADP+), solu | 10 |
| | 129554 | BE222078 | Hs.113069 | ESTs | 10 |
| | 130085 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 10 |
| | 130243 | D88435 | Hs.153227 | cyclin G associated kinase | 10 |
| | 130400 | V00517 | Hs.283108 | hemoglobin, gamma G | 10 |
| 15 | 130436 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 10 |
| | 130563 | BE270472 | Hs.279900 | HSPC015 protein | 10 |
| | 130589 | AL110226 | Hs.16441 | DKFZP434H204 protein | 10 |
| | 130683 | AA993269 | Hs.17872 | Homo sapiens, clone IMAGE:3875012, mRNA | 10 |
| | 130689 | NM_006691 | Hs.17917 | extracellular link domain-containing 1 | 10 |
| 20 | 130689 | AA046747 | Hs.17917 | extracellular link domain-containing 1 | 10 |
| | 130718 | N70196 | Hs.18376 | KIAA1319 protein | 10 |
| | 130798 | M81349 | Hs.1955 | serum amyloid A4, constitutive | 10 |
| | 130840 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 10 |
| | 131184 | AB040935 | Hs.23954 | cerebral cell adhesion molecule | 10 |
| 25 | 131282 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 10 |
| | 131328 | AW939251 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 10 |
| | 131543 | AW966881 | Hs.41639 | programmed cell death 2 | 10 |
| | 131753 | AA829286 | Hs.332053 | serum amyloid A1 | 10 |
| | 131785 | H69342 | Hs.26320 | TRABID protein | 10 |
| 30 | 131828 | AJ000263 | Hs.278658 | keratin, hair, basic, 6 (monilethrix) | 10 |
| | 132426 | AW118072 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 10 |
| | 132675 | AI291496 | Hs.5476 | Homo sapiens, clone IMAGE:3530123, mRNA, | 10 |
| | 132898 | W28548 | Hs.224829 | ESTs | 10 |
| | 132905 | NM_004235 | Hs.7934 | Kruppel-like factor 4 (gut) | 10 |
| 35 | 133120 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 10 |
| | 133407 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 10 |
| | 133719 | H26904 | Hs.75736 | apolipoprotein D | 10 |
| | 134007 | AF072441 | Hs.7840 | calcineurin binding protein 1 | 10 |
| | 134055 | D86062 | Hs.182423 | ES1 (zebrafish) protein, human homolog o | 10 |
| 40 | 134111 | AI372588 | Hs.8022 | TU3A protein | 5 |
| | 134117 | AA081846 | Hs.7921 | Homo sapiens mRNA; cDNA DKFZp566E183 (fr | 5 |
| | 134177 | BE243319 | Hs.79672 | KIAA0652 gene product | 10 |
| | 134369 | AF207664 | Hs.8230 | a disintegrin-like and metalloprotease (| 10 |
| | 134496 | M64936 | | gb:Homo sapiens retinoic acid-inducible | 10 |
| 45 | 134510 | NM_002757 | Hs.250870 | mitogen-activated protein kinase kinase | 10 |
| | 134550 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 5 |
| | 134758 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 5 |
| | 134963 | NM_003394 | Hs.91985 | wingless-type MMTV integration site fami | 10 |
| | 135066 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 10 |
| 50 | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, type 2 | 10 |
| | 446674 | AA563892 | Hs.306000 | solute carrier family 4 (anion exchanger), memb | 10 |

TABLE 2A

Table 2A shows the accession numbers for those pkeys lacking unigeneID's for Table 2.

- 5 For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15

Pkey CAT number Accessions

20

111168 38585_1 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567
 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384
 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718
 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254
 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215
 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
 BE081531 H59570

25

103747 117944_1 AA081995 AA101099
 134496 46501_1 M64936 AI025512 AI382987 BE061777 AA089966 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311
 AI684569 AA257011 AI079277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514
 105239 34624_1 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627
 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241
 30 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904
 C16859

35

100654 tigr_HT2969 A03758 A06977 A15293 D17029 D17107 D17171 L00132 L00133 M12523 M13075 M13076 M92816 U22961 V00494 V00495
 X51363 X51364 X51365

40

102208 6735_9 U22961 AA203623 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195
 AI209170 AI186653 AI127795 AI183846 H77389 AI589465 AA629390 H94306 AI018388 R68584 AA027196 AI745413
 AI685092 AI093426 AI623873 AI074570 N50096 AA047486 N25060 AA327614 AI042512 AI383957 AA156873 AI333101
 N70806 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265
 AA877103 W84464 AA625146 R68379 AI133207 AI132980 AI133214 AI064826 AI061615 AI133473 AI174852 AI133404
 AI133272 V00494 M12523 AI207526 AI133120 AI064802 AI174993 AI114729 AI061645 AI064716 AI064959 H77388
 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248416 AI207432 AI133684 AI133345 AI174710
 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF063516 AI110642 AI114559 AI114498 AI114759
 AI207568 AI064960 AI174753 AI114666 R69184 R00011 AI064997 T60501 AI207701 T71735 AA385318 H73569 T60496
 H94399 AI133158 T74675 AA484750 T73413 T55909 R50261 T72061 N80533 T51189 T74936 AI207490 AI132925 AI064701
 AI174748 AI114663 AI133104 AI132999 AI133100 AI064925 AI064979 AI133063 AA343347 T69091 AA233989 T39772
 45 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091136 AA334608 T57411 Z20979
 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468
 AA332728 T51362 AI114589 R06691 AI110629 AF063503 AI140543 AA334661 AA332720 AA343262 T73513 T86549
 AI114840 T57284 T39981 T61407 T72757 T51749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174786
 AI132926 R09237 AI064838 AI133660 T60398 T88753 T55930 T92126 AI444602 T60996 AI114792 H93911 AI133106
 R10779 AI065020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI064857 AI110730 AF074637 AI207567
 H71080 T73217 AA343950 AI174743 AA334224 AA334281 R06692 T64739 T40163 T60628 T81661 T73179 R01842
 AA501730 T39931 T39662 T40136 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951
 AA005016 T60361 T69176 T73356 T58795 T61233 T39955 T60612 AI114676 AI064778 AA035710 W52763 AI114786
 T83564 AA341859 T81684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305675
 50 AA343592 T53836 T46869 T64721 T55508 W05241 T54019 T57945 T60513 T48364 AF075308 W86731 T82851 T48269
 H54053 T73211 AI114590 T48317 T55965 T74857 R84226 T56552 T52231 T74946 T76976 R02576 T95666 AI203974
 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI064737 AW051713 AA936693 AI133117 AI766232 AI913646
 T83962 AI065112 AI207689 AI174684 AI207702 T81475 AI133325 AI032512 AA701169 AI936354 AI114720 AI433289
 AA046980 AI823482 AI114536 AA860651 AW242644 R07469 AW300438 AI133416 AW271670 AI991363 T78943 AI823481
 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T62890 T71374 T68294 AI174774 T67411 T68318
 AI064689 T56624 T69010 T68982 T68302 AI332829 T72908 AI064819 AI205880 T62895 T69430 T95111 AA025050 T73330
 60 W52657 T71984 T69118 W92684 AI114860 T62093 T61797 AI522333 T73322 H92981 T56018 T57232 AI336158

5

T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R94581 T71311 T61819 T89358 T67708 T70918
T59166 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T67908 R16809 T69394
AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890
T67751 AI174983 T51679 T54851 H69880 N73734 AA443453 T73466 H69672 N53869 T68447 D11809 D12412 T64300
T28321 T55864
102800 14782_20 AA313538 U88895 U88902
108351 genbank_AA071193 AA071193
101447 entrez_M21305 M21305

TABLE 3: Figure 3 from BRCA 001 US

Table 3 shows genes downregulated in tumor tissue compared to normal breast tissue.

5

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal breast tissue to tumor

15

| | Pkey | ExAccn | UnigenelD | UnigeneTitle | R1 |
|----|--------|-----------|-----------|--|------|
| | 101336 | NM_006732 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 10.0 |
| | 102208 | U22961 | | gb:Human mRNA clone with similarity to L | 10.0 |
| 20 | 102990 | AA829286 | Hs.332053 | serum amyloid A1 | 10.0 |
| | 111168 | AI798376 | | gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens | 10.0 |
| | 111803 | AA593731 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 10.0 |
| | 130085 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 10.0 |
| | 130840 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 10.0 |
| 25 | 131543 | AW966881 | Hs.41639 | programmed cell death 2 | 10.0 |
| | 133120 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 10.0 |
| | 134758 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 10.0 |

TABLE 3A

Table 3A shows the accession numbers for those pkeys lacking unigeneID's for Table 3. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

| | | | |
|----|------------------------------------|---|---|
| 10 | Pkey: CAT number: Accession: | Unique Eos probeset identifier number Gene cluster number Genbank accession numbers | |
| 15 | Pkey | CAT number | Accessions |
| 20 | 111168 | 38585_1 | AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 |
| 25 | 102208 | 6735_9 | U22961 AA203623 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195 AI209170 AI186653 AI127795 AI183846 H77389 AI589465 AA629390 H94306 AI018388 R68584 AA027196 AI745413 AI685092 AI093426 AI623873 AI074570 N50096 AA047486 N25060 AA327614 AI042512 AI383957 AA156873 AI333101 N70806 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265 AA877103 W84464 AA625146 R68379 AI133207 AI132980 AI133214 AI064826 AI061615 AI133473 AI174852 AI133404 AI133272 V00494 M12523 M12523 AI207526 AI133120 AI064802 AI174993 AI114729 AI061645 AI064716 AI064959 H77388 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248416 AI207432 AI133684 AI133345 AI174710 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF063516 AI110642 AI114559 AI114498 AI114759 AI207568 AI064960 AI174753 AI114666 R69184 R00011 AI064997 T60501 AI207701 T71735 AA385318 H73569 T60496 H94399 AI133158 T74675 AA484750 T73413 T55909 R50261 T72061 N80533 T51189 T74936 AI207490 AI132925 AI064701 AI174748 AI114663 AI133104 AI132999 AI133100 AI064925 AI064979 AI133063 AA343347 T69091 AA233989 T39772 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091136 AA334608 T57411 Z20979 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468 AA332728 T51362 AI114589 R06691 AI110629 AF063503 AI140543 AA334661 AA332720 AA343262 T73513 T86549 AI114840 T57284 T39981 T61407 T72757 T51749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174786 AI132926 R09237 AI064838 AI133660 T60398 T88753 T55930 T92126 AI444602 T60996 AI114792 H93911 AI133106 R10779 AI065020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI064857 AI110730 AF074637 AI207567 H71080 T73217 AA343950 AI174743 AA334224 AA334281 R06692 T64739 T40163 T60628 T81661 T73179 R01842 AA501730 T39931 T39662 T40136 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951 AA005016 T60361 T69176 T73356 T58795 T61233 T39955 T60612 AI114676 AI064778 AA035710 W52763 AI114786 T83564 AA341859 T81684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305675 AA343592 T53836 T46869 T64721 T55508 W05241 T54019 T57945 T60513 T48364 AF075308 W86731 T82851 T48269 H54053 T73211 AI114590 T48317 T55965 T74857 R84226 T56552 T52231 T74946 T6976 R02576 T95666 AI203974 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI064737 AW051713 AA936693 AI133117 AI766232 AI913646 T83962 AI065112 AI207689 AI174684 AI207702 T81475 AI133325 AI032512 AA701169 AI936354 AI114720 AI433289 AA046980 AI823482 AI114536 AA860651 AW242644 R07469 AW300438 AI133416 AW271670 AI991363 T78943 AI823481 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T62890 T71374 T68294 AI174774 T67411 T68318 AI064689 T56624 T69010 T68982 T68302 AI332829 T72908 AI064819 AI205880 T62895 T69430 T95111 AA025050 T73330 W52657 T71984 T69118 W92684 AI114860 T62093 T61797 AI522333 T73322 H92981 T56018 T61811 T57232 AI336158 T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R94581 T71311 T61819 T89358 T67708 T70918 T59166 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T67908 R16809 T69394 AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890 T67751 AI174983 T51679 T54851 H69880 N73734 AA443453 T73466 H69672 N53869 T68447 D11809 D12412 T64300 T28321 T55864 |
| 30 | | | |
| 35 | | | |
| 40 | | | |
| 45 | | | |
| 50 | | | |
| 55 | | | |

TABLE 4: Figure 4 from BRCA 001 US

5 Table 4 shows genes upregulated in tumor tissue compared to normal breast tissue.

| | | | | | |
|----|----------------|---|-----------|---|------|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal breast tissue | | | |
| 15 | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
| 20 | 100113 | NM_001269 | Hs.84746 | chromosome condensation 1 | 2.3 |
| | 100114 | X02308 | Hs.82962 | thymidylate synthetase | 2.9 |
| | 100131 | D12485 | Hs.11951 | ectonucleotide pyrophosphatase/phosphodiesterase 1 | 1.9 |
| | 100146 | BE185499 | Hs.2471 | KIAA0020 gene product | 1.9 |
| | 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fascin-like) (periostin) | 7.5 |
| 25 | 100154 | H60720 | Hs.81892 | KIAA0101 gene product | 9.2 |
| | 100163 | W44671 | Hs.124 | gene predicted from cDNA with a complete coding sequence | 1.6 |
| | 100220 | AW015534 | Hs.217493 | annexin A2 | 2.0 |
| | 100265 | D38521 | Hs.112396 | KIAA0077 protein | 1.5 |
| | 100271 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgizzarin) | 13.5 |
| 30 | 100275 | BE242802 | Hs.154797 | KIAA0090 protein | 5.1 |
| | 100323 | D50920 | Hs.23106 | KIAA0130 gene product | 1.9 |
| | 100335 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD) | 2.7 |
| | 100364 | NM_004341 | Hs.154868 | carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase | 2.0 |
| | 100372 | NM_014791 | Hs.184339 | KIAA0175 gene product | 2.6 |
| 35 | 100393 | D84145 | Hs.39913 | novel RGD-containing protein | 3.2 |
| | 100400 | AW954324 | Hs.75790 | phosphatidylinositol glycan, class C | 1.5 |
| | 100418 | D86978 | Hs.84790 | KIAA0225 protein | 2.0 |
| | 100482 | M65028 | Hs.81361 | heterogeneous nuclear ribonucleoprotein A/B | 2.9 |
| | 100518 | NM_004415 | Hs.74316 | desmoplakin (DP1, DP11) | 1.9 |
| 40 | 100666 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian blood group system) | 5.7 |
| | 100667 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian blood group system) | 9.0 |
| | 100668 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian blood group system) | 7.6 |
| | 100678 | AW502935 | Hs.740 | PTK2 protein tyrosine kinase 2 | 53.2 |
| | 100685 | AA328229 | Hs.184582 | ribosomal protein L24 | 1.8 |
| 45 | 100690 | AA383256 | Hs.1657 | estrogen receptor 1 | 1.6 |
| | 100783 | AF078847 | Hs.191356 | general transcription factor IIH, polypeptide 2 (44kD subunit) | 5.9 |
| | 100850 | AA836472 | Hs.297939 | cathepsin B | 1.7 |
| | 100892 | BE245294 | Hs.180789 | S164 protein | 1.7 |
| | 100945 | AF002225 | Hs.180686 | ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) | 1.5 |
| 50 | 100969 | AA157634 | Hs.79172 | solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 | 6.3 |
| | 100988 | AK000405 | Hs.76480 | ubiquitin-like 4 | 11.4 |
| | 100999 | H38765 | Hs.80706 | diaphorase (NADH/NADPH) (cytochrome b-5 reductase) | 1.6 |
| | 101031 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) | 8.2 |
| | 101045 | J05614 | | gb:Human proliferating cell nuclear antigen (PCNA) gene, promoter region. | 5.0 |
| 55 | 101077 | N99692 | Hs.75227 | Empirically selected from AFFX single probeset | 2.6 |
| | 101093 | L06419 | Hs.75093 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) | 1.4 |
| | 101161 | NM_006262 | Hs.37044 | peripherin | 16.9 |
| | 101186 | AA020956 | Hs.179881 | core-binding factor, beta subunit | 2.0 |
| | 101216 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) | 1.8 |
| 60 | 101228 | AA333387 | Hs.82916 | chaperonin containing TCP1, subunit 6A (zeta 1) | 1.7 |
| | 101247 | AA132666 | Hs.78802 | glycogen synthase kinase 3 beta | 1.9 |
| | 101249 | L18964 | Hs.1904 | protein kinase C, iota | 1.5 |
| | 101332 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 5.2 |
| | 101332 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 3.4 |
| 65 | 101352 | AI494299 | Hs.16297 | COX17 (yeast) homolog, cytochrome c oxidase assembly protein | 6.3 |
| | 101396 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 4.2 |
| | 101445 | M21259 | | gb:Human Alu repeats in the region 5' to the small nuclear rib | 1.9 |
| | 101470 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 1.6 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 101478 | NM_002890 | Hs.758 | RAS p21 protein activator (GTPase activating protein) 1 | 2.5 |
| | 101483 | M24486 | Hs.76768 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I | 5.5 |
| | 101540 | J04977 | Hs.84981 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining 2.1 | |
| | 101573 | AW248421 | Hs.250758 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 | 1.6 |
| 5 | 101580 | NM_012151 | Hs.83363 | coagulation factor VIII-associated (intronic transcript) | 5.7 |
| | 101592 | AF064853 | Hs.91299 | guanine nucleotide binding protein (G protein), beta polypeptide 2 | 1.8 |
| | 101592 | AF064853 | Hs.91299 | guanine nucleotide binding protein (G pr | 5.6 |
| | 101621 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon-inducible, 67kD | 2.4 |
| | 101702 | AW504089 | Hs.179574 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | 1.3 |
| 10 | 101734 | M74099 | Hs.147049 | cut (Drosophila)-like 1 (CCAAT displacement protein) | 2.1 |
| | 101759 | M80244 | Hs.184601 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 | 5.0 |
| | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 14.4 |
| | 101782 | AA306495 | Hs.1869 | phosphoglucomutase 1 | 5.2 |
| | 101805 | AW409747 | Hs.75612 | stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) | 8.6 |
| 15 | 101806 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psoriasin 1) | 8.9 |
| | 101810 | NM_000318 | Hs.180612 | peroxisomal membrane protein 3 (35kD, Zellweger syndrome) | 3.2 |
| | 101879 | AA176374 | Hs.243886 | nuclear autoantigenic sperm protein (histone-binding) | 1.6 |
| | 101911 | AA441787 | Hs.119689 | glycoprotein hormones, alpha polypeptide | 31.3 |
| | 101920 | AF182645 | Hs.8024 | IK cytokine, down-regulator of HLA II | 1.8 |
| 20 | 101973 | U41514 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | 2.4 |
| | 101983 | AI904232 | Hs.75323 | prohibitin | 8.4 |
| | 102009 | BE245149 | Hs.82643 | protein tyrosine kinase 9 | 1.3 |
| | 102036 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevisiae, homolog) | 2.0 |
| | 102083 | T35901 | Hs.75117 | interleukin enhancer binding factor 2, 45kD | 1.6 |
| 25 | 102083 | T35901 | Hs.75117 | interleukin enhancer binding factor 2, 4 | 1.3 |
| | 102107 | BE258602 | Hs.182366 | heat shock protein 75 | 1.4 |
| | 102123 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 1.8 |
| | 102165 | BE313280 | Hs.159627 | death associated protein 3 | 4.6 |
| | 102198 | AW950852 | Hs.74598 | polymerase (DNA directed), delta 2, regulatory subunit (50kD) | 4.3 |
| 30 | 102217 | AA829978 | Hs.301613 | JTV1 gene | 6.7 |
| | 102220 | U24389 | Hs.65436 | lysosomal | 4.3 |
| | 102234 | AW163390 | Hs.278554 | heterochromatin-like protein 1 | 1.9 |
| | 102260 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, Importin alpha 1) | 4.4 |
| | 102302 | AA306342 | Hs.69171 | protein kinase C-like 2 | 2.7 |
| 35 | 102330 | BE298063 | Hs.77254 | chromobox homolog 1 (Drosophila HP1 beta) | 1.5 |
| | 102339 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 2.3 |
| | 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member B2 | 2.0 |
| | 102349 | AU077055 | Hs.289107 | baculoviral IAP repeat-containing 2 | 3.2 |
| | 102369 | U39840 | Hs.299867 | hepatocyte nuclear factor 3, alpha | 2.0 |
| 40 | 102374 | U33635 | Hs.90572 | PTK7 protein tyrosine kinase 7 | 6.2 |
| | 102391 | AA296874 | Hs.77494 | deoxyguanosine kinase | 1.5 |
| | 102455 | U48705 | Hs.75562 | discoidin domain receptor family, member 1 | 6.9 |
| | 102465 | NM_001359 | Hs.81548 | 2,4-dienoyl CoA reductase 1, mitochondrial | 1.8 |
| | 102488 | U50939 | Hs.61828 | amyloid beta precursor protein-binding protein 1, 59kD | 1.5 |
| 45 | 102489 | AL080116 | Hs.74420 | origin recognition complex, subunit 3 (yeast homolog)-like | 3.3 |
| | 102494 | AI188137 | Hs.75193 | COP9 homolog | 2.1 |
| | 102501 | AF217197 | Hs.74562 | slah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing | 3.2 |
| | 102522 | BE250944 | Hs.183556 | solute carrier family 1 (neutral amino acid transporter), member 5 | 2.8 |
| | 102532 | AF040253 | Hs.70186 | suppressor of Ty (S.cerevisiae) 5 homolog | 5.7 |
| 50 | 102564 | U59423 | Hs.79067 | MAD (mothers against decapentaplegic, Drosophila) homolog 1 | 2.3 |
| | 102568 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 5.3 |
| | 102580 | U60808 | Hs.152981 | CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1 | 2.1 |
| | 102581 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 1.6 |
| | 102582 | U61232 | Hs.32675 | tubulin-specific chaperone e | 2.1 |
| 55 | 102617 | AW161453 | Hs.198767 | COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 | 1.8 |
| | 102618 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 5.8 |
| | 102627 | AL021918 | Hs.158174 | zinc finger protein 184 (Krueppel-like) | 1.3 |
| | 102663 | NM_002270 | Hs.168075 | karyopherin (importin) beta 2 | 1.8 |
| | 102676 | BE262989 | Hs.12045 | putative protein | 2.3 |
| 60 | 102687 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 4.3 |
| | 102689 | U96132 | Hs.171280 | hydroxyacyl-Coenzyme A dehydrogenase, type II | 6.0 |
| | 102696 | BE540274 | Hs.239 | forkhead box M1 | 4.2 |
| | 102704 | AU077058 | Hs.54089 | BRCA1 associated RING domain 1 | 1.9 |
| | 102705 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cys-Cys), member 19 | 2.3 |
| 65 | 102750 | AB014460 | Hs.66196 | nth (E.coli endonuclease III)-like 1 | 1.2 |
| | 102801 | BE252241 | Hs.38041 | pyridoxal (pyridoxine, vitamin B6) kinase | 6.4 |
| | 102812 | U90549 | Hs.236774 | high-mobility group (nonhistone chromosomal) protein 17-like 3 | 1.6 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 102827 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (beta) | 5.6 |
| | 102831 | AA262170 | Hs.80917 | adaptor-related protein complex 3, sigma 1 subunit | 2.0 |
| | 102844 | AV653790 | Hs.324275 | WW domain-containing protein 1 | 1.3 |
| | 102868 | X02419 | Hs.77274 | plasminogen activator, urokinase | 4.4 |
| 5 | 102925 | BE440142 | Hs.2943 | signal recognition particle 19kD | 1.9 |
| | 102935 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypeptide A' | 2.4 |
| | 102968 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase2.7 | |
| | 102983 | BE387202 | Hs.118638 | non-metastatic cells 1, protein (NM23A) expressed in | 3.1 |
| | 102985 | U95742 | Hs.2707 | G1 to S phase transition 1 | 5.2 |
| 10 | 103023 | AW500470 | Hs.117950 | multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase | 1.6 |
| | 103038 | AA926960 | Hs.334883 | CDC28 protein kinase 1 | 2.5 |
| | 103060 | NM_005940 | Hs.155324 | matrix metalloproteinase 11 (MMP11; stromelysin 3) | 4.5 |
| | 103080 | AU077231 | Hs.82932 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | 3.1 |
| | 103089 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) | 2.4 |
| 15 | 103177 | BE244377 | Hs.48876 | farnesyl-diphosphate farnesyltransferase 1 | 3.5 |
| | 103178 | AA205475 | Hs.275865 | ribosomal protein S18 | 9.9 |
| | 103179 | NM_001777 | Hs.82685 | CD47 antigen (Rh-related antigen, integrin-associated signal transducer) | 1.3 |
| | 103181 | X69636 | Hs.334731 | Homo sapiens, clone IMAGE:3448306, mRNA, partial cds | 2.0 |
| | 103185 | NM_006825 | Hs.74368 | transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment | 1.6 |
| 20 | 103191 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), catalytic subunit | 2.5 |
| | 103193 | NM_004766 | Hs.75724 | coatamer protein complex, subunit beta 2 (beta prime) | 2.2 |
| | 103194 | NM_004939 | Hs.78580 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 | 6.3 |
| | 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 8.8 |
| | 103223 | BE275607 | Hs.1708 | chaperonin containing TCP1, subunit 3 (gamma) | 3.0 |
| 25 | 103232 | X75962 | Hs.129780 | tumor necrosis factor receptor superfamily, member 4 | 1.8 |
| | 103238 | AI369285 | Hs.75189 | death-associated protein | 5.6 |
| | 103297 | NM_001545 | Hs.9078 | immature colon carcinoma transcript 1 | 1.9 |
| | 103330 | AI803447 | Hs.77496 | small nuclear ribonucleoprotein polypeptide G | 2.5 |
| | 103349 | X89059 | | gb:hs.sapiens mRNA for unknown protein expressed in macrophage | 1.6 |
| 30 | 103376 | AL036166 | Hs.323378 | coated vesicle membrane protein | 1.8 |
| | 103391 | X94453 | Hs.114366 | pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) | 2.3 |
| | 103392 | X94563 | | gb:hs.sapiens dbi/acbp gene exon 1 & 2. | 4.0 |
| | 103430 | BE564090 | Hs.20716 | translocase of inner mitochondrial membrane 17 (yeast) homolog A | 1.3 |
| | 103491 | AF264750 | Hs.288971 | myeloid/lymphoid or mixed-lineage leukemia 3 | 5.6 |
| 35 | 103505 | AL031224 | Hs.33102 | transcription factor AP-2 beta (activating enhancer-binding protein 2 beta) | 5.1 |
| | 103547 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) | 9.7 |
| | 103588 | NM_006218 | Hs.85701 | phosphoinositide-3-kinase, catalytic, alpha polypeptide | 2.0 |
| | 103613 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) | 1.3 |
| | 103621 | BE379766 | Hs.150675 | polymerase (RNA) II (DNA directed) polypeptide K (7.0kD) | 2.0 |
| 40 | 103622 | AA609685 | Hs.278672 | membrane component, chromosome 11, surface marker 1 | 2.3 |
| | 103727 | AI878883 | Hs.296381 | growth factor receptor-bound protein 2 | 1.3 |
| | 103749 | AL135301 | Hs.8768 | hypothetical protein FLJ10849 | 1.8 |
| | 103754 | AI015709 | Hs.172089 | Homo sapiens mRNA; cDNA DKFZp58612022 (from clone DKFZp58612022) | 1.3 |
| | 103780 | AA094752 | Hs.169992 | hypothetical 43.2 Kd protein | 7.5 |
| 45 | 103795 | H26531 | Hs.7367 | Homo sapiens BTB domain protein (BDPL) mRNA, partial cds | 1.2 |
| | 103797 | AA080912 | | gb:zn04d03.r1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone 5' similar | 1.5 |
| | 103813 | AI042582 | Hs.181271 | CGI-120 protein | 1.5 |
| | 103855 | W02363 | Hs.302267 | hypothetical protein FLJ10330 | 1.5 |
| | 103886 | AK001278 | Hs.105737 | hypothetical protein FLJ10416 similar to constitutive photomorphogenic protein 1 | 6.5 |
| 50 | 104052 | NM_002407 | Hs.97644 | mammaglobin 2 | 2.9 |
| | 104079 | AA251242 | Hs.103238 | ESTs | 1.4 |
| | 104174 | AA478984 | Hs.6451 | PRO0659 protein | 5.6 |
| | 104227 | AB002343 | Hs.98938 | protocadherin alpha 9 | 1.6 |
| | 104275 | AI751970 | Hs.101067 | GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 | 5.4 |
| 55 | 104325 | BE379766 | Hs.150675 | polymerase (RNA) II (DNA directed) polypeptide K (7.0kD) | 6.3 |
| | 104370 | AA324597 | Hs.21851 | Homo sapiens cDNA FLJ12900 fs, clone NT2RP2004321 | 1.6 |
| | 104423 | R83113 | Hs.1432 | protein kinase C substrate 80K-H | 5.2 |
| | 104482 | AB037762 | Hs.44268 | myelin gene expression factor 2 | 1.2 |
| | 104532 | AI498763 | Hs.203013 | hypothetical protein FLJ12748 | 2.1 |
| 60 | 104563 | AL117403 | Hs.306189 | DKFZP434F1735 protein | 1.2 |
| | 104667 | AI239923 | Hs.30098 | ESTs | 1.3 |
| | 104757 | AI694413 | Hs.332649 | olfactory receptor, family 2, subfamily I, member 6 | 2.3 |
| | 104804 | AI858702 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapiens] | 1.3 |
| | 104806 | AB023175 | Hs.22982 | KIAA0958 protein | 2.3 |
| 65 | 104827 | AW052006 | Hs.8551 | PRP4/STKWD splicing factor | 10.9 |
| | 104846 | AI250789 | Hs.32478 | ESTs | 5.6 |
| | 104854 | AA041276 | Hs.154729 | 3-phosphoinositide dependent protein kinase-1 | 12.3 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 104867 | AA278898 | Hs.225979 | hypothetical protein similar to small G proteins, especially RAP-2A | 2.0 |
| | 104871 | T78044 | Hs.28893 | Homo sapiens mRNA; cDNA DKFZp564O2364 (from clone DKFZp564O2364) | 1.3 |
| | 104896 | AW015318 | Hs.23165 | ESTs | 17.7 |
| | 104909 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 5.0 |
| 5 | 104916 | AW958157 | Hs.155489 | NS1-associated protein 1 | 1.7 |
| | 104919 | AA026880 | Hs.25252 | prolactin receptor | 1.4 |
| | 104930 | AF043467 | Hs.32893 | neurexophilin 2 | 2.2 |
| | 104973 | NM_015310 | Hs.6763 | KIAA0942 protein | 5.0 |
| | 104974 | Y12059 | Hs.278675 | bromodomain-containing 4 | 1.4 |
| 10 | 104975 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 | 2.4 |
| | 104975 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 2.3 |
| | 104978 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010317E24 gene, clone IMAGE:3502019, mRNA, partial cds | 7.2 |
| | 104979 | AA937934 | Hs.321062 | ESTs | 1.3 |
| | 104994 | AI499930 | Hs.334885 | mitochondrial GTP binding protein | 3.5 |
| 15 | 105009 | BE379584 | Hs.34789 | dolichyl-diphosphooligosaccharide-protein glycosyltransferase | 5.5 |
| | 105012 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.3 |
| | 105028 | AI050715 | Hs.2331 | E2F transcription factor 5, p130-binding | 2.2 |
| | 105032 | AA127818 | Hs.36475 | gbz12a02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:501674 3' | 6.8 |
| | 105039 | AA907305 | Hs.36475 | ESTs | 2.5 |
| 20 | 105041 | AB037716 | Hs.26204 | KIAA1295 protein | 2.2 |
| | 105045 | BE242899 | Hs.129951 | speckle-type POZ protein | 3.8 |
| | 105079 | AA151342 | Hs.12677 | CGI-147 protein | 9.5 |
| | 105087 | AA147884 | Hs.9812 | Homo sapiens cDNA FLJ14388 fis, clone HEMBA1002716 | 5.6 |
| | 105088 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114 | 2.2 |
| 25 | 105096 | Z78407 | Hs.27023 | vesicle transport-related protein | 2.2 |
| | 105110 | BE387350 | Hs.33122 | KIAA1160 protein | 1.6 |
| | 105126 | AW975433 | Hs.36288 | ESTs | 6.3 |
| | 105127 | AA045648 | Hs.301957 | nudix (nucleoside diphosphate linked motely X)-type motif 5 | 2.1 |
| | 105141 | AA164687 | Hs.177576 | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A | 2.7 |
| 30 | 105158 | AW976357 | Hs.234545 | hypothetical protein NUF2R | 1.9 |
| | 105169 | BE245294 | Hs.180789 | S164 protein | 1.7 |
| | 105186 | AA191512 | Hs.28005 | Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076 | 4.8 |
| | 105254 | AA071276 | Hs.19469 | KIAA0859 protein | 1.9 |
| | 105281 | AA263143 | Hs.24596 | RAD51-interacting protein | 2.8 |
| 35 | 105288 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DNAJ domain-containing protein MCJ [H.sapiens] | 1.9 |
| | 105302 | AA700122 | Hs.3355 | sentrin-specific protease | 8.0 |
| | 105331 | AW270037 | Hs.179507 | KIAA0779 protein | 1.8 |
| | 105359 | NM_016015 | Hs.8054 | CGI-68 protein | 8.2 |
| | 105366 | BE264645 | Hs.282093 | hypothetical protein FLJ21918 | 5.0 |
| 40 | 105373 | AW887701 | Hs.32356 | hypothetical protein FLJ20628 | 2.5 |
| | 105374 | BE242803 | Hs.262823 | hypothetical protein FLJ10326 | 2.2 |
| | 105387 | AW592146 | Hs.108636 | membrane protein CH1 | 2.3 |
| | 105393 | AF167570 | Hs.256583 | interleukin enhancer binding factor 3, 90kD | 5.4 |
| | 105399 | BE386877 | Hs.334811 | Npw38-binding protein NpwBP | 1.6 |
| 45 | 105400 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 1.6 |
| | 105445 | AA252395 | Hs.226318 | gb:zs12g10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685026 3', mRNA sequence, | 5.0 |
| | 105507 | BE268348 | Hs.226318 | CCR4-NOT transcription complex, subunit 7 | 1.6 |
| | 105529 | AA113449 | Hs.32471 | hypothetical protein FLJ20364 | 1.3 |
| | 105530 | AB023179 | Hs.9059 | KIAA0962 protein | 3.4 |
| 50 | 105547 | AA262640 | Hs.27445 | unknown | 9.3 |
| | 105564 | BE616694 | Hs.288042 | hypothetical protein FLJ14299 | 1.4 |
| | 105596 | AA579535 | Hs.18490 | hypothetical protein FLJ20452 | 10.9 |
| | 105597 | AF054284 | Hs.334826 | splicing factor 3b, subunit 1, 155kD | 2.9 |
| | 105608 | AI808201 | Hs.287863 | hypothetical protein FLJ12475 | 1.7 |
| 55 | 105610 | AA280072 | Hs.99872 | fetal Alzheimer antigen | 1.4 |
| | 105617 | AK000892 | Hs.4069 | glucocorticoid modulatory element binding protein 1 | 1.7 |
| | 105620 | AW302245 | Hs.181390 | casein kinase 1, gamma 2 | 5.5 |
| | 105658 | AA985190 | Hs.246875 | hypothetical protein FLJ20059 | 9.4 |
| | 105697 | AW499988 | Hs.27801 | zinc finger protein 278 | 2.0 |
| 60 | 105708 | R26944 | Hs.180777 | Homo sapiens mRNA; cDNA DKFZp564M0264 (from clone DKFZp564M0264) | 1.7 |
| | 105743 | BE246502 | Hs.9598 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short | 2.6 |
| | 105746 | AW151952 | Hs.46679 | hypothetical protein FLJ20739 | 1.5 |
| | 105759 | AI123118 | Hs.15159 | chemokine-like factor, alternatively spliced | 1.3 |
| | 105771 | AI267720 | Hs.153221 | synovial sarcoma, translocated to X chromosome | 1.6 |
| 65 | 105820 | AA741336 | Hs.152108 | transcriptional unit N143 | 2.2 |
| | 105826 | AA478756 | Hs.194477 | E3 ubiquitin ligase SMURF2 | 1.3 |
| | 105856 | AI262106 | Hs.12653 | ESTs | 2.4 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 105858 | AF151066 | Hs.281428 | hypothetical protein | 2.9 |
| | 105875 | AK001708 | Hs.32271 | hypothetical protein FLJ10846 | 1.4 |
| | 105930 | AF016371 | Hs.9880 | peptidyl prolyl isomerase H (cyclophilin H) | 5.2 |
| | 106000 | AW194426 | Hs.20726 | ESTs | 1.7 |
| 5 | 106011 | AW081202 | Hs.12284 | Homo sapiens, clone IMAGE:2989556, mRNA, partial cds | 2.8 |
| | 106017 | AA477956 | Hs.26268 | ESTs | 1.4 |
| | 106073 | AL157441 | Hs.17834 | downstream neighbor of SON | 1.4 |
| | 106078 | AA130158 | Hs.19977 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION | 1.6 |
| | 106094 | AA533491 | Hs.23317 | hypothetical protein FLJ14681 | 6.8 |
| 10 | 106140 | AB006624 | Hs.14912 | KIAA0286 protein | 1.6 |
| | 106271 | AA251393 | Hs.289052 | Homo sapiens, Similar to RIKEN cDNA 5430429M05 gene, clone MGC:13155, mRNA, complete cds | 10.8 |
| | 106288 | AB037742 | Hs.24336 | KIAA1321 protein | 1.3 |
| | 106300 | Y10043 | Hs.19114 | high-mobility group (nonhistone chromosomal) protein 4 | 3.6 |
| | 106333 | AL043114 | Hs.22410 | ESTs, Weakly similar to A54849 collagen alpha 1(VII) chain precursor [H.sapiens] | 5.4 |
| 15 | 106350 | AK001404 | Hs.194698 | cyclin B2 | 5.7 |
| | 106359 | AW390282 | Hs.31130 | transmembrane 7 superfamily member 2 | 6.3 |
| | 106381 | AB040916 | Hs.24106 | KIAA1483 protein | 6.5 |
| | 106389 | AW748420 | Hs.6236 | Homo sapiens cDNA: FLJ21487 fis, clone COL05419 | 2.2 |
| | 106457 | AF119256 | Hs.27801 | zinc finger protein 278 | 2.7 |
| 20 | 106470 | D63078 | Hs.186180 | Homo sapiens cDNA: FLJ23038 fis, clone LNG02039 | 2.3 |
| | 106531 | AA454036 | Hs.8832 | ESTs | 1.6 |
| | 106586 | AA243837 | Hs.57787 | ESTs | 1.6 |
| | 106589 | AK000933 | Hs.28661 | Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702 | 2.4 |
| | 106610 | AA458882 | Hs.79732 | fibulin 1 | 7.9 |
| 25 | 106624 | NM_003595 | Hs.26350 | tyrosylprotein sulfotransferase 2 | 7.7 |
| | 106650 | AL049951 | Hs.22370 | Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122) | 1.8 |
| | 106669 | AV657117 | Hs.184164 | ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens] | 1.3 |
| | 106713 | BE614802 | Hs.184352 | hypothetical protein FLJ12549 | 4.5 |
| | 106717 | AA600357 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-binding protein | 1.3 |
| 30 | 106723 | BE388094 | Hs.21857 | ESTs | 1.6 |
| | 106795 | AF174487 | Hs.293753 | Bcl-2-related ovarian killer protein-like | 5.7 |
| | 106829 | AW959893 | Hs.27099 | hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2 | 16.2 |
| | 106831 | BE564871 | Hs.29463 | centrin, EF-hand protein, 3 (CDC31 yeast homolog) | 1.5 |
| | 106846 | AB037744 | Hs.34892 | KIAA1323 protein | 2.2 |
| 35 | 106852 | AF151031 | Hs.300631 | hypothetical protein | 1.3 |
| | 106873 | N49809 | Hs.11197 | Homo sapiens, clone IMAGE:3343149, mRNA, partial cds | 16.8 |
| | 106886 | W79171 | Hs.9567 | GL002 protein | 1.5 |
| | 106906 | AA861271 | Hs.222024 | transcription factor BMAL2 | 2.2 |
| 40 | 106920 | AK001838 | Hs.296323 | serum/glucocorticoid regulated kinase | 3.3 |
| | 106945 | AK000511 | Hs.6294 | hypothetical protein DKFZp434L1435 similar to valyl tRNA synthetase | 6.8 |
| | 106973 | BE156256 | Hs.11923 | hypothetical protein | 6.6 |
| | 106977 | AL043152 | Hs.50421 | KIAA0203 gene product | 4.8 |
| | 106978 | AW631480 | Hs.8688 | ESTs | 6.0 |
| | 107004 | AA146872 | Hs.300700 | hypothetical protein FLJ20727 | 1.3 |
| 45 | 107029 | AF264750 | Hs.288971 | myeloid/lymphoid or mixed-lineage leukemia 3 | 1.8 |
| | 107071 | AW385224 | Hs.35198 | ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) | 1.7 |
| | 107113 | AK000733 | Hs.23900 | GTPase activating protein | 2.5 |
| | 107125 | AK000512 | Hs.69388 | hypothetical protein FLJ20505 | 1.7 |
| 50 | 107136 | AV661958 | Hs.8207 | GK001 protein | 4.6 |
| | 107136 | AV661958 | Hs.8207 | GK001 protein | 3.3 |
| | 107146 | AK001455 | Hs.5198 | Down syndrome critical region gene 2 | 2.0 |
| | 107151 | AW378065 | Hs.8687 | ESTs | 6.3 |
| | 107155 | AW391927 | Hs.7946 | KIAA1288 protein | 33.5 |
| | 107174 | BE122762 | Hs.25338 | ESTs | 5.2 |
| 55 | 107197 | W15477 | Hs.64639 | glioma pathogenesis-related protein | 6.1 |
| | 107221 | AW888411 | Hs.81915 | leukemia-associated phosphoprotein p18 (stathmin) | 17.4 |
| | 107243 | BE219716 | Hs.34727 | ESTs, Moderately similar to I38759 zinc finger/leucine zipper protein [H.sapiens] | 7.4 |
| | 107248 | AW263124 | Hs.315111 | nuclear receptor co-repressor/HDAC3 complex subunit | 1.8 |
| | 107263 | D60341 | Hs.21198 | translocase of outer mitochondrial membrane 70 (yeast) homolog A | 6.6 |
| 60 | 107265 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION | 2.5 |
| | 107298 | N95657 | Hs.6820 | ESTs, Moderately similar to YOJ1_CAEEL HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN | 2.5 |
| | 107298 | N95657 | Hs.6820 | ESTs, Moderately similar to YOJ1_CAEEL H | 1.7 |
| | 107299 | BE277457 | Hs.30661 | hypothetical protein MGC4606 | 3.2 |
| | 107316 | T63174 | Hs.193700 | Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324) | 2.0 |
| 65 | 107354 | NM_006299 | Hs.96448 | zinc finger protein 193 | 5.0 |
| | 107392 | AW299900 | Hs.267632 | TATA element modulatory factor 1 | 1.2 |
| | 107481 | AA307703 | Hs.279766 | kinesin family member 4A | 1.6 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|--|
| | 107529 | BE515065 | Hs.296585 | nucleolar protein (KKE/D repeat) | 3.0 | |
| | 107554 | AA001386 | Hs.59844 | ESTs | 1.3 | |
| | 107681 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION | 2.2 | |
| | 107772 | AA018587 | Hs.303055 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION | 2.1 | |
| 5 | 107859 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 | 8.4 | |
| | 107901 | L42612 | Hs.335952 | keratin 6B | 2.5 | |
| | 107901 | L42612 | Hs.335952 | keratin 6B | 1.6 | |
| | 107922 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 2.2 | |
| | 107974 | AW956103 | Hs.61712 | pyruvate dehydrogenase kinase, isoenzyme 1 | 6.7 | |
| 10 | 108040 | AL121031 | Hs.159971 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 | 1.5 | |
| | 108230 | AA054224 | Hs.59847 | ESTs | 1.3 | |
| | 108274 | AF129535 | Hs.272027 | F-box only protein 5 | 7.1 | |
| | 108296 | N31256 | Hs.161623 | ESTs | 2.5 | |
| | 108496 | AA083069 | Hs.339659 | ESTs | 3.5 | |
| 15 | 108607 | BE300380 | Hs.69476 | Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328 | 3.4 | |
| | 108621 | AA101809 | Hs.182685 | ESTs | 1.6 | |
| | 108634 | AW022410 | Hs.69507 | ESTs | 1.7 | |
| | 108647 | BE546947 | Hs.44276 | homeo box C10 | 9.8 | |
| | 108695 | AB029000 | Hs.70823 | KIAA1077 protein | 7.2 | |
| 20 | 108717 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 1.3 | |
| | 108740 | AI089575 | Hs.9071 | progesterone membrane binding protein | 2.7 | |
| | 108828 | AK001693 | Hs.273344 | DKFZP564O0463 protein | 1.8 | |
| | 108859 | AL121500 | Hs.178904 | ESTs | 1.5 | |
| | 108872 | H06720 | Hs.111680 | endosulfine alpha | 2.1 | |
| 25 | 108891 | AI801235 | Hs.48480 | ESTs | 5.3 | |
| | 108894 | AK001431 | Hs.5105 | hypothetical protein FLJ10569 | 4.0 | |
| | 108955 | AA149754 | Hs.195155 | Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds | 5.6 | |
| | 108982 | AA151708 | Hs.171980 | homeo box (expressed in ES cells) 1 | 1.6 | |
| | 108987 | AA152178 | Hs.23467 | hypothetical protein FLJ10633 | 6.2 | |
| 30 | 109002 | AB028987 | Hs.72134 | KIAA1064 protein | 1.7 | |
| | 109011 | AA156542 | Hs.72127 | ESTs | 1.4 | |
| | 109026 | AA157811 | | gb:zo35d07.s1 Stratagene colon (937204) Homo sapiens cDNA clone 3' similar to contains Alu repetitive | 5.3 | |
| | 109058 | AA164293 | Hs.72545 | ESTs | 2.9 | |
| | 109101 | AW608930 | Hs.52184 | hypothetical protein FLJ20618 | 1.6 | |
| 35 | 109112 | AW419196 | Hs.257924 | hypothetical protein FLJ13782 | 3.2 | |
| | 109124 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 1.7 | |
| | 109139 | AJ132592 | Hs.59757 | zinc finger protein 281 | 2.6 | |
| | 109166 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkinesin 6) | 2.9 | |
| | 109198 | BE566742 | Hs.58169 | highly expressed in cancer, rich in leucine heptad repeats | 2.0 | |
| 40 | 109213 | NM_016603 | Hs.82035 | potential nuclear protein C5ORF5; GAP-like protein | 5.3 | |
| | 109220 | AW958181 | Hs.189998 | ESTs | 5.7 | |
| | 109233 | AL077281 | Hs.170285 | nucleoporin 214kD (CAIN) | 5.3 | |
| | 109270 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DNAJ domain-containing protein MCJ [H.sapiens] | 1.4 | |
| | 109273 | AA375752 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (from clone DKFZp586F1822) | 2.9 | |
| 45 | 109313 | AF153201 | Hs.86276 | C2H2 (Kruppel-type) zinc finger protein | 1.3 | |
| | 109341 | AA213506 | Hs.115099 | EST | 2.9 | |
| | 109391 | AL096858 | Hs.184245 | KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog | 1.5 | |
| | 109420 | H83603 | Hs.40408 | homeo box C9 | 2.2 | |
| | 109426 | N30531 | Hs.42215 | protein phosphatase 1, regulatory subunit 6 | 3.0 | |
| 50 | 109429 | AI160029 | Hs.61438 | ESTs | 1.9 | |
| | 109445 | AA232103 | Hs.189915 | ESTs | 1.8 | |
| | 109450 | AB032969 | Hs.173042 | KIAA1143 protein | 3.7 | |
| | 109468 | NM_015310 | Hs.6763 | KIAA0942 protein | 3.2 | |
| | 109478 | AW074143 | Hs.87134 | ESTs | 2.0 | |
| 55 | 109570 | L40027 | Hs.118890 | glycogen synthase kinase 3 alpha | 2.1 | |
| | 109662 | F02614 | Hs.27319 | ESTs | 1.4 | |
| | 109825 | R71264 | Hs.16798 | ESTs | 1.3 | |
| | 110039 | H11938 | Hs.21907 | histone acetyltransferase | 2.0 | |
| | 110056 | AA503041 | Hs.279009 | matrix Gla protein | 2.5 | |
| 60 | 110085 | AA603840 | Hs.29956 | KIAA0460 protein | 1.7 | |
| | 110110 | T07353 | Hs.7948 | ESTs | 2.9 | |
| | 110129 | R51853 | Hs.226429 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION | 1.7 | |
| | 110154 | NM_014521 | Hs.17667 | SH3-domain binding protein 4 | 4.2 | |
| | 110240 | AI668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME P450 4A11 PRECURSOR [H.sapiens] | 4.2 | |
| 65 | 110242 | N41744 | Hs.19978 | CGI-30 protein | 1.3 | |
| | 110259 | H28428 | Hs.32406 | ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] | 2.2 | |
| | 110312 | BE256986 | Hs.11896 | hypothetical protein FLJ12089 | 2.1 | |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 110330 | AI288666 | Hs.16621 | DKFZP4341116 protein | 6.2 |
| | 110501 | H55748 | | gb:yq94a01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:203400 3' | 6.1 |
| | 110504 | H55915 | Hs.210859 | hypothetical protein FLJ11016 | 6.1 |
| | 110525 | H57330 | Hs.37430 | EST | 6.3 |
| 5 | 110568 | AK001160 | Hs.5999 | hypothetical protein FLJ10298 | 1.3 |
| | 110699 | T97586 | Hs.18090 | ESTs | 1.8 |
| | 110705 | AB007902 | Hs.32168 | KIAA0442 protein | 1.6 |
| | 110742 | AW190338 | Hs.28029 | hypothetical protein MGC11256 | 7.6 |
| | 110761 | AL138077 | Hs.16157 | hypothetical protein FLJ12707 | 2.5 |
| 10 | 110762 | BE044245 | Hs.30011 | hypothetical protein MGC2963 | 9.3 |
| | 110765 | AK000322 | Hs.18457 | hypothetical protein FLJ20315 | 5.5 |
| | 110769 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HEMBA1006364 | 2.1 |
| | 110799 | AI089660 | Hs.323401 | dpy-30-like protein | 1.5 |
| | 110805 | T25829 | Hs.24048 | FK506 binding protein precursor | 6.6 |
| 15 | 110813 | AA767373 | Hs.35669 | ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION | 5.7 |
| | 110820 | R33261 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens] | 3.4 |
| | 110840 | N31598 | Hs.12727 | hypothetical protein FLJ21610 | 1.7 |
| | 110844 | AI740792 | Hs.167531 | methylenetetrahydrofolate-Coenzyme A carboxylase 2 (beta) | 1.7 |
| | 110854 | BE612992 | Hs.27931 | hypothetical protein FLJ10607, similar to glucosamine-phosphate N-acetyltransferase | 4.7 |
| 20 | 110856 | AA992380 | | gb:cl37g06.s1 Soares_testis_NHT Homo sapiens cDNA clone 3' similar to contains element | 2.3 |
| | 110885 | BE384447 | Hs.16034 | hypothetical protein MGC13186 | 3.5 |
| | 110897 | AL117430 | Hs.6880 | DKFZP434D156 protein | 2.2 |
| | 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 2.6 |
| | 110918 | H04360 | Hs.24283 | ESTs, Moderately similar to reduced expression in cancer [H.sapiens] | 1.9 |
| 25 | 110958 | NM_005864 | Hs.24587 | signal transduction protein (SH3 containing) | 6.7 |
| | 110963 | AK002180 | Hs.11449 | DKFZP564O123 protein | 2.0 |
| | 110981 | AK001980 | Hs.24284 | ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 2 | 1.3 |
| | 110984 | AW613287 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | 1.8 |
| | 111125 | N63823 | Hs.269115 | ESTs, Moderately similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens] | 3.6 |
| 30 | 111132 | AB037807 | Hs.83293 | hypothetical protein | 2.1 |
| | 111164 | N46180 | Hs.122489 | Homo sapiens cDNA FLJ13289 fis, clone OVARC1001170 | 2.3 |
| | 111172 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321 | 3.7 |
| | 111174 | AL050166 | Hs.26295 | Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122) | 7.5 |
| | 111179 | AK000136 | Hs.10760 | asporin (LRR class 1) | 7.1 |
| 35 | 111184 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HEP08257 | 6.7 |
| | 111184 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 3.3 |
| | 111189 | N67603 | Hs.272130 | ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens] | 3.6 |
| | 111216 | AW139408 | Hs.152940 | ESTs | 1.5 |
| | 111221 | AB037782 | Hs.15119 | KIAA1361 protein | 2.6 |
| 40 | 111223 | AA852773 | Hs.334838 | KIAA1866 protein | 4.6 |
| | 111239 | N90956 | Hs.17230 | hypothetical protein FLJ22087 | 7.9 |
| | 111285 | AA778711 | Hs.4310 | eukaryotic translation initiation factor 1A | 6.9 |
| | 111299 | AB033091 | Hs.74313 | KIAA1265 protein | 5.0 |
| | 111312 | AI523913 | Hs.34504 | ESTs | 3.8 |
| 45 | 111318 | T99755 | Hs.334728 | ESTs | 1.2 |
| | 111337 | AA837396 | Hs.263925 | LIS1-interacting protein NUDE1, rat homolog | 5.1 |
| | 111352 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114 | 2.2 |
| | 111370 | AI478658 | Hs.94631 | brefeldin A-inhibited guanine nucleotide-exchange protein 1 | 2.8 |
| | 111384 | N94606 | Hs.288969 | HSCARG protein | 2.2 |
| 50 | 111389 | AK000987 | Hs.169111 | oxidation resistance 1 | 2.1 |
| | 111391 | NM_003896 | Hs.225939 | sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) | 5.1 |
| | 111392 | W46342 | Hs.325081 | Homo sapiens, clone IMAGE:3659680, mRNA, partial cds | 8.4 |
| | 111452 | R02354 | Hs.15999 | ESTs | 2.7 |
| | 111486 | AI051194 | Hs.227978 | EST | 6.5 |
| 55 | 111549 | W90638 | Hs.20321 | ESTs, Moderately similar to ZRF1_HUMAN ZUOTIN RELATED FACTOR-1 (M-PHASE | 1.4 |
| | 111585 | R10720 | Hs.20670 | EST | 1.6 |
| | 111627 | R52656 | Hs.21691 | ESTs | 1.6 |
| | 111870 | AB037834 | Hs.18685 | Homo sapiens mRNA for KIAA1413 protein, partial cds | 2.4 |
| | 111937 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016) | 10.6 |
| 60 | 111944 | AW083791 | Hs.21263 | suppressor of potassium transport defect 3 | 6.6 |
| | 111987 | NM_015310 | Hs.6763 | KIAA0942 protein | 5.1 |
| | 112134 | R41823 | Hs.7413 | ESTs; calyntenin-2 | 2.8 |
| | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 14.6 |
| | 112388 | R46071 | Hs.301693 | Homo sapiens, clone IMAGE:3638994, mRNA, partial cds | 9.0 |
| 65 | 112456 | NM_016248 | Hs.232076 | A kinase (PRKA) anchor protein 11 | 1.4 |
| | 112464 | AW007287 | Hs.28538 | Homo sapiens cDNA: FLJ21086 fis, clone CAS03272 | 1.4 |
| | 112506 | AI742756 | Hs.26079 | ESTs | 3.2 |

| | | | | | | |
|----|--------|----------|-----------|--|------|--|
| | 112513 | R68425 | Hs.13809 | hypothetical protein FLJ10648 | 2.0 | |
| | 112752 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 1.8 | |
| | 112884 | AK000004 | Hs.5013 | Homo sapiens mRNA for FLJ00004 protein, partial cds | 6.6 | |
| | 112923 | T10258 | Hs.5037 | EST | 1.5 | |
| 5 | 112936 | AW970826 | Hs.6185 | KIAA1557 protein | 3.2 | |
| | 112958 | R61388 | Hs.6724 | ESTs | 6.0 | |
| | 112966 | Z44718 | Hs.102548 | glucocorticoid receptor DNA binding factor 1 | 6.4 | |
| | 112978 | AK000272 | Hs.7099 | hypothetical protein FLJ20265 | 1.2 | |
| | 112995 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYKl protein [M.musculus] | 5.6 | |
| 10 | 112996 | BE276112 | Hs.7165 | zinc finger protein 259 | 2.0 | |
| | 113047 | AI571940 | Hs.7549 | ESTs | 1.9 | |
| | 113049 | AW965190 | Hs.7560 | Homo sapiens mRNA for KIAA1729 protein, partial cds | 2.4 | |
| | 113089 | T40707 | Hs.270862 | ESTs | 1.3 | |
| 15 | 113196 | T57317 | | gb:yb51a03.s1 Stratagene fetal spleen (937205) Homo sapiens cDNA clone IMAGE:74668 3', | 1.7 | |
| | 113248 | T63857 | | gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens cDNA clone 3', mRNA sequence | 2.8 | |
| | 113254 | AK002180 | Hs.11449 | DKFZP564O123 protein | 1.3 | |
| | 113277 | AW971049 | Hs.11774 | protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) | 3.2 | |
| | 113429 | AA688021 | Hs.179808 | ESTs | 1.2 | |
| | 113499 | AI467908 | Hs.8882 | ESTs | 5.9 | |
| 20 | 113547 | H59588 | Hs.15233 | ESTs | 2.0 | |
| | 113554 | AW503990 | Hs.142442 | HP1-BP74 | 3.6 | |
| | 113647 | AA813887 | Hs.188173 | Homo sapiens cDNA FLJ12187 fis, clone MAMMA1000831 | 1.3 | |
| | 113702 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121497 3', | 4.4 | |
| | 113722 | AV653556 | Hs.184411 | albumin | 1.3 | |
| 25 | 113759 | AW499665 | Hs.9456 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 | 1.2 | |
| | 113777 | BE266947 | Hs.10590 | zinc finger protein 313 | 13.4 | |
| | 113783 | AL359588 | Hs.7041 | hypothetical protein DKFZp762B226 | 1.7 | |
| | 113791 | AI269096 | Hs.135578 | chitinase, di-N-acetyl- | 1.3 | |
| | 113808 | W44735 | Hs.9286 | Homo sapiens cDNA: FLJ21278 fis, clone COL01832 | 3.3 | |
| 30 | 113811 | BE207480 | Hs.6994 | Homo sapiens cDNA: FLJ22044 fis, clone HEP09141 | 3.1 | |
| | 113817 | H13325 | Hs.332795 | hypothetical protein DKFZp761O17121 | 3.2 | |
| | 113826 | AW378212 | Hs.24809 | hypothetical protein FLJ10826 | 2.3 | |
| | 113834 | T26483 | Hs.6059 | EGF-containing fibulin-like extracellular matrix protein 2 | 11.3 | |
| | 113868 | W57902 | Hs.90744 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | 2.7 | |
| 35 | 113870 | AL079314 | Hs.16537 | hypothetical protein, similar to (U06944) PRAJA1 | 6.1 | |
| | 113885 | AW959486 | Hs.21732 | ESTs | 6.6 | |
| | 113923 | AW953484 | Hs.3849 | hypothetical protein FLJ22041 similar to FK506 binding proteins | 1.9 | |
| | 113989 | W87544 | Hs.268828 | ESTs | 1.2 | |
| | 114022 | AI539519 | Hs.120969 | Homo sapiens cDNA FLJ11562 fis, clone HEMBA1003197 | 5.4 | |
| 40 | 114030 | AI825386 | Hs.164478 | hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 | 9.4 | |
| | 114060 | AB029551 | Hs.7910 | RING1 and YY1 binding protein | 1.8 | |
| | 114196 | AF017445 | Hs.150926 | lucose-1-phosphate guanylyltransferase | 1.5 | |
| | 114226 | AB028968 | Hs.7989 | KIAA1045 protein | 1.8 | |
| | 114253 | BE149866 | Hs.14831 | Homo sapiens, Similar to zinc finger protein 136 (clone pHZ-20), clone MGC:10647, mRNA, complete cds | 2.3 | |
| 45 | 114262 | AL117518 | Hs.3686 | KIAA0978 protein | 1.4 | |
| | 114275 | AW515443 | Hs.306117 | KIAA0306 protein | 15.8 | |
| | 114292 | AI815395 | Hs.184641 | fatty acid desaturase 2 | 1.9 | |
| | 114309 | AA332453 | Hs.20824 | CGI-85 protein | 2.4 | |
| | 114392 | AA249590 | Hs.100748 | ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus] | 1.8 | |
| 50 | 114407 | BE539976 | Hs.103305 | Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425) | 1.2 | |
| | 114455 | H37908 | Hs.271616 | ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE | 5.5 | |
| | 114463 | AL120247 | Hs.40109 | KIAA0872 protein | 5.2 | |
| | 114464 | AI091713 | Hs.106597 | Homo sapiens, Similar to RIKEN cDNA 1110012M11 gene, clone IMAGE:3688605, mRNA, partial cds | 1.2 | |
| | 114471 | AA028074 | Hs.104613 | RP42 homolog | 1.8 | |
| 55 | 114480 | BE066778 | Hs.151678 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) | 13.4 | |
| | 114671 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 1.9 | |
| | 114698 | AA476966 | Hs.110857 | polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa) | 3.5 | |
| | 114730 | AI373544 | Hs.331328 | intermediate filament protein syncoilin | 3.8 | |
| | 114767 | AI859865 | Hs.154443 | minichromosome maintenance deficient (S. cerevisiae) 4 | 1.6 | |
| 60 | 114774 | AV656017 | Hs.184325 | CGI-76 protein | 3.1 | |
| | 114798 | AA159181 | Hs.54900 | serologically defined colon cancer antigen 1 | 3.5 | |
| | 114860 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.3 | |
| | 114895 | AA236177 | Hs.76591 | KIAA0887 protein | 7.1 | |
| | 114896 | BE539101 | Hs.5324 | hypothetical protein | 1.3 | |
| 65 | 114911 | AA236672 | | gb:zt29f02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:723771 3', mRNA sequence. | 1.5 | |
| | 114930 | AA237022 | Hs.188717 | ESTs | 2.0 | |
| | 114938 | AA242834 | Hs.58384 | ESTs | 2.9 | |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 114965 | AI733881 | Hs.72472 | BMP-R1B | 2.3 |
| | 115023 | AF102546 | Hs.63931 | dachshund (Drosophila) homolog | 1.3 |
| | 115038 | AA252360 | Hs.87968 | tol-like receptor 9 | 1.6 |
| | 115061 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1913076 | 11.8 |
| 5 | 115062 | AA253314 | Hs.154103 | LIM protein (similar to rat protein kina | 1.5 |
| | 115117 | AI670847 | Hs.5324 | hypothetical protein | 1.5 |
| | 115121 | AI634549 | Hs.88155 | ESTs | 2.8 |
| | 115206 | AW183695 | Hs.186572 | ESTs | 2.5 |
| | 115221 | AW365434 | Hs.79741 | hypothetical protein FLJ10116 | 1.5 |
| 10 | 115239 | BE251328 | Hs.73291 | hypothetical protein FLJ10881 | 1.3 |
| | 115242 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE | 1.4 |
| | 115278 | AK002163 | Hs.301724 | hypothetical protein FLJ11301 | 1.5 |
| | 115285 | AW972872 | Hs.293736 | ESTs | 2.4 |
| | 115291 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 6.2 |
| 15 | 115400 | AI215069 | Hs.89113 | ESTs | 6.6 |
| | 115468 | AA314349 | Hs.48499 | tumor antigen SLP-8p | 7.4 |
| | 115471 | AK001376 | Hs.59346 | hypothetical protein FLJ10514 | 1.4 |
| | 115479 | AW301608 | Hs.278188 | ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens] | 4.0 |
| | 115496 | AW247593 | Hs.71819 | eukaryotic translation initiation factor 4E binding protein 1 | 16.3 |
| 20 | 115500 | Y14443 | Hs.88219 | zinc finger protein 200 | 5.0 |
| | 115553 | AJ275986 | Hs.71414 | transcription factor (SMIF gene) | 2.5 |
| | 115581 | AI540842 | Hs.61082 | ESTs | 6.1 |
| | 115587 | BE081342 | Hs.283037 | HSPC039 protein | 2.9 |
| | 115590 | AA399477 | Hs.67896 | 7-60 protein | 5.3 |
| 25 | 115646 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glucose transporter), member 10 | 4.7 |
| | 115652 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 10.6 |
| | 115655 | AL048269 | Hs.288544 | Homo sapiens, clone MGC:16063, mRNA, complete cds | 12.7 |
| | 115663 | AI138785 | Hs.40507 | ESTs | 2.0 |
| | 115676 | AA953006 | Hs.88143 | ESTs | 3.0 |
| 30 | 115690 | AA625132 | Hs.44159 | hypothetical protein FLJ21615 | 1.7 |
| | 115693 | AF231023 | Hs.55173 | cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog | 6.8 |
| | 115715 | BE395161 | Hs.1390 | proteasome (prosome, macropain) subunit, beta type, 2 | 1.7 |
| | 115734 | AI950339 | Hs.40782 | ESTs | 2.6 |
| | 115811 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.1 |
| 35 | 115823 | AI732742 | Hs.87440 | ESTs | 2.1 |
| | 115837 | AI675217 | Hs.42761 | ESTs | 1.3 |
| | 115844 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 4.4 |
| | 115866 | AW062629 | Hs.52081 | KIAA0867 protein | 7.2 |
| | 115875 | N55669 | Hs.333823 | mitochondrial ribosomal protein L13 | 1.2 |
| 40 | 115941 | AI867451 | Hs.46679 | hypothetical protein FLJ20739 | 5.5 |
| | 115968 | AB037753 | Hs.62767 | KIAA1332 protein | 9.8 |
| | 116003 | BE275469 | Hs.66493 | Down syndrome critical region gene 5 | 1.4 |
| | 116011 | AL359053 | Hs.57664 | Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735 | 2.4 |
| | 116108 | AA770688 | Hs.28777 | H2A histone family, member L | 1.8 |
| 45 | 116134 | BE243834 | Hs.50441 | CGI-04 protein | 1.4 |
| | 116189 | N35719 | Hs.44749 | ESTs, Moderately similar to T00358 hypothetical protein KIAA0684 [H.sapiens] | 1.2 |
| | 116195 | AW821113 | Hs.72402 | ESTs | 2.1 |
| | 116238 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 1.7 |
| | 116246 | AF265555 | Hs.250646 | baculoviral IAP repeat-containing 6 | 1.7 |
| 50 | 116262 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 1.7 |
| | 116298 | AI955411 | Hs.94109 | Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133 | 1.9 |
| | 116318 | AF097645 | Hs.58570 | deleted in cancer 1; RNA helicase HDB/DICE1 | 4.9 |
| | 116325 | AI472106 | Hs.49303 | Homo sapiens cDNA FLJ11663 fis, clone HEMBA1004631 | 1.4 |
| | 116336 | AL133033 | Hs.4084 | KIAA1025 protein | 1.9 |
| 55 | 116339 | AK000290 | Hs.44033 | dipeptidyl peptidase 8 | 1.5 |
| | 116350 | AA497129 | Hs.184771 | nuclear factor I/C (CCAAT-binding transcription factor) | 1.9 |
| | 116358 | AI149586 | Hs.38125 | interferon-induced protein 75, 52kD | 1.9 |
| | 116365 | N50174 | Hs.46765 | ESTs | 6.1 |
| | 116368 | N90466 | Hs.71109 | KIAA1229 protein | 1.6 |
| 60 | 116417 | AW499664 | Hs.12484 | Human clone 23826 mRNA sequence | 7.4 |
| | 116436 | AA161411 | Hs.58668 | chromosome 21 open reading frame 57 | 2.1 |
| | 116462 | AF218313 | Hs.236828 | putative helicase RUVBL | 1.5 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.1 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 1.2 |
| 65 | 116575 | AA312572 | Hs.6241 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) | 1.5 |
| | 116637 | AK001043 | Hs.92033 | integrin-linked kinase-associated serine/threonine phosphatase 2C | 2.7 |
| | 116640 | X89984 | Hs.211563 | B-cell CLL/lymphoma 7A | 2.3 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|--|
| | 116700 | AI800202 | Hs.317589 | hypothetical protein MGC10765 | 1.4 | |
| | 116705 | AW074819 | Hs.12313 | hypothetical protein FLJ14566 | 3.4 | |
| | 116732 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] | 2.9 | |
| | 116921 | AW068115 | Hs.821 | biglycan | 8.3 | |
| 5 | 116926 | H73608 | Hs.290830 | ESTs | 1.7 | |
| | 117034 | U72209 | Hs.180324 | YY1-associated factor 2 | 3.4 | |
| | 117132 | AI393666 | Hs.42315 | p10-binding protein | 5.2 | |
| | 117247 | N21032 | | gb:yx46f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264803 3', mRNA sequence. | 5.5 | |
| | 117276 | N71183 | Hs.121806 | Homo sapiens cDNA FLJ11971 fis, clone HEMBB1001208 | 1.5 | |
| 10 | 117284 | AK001701 | Hs.183779 | Homo sapiens cDNA FLJ10590 fis, clone NT2RP2004392, weakly similar to MNN4 PROTEIN | 2.0 | |
| | 117367 | AI041793 | Hs.42502 | ESTs | 2.0 | |
| | 117368 | AI878942 | Hs.90336 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J | 2.1 | |
| | 117382 | AF150275 | Hs.40173 | ESTs | 2.7 | |
| | 117412 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic acid transporters), member 6 | 1.4 | |
| 15 | 117557 | AF123050 | Hs.44532 | diubiquitin | 3.4 | |
| | 117588 | N34895 | Hs.44648 | ESTs | 3.4 | |
| | 117745 | BE294925 | Hs.46680 | CGI-12 protein | 3.0 | |
| | 117754 | AA121673 | Hs.59757 | zinc finger protein 281 | 1.9 | |
| | 117879 | N54706 | Hs.303025 | chromosome 11 open reading frame 24 | 1.8 | |
| 20 | 117881 | AF161470 | Hs.260622 | butyrate-induced transcript 1 | 5.7 | |
| | 117904 | BE540675 | Hs.332938 | hypothetical protein MGC5370 | 5.9 | |
| | 117911 | AL137379 | Hs.47125 | hypothetical protein FLJ13912 | 1.7 | |
| | 117933 | Y10518 | Hs.116470 | hypothetical protein FLJ20048 | 1.7 | |
| | 117983 | AL110246 | Hs.47367 | KIAA1785 protein | 5.4 | |
| 25 | 118078 | N54321 | Hs.47790 | EST | 5.2 | |
| | 118301 | AA453902 | Hs.293264 | ESTs | 2.6 | |
| | 118429 | AA243332 | Hs.74649 | cytochrome c oxidase subunit VIc | 2.5 | |
| | 118472 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.1 | |
| | 118488 | AJ277275 | Hs.50102 | rapa-2 (rapa gene) | 1.2 | |
| 30 | 118509 | N22617 | Hs.43228 | Homo sapiens cDNA FLJ11835 fis, clone HEMBA1006595 | 1.5 | |
| | 118528 | AI949952 | Hs.49397 | ESTs | 7.4 | |
| | 118656 | AI458020 | Hs.293287 | ESTs | 2.5 | |
| | 118670 | AA332845 | Hs.152618 | ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens] | 1.2 | |
| | 118698 | AB033113 | Hs.50187 | KIAA1287 protein | 2.1 | |
| 35 | 118737 | AA199686 | | gb:zq75g09.r1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone IMAGE:647488 5' | 5.2 | |
| | 118925 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION | 1.4 | |
| | 118984 | AI668709 | Hs.240722 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION | 3.6 | |
| | 118986 | AF148713 | Hs.125830 | bladder cancer overexpressed protein | 4.8 | |
| | 119206 | W24781 | Hs.293798 | KIAA1710 protein | 1.7 | |
| 40 | 119235 | AW453069 | Hs.3657 | activity-dependent neuroprotective protein | 2.2 | |
| | 119235 | AW453069 | Hs.3657 | activity-dependent neuroprotective prote | 1.6 | |
| | 119265 | BE539706 | Hs.285363 | ESTs | 1.4 | |
| | 119279 | N57568 | Hs.48028 | EST | 25.1 | |
| | 119298 | NM_001241 | Hs.155478 | cyclin T2 | 1.6 | |
| 45 | 119338 | AI417240 | Hs.320836 | ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens] | 1.3 | |
| | 119349 | T65004 | Hs.163561 | ESTs | 8.4 | |
| | 119403 | AL117554 | Hs.119908 | nucleolar protein NOP5/NOP58 | 6.7 | |
| | 119478 | AI624342 | Hs.170042 | ESTs | 2.4 | |
| | 119486 | AI796730 | Hs.55513 | ESTs | 2.1 | |
| 50 | 119513 | W37933 | | Empirically selected from AFFX single probeset | 1.9 | |
| | 119601 | AK000155 | Hs.91684 | Homo sapiens mRNA; cDNA DKFZp6671103 (from clone DKFZp6671103) | 3.7 | |
| | 119602 | AW675298 | Hs.233694 | hypothetical protein FLJ11350 | 3.0 | |
| | 119676 | AA243837 | Hs.57787 | ESTs | 1.4 | |
| | 119682 | W61019 | Hs.57811 | ESTs | 1.2 | |
| 55 | 119774 | AB032977 | Hs.6298 | KIAA1151 protein | 1.8 | |
| | 119780 | NM_016625 | Hs.191381 | hypothetical protein | 3.1 | |
| | 119789 | BE393948 | Hs.50915 | kallikrein 5 (KLK5; KLK-L2; stratum comeum tryptic enzyme) | 9.2 | |
| | 119805 | AJ223810 | Hs.43213 | ESTs, Weakly similar to IEFS_HUMAN TRANSFORMATION-SENSITIVE PROTEIN IEF SSP | 3.6 | |
| | 119818 | AA130970 | Hs.58382 | hypothetical protein FLJ11101 | 2.5 | |
| 60 | 119863 | AA081218 | Hs.58608 | Homo sapiens cDNA FLJ14206 fis, clone NT2RP3003157 | 2.7 | |
| | 119905 | AW449064 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | 2.6 | |
| | 119966 | AA703129 | Hs.58963 | ESTs | 2.7 | |
| | 120132 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 1.2 | |
| | 120206 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 45.7 | |
| 65 | 120248 | AI924294 | Hs.173259 | uncharacterized bone marrow protein BM033 | 1.2 | |
| | 120253 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 38.9 | |
| | 120269 | AW131940 | Hs.104030 | ESTs | 9.6 | |

| | | | | |
|----|--------|----------|--|------|
| | 120274 | AA177051 | gb:nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:194 similar to contains Alu | 4.6 |
| | 120280 | AA190577 | gb:zp52g02.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 3', mRNA sequence | 2.0 |
| | 120296 | AW995911 | Hs.299883 hypothetical protein FLJ23399 | 1.8 |
| 5 | 120297 | AA191384 | Hs.104072 ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens] | 15.2 |
| | 120324 | AA195517 | Hs.191643 ESTs | 5.5 |
| | 120325 | AA195651 | Hs.104106 ESTs | 6.4 |
| | 120327 | AK000292 | Hs.278732 hypothetical protein FLJ20285 | 16.1 |
| | 120336 | N85785 | Hs.181165 eukaryotic translation elongation factor 1 alpha 1 | 2.9 |
| | 120342 | AW450669 | Hs.45068 hypothetical protein DKFZp434143 | 5.7 |
| 10 | 120345 | AA210722 | Hs.104158 ESTs | 4.5 |
| | 120349 | AW969481 | Hs.55189 hypothetical protein | 16.8 |
| | 120352 | R06859 | Hs.193172 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] | 5.0 |
| | 120356 | AF000545 | Hs.296433 putative purinergic receptor | 28.1 |
| | 120371 | AA219305 | Hs.104196 EST | 12.4 |
| 15 | 120382 | AA228026 | Hs.38774 ESTs | 4.0 |
| | 120383 | AL109963 | Hs.123122 FSH primary response (LRPR1, rat) homolog 1 | 9.7 |
| | 120386 | AW969665 | Hs.154848 hypothetical protein DKFZp434D0127 | 32.6 |
| | 120388 | AA232874 | Hs.104245 ESTs | 3.1 |
| 20 | 120389 | AW967985 | Hs.325572 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION | 21.7 |
| | 120396 | AA134006 | Hs.79306 eukaryotic translation initiation factor 4E | 12.5 |
| | 120404 | AB023230 | Hs.96427 KIAA1013 protein | 7.2 |
| | 120418 | AW966893 | Hs.26613 Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323) | 11.4 |
| | 120423 | AA236453 | Hs.18978 Homo sapiens cDNA: FLJ22822 fis, clone KAJA3968 | 1.9 |
| 25 | 120472 | AI950087 | gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone 3', mRNA sequence | 19.4 |
| | 120473 | AA251973 | Hs.269988 ESTs | 5.4 |
| | 120484 | AA253170 | Hs.96473 EST | 10.4 |
| | 120504 | AA256837 | gb:zr84d10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:682387 3', mRNA sequence | 3.9 |
| | 120509 | BE047718 | Hs.96545 ESTs | 9.4 |
| 30 | 120520 | AA258601 | Hs.161731 EST | 2.4 |
| | 120535 | BE350244 | Hs.96547 ESTs | 2.5 |
| | 120551 | AA279160 | Hs.111407 Homo sapiens, clone IMAGE:3613029, mRNA, partial cds | 5.2 |
| | 120570 | AA280679 | Hs.271445 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION | 14.4 |
| | 120582 | BE244830 | Hs.284228 ZNF135-like protein | 10.2 |
| 35 | 120590 | AW372799 | Hs.125790 leucine-rich repeat-containing 2 | 2.1 |
| | 120596 | AA282074 | Hs.237323 N-acetylglucosamine-phosphate mutase | 7.5 |
| | 120619 | AW965339 | Hs.111471 ESTs | 2.5 |
| | 120624 | AW407987 | Hs.173518 M-phase phosphoprotein homolog | 52.0 |
| | 120639 | AA286942 | gb:zs56f05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701505 3' similar to contains Alu2.4 | 2.4 |
| 40 | 120648 | AA287095 | Hs.140309 Homo sapiens, clone IMAGE:3677194, mRNA, partial cds | 5.0 |
| | 120653 | AW063659 | Hs.191649 ESTs | 2.2 |
| | 120668 | AW969638 | Hs.112318 6.2 kd protein | 2.2 |
| | 120669 | BE536739 | Hs.109909 ESTs | 1.9 |
| | 120695 | AA976503 | gb:oq30a04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3' similar to contains PTR7.t1 PTR7 | 46.8 |
| 45 | 120696 | AI821539 | Hs.97249 ESTs | 2.5 |
| | 120713 | AW449855 | Hs.96557 Homo sapiens cDNA FLJ12727 fis, clone NT2RP2000027 | 5.9 |
| | 120718 | AA292747 | Hs.97296 ESTs | 2.9 |
| | 120750 | AI191410 | Hs.96693 ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens] | 7.0 |
| | 120774 | AI608909 | Hs.193985 ESTs | 7.8 |
| | 120807 | AA346385 | Hs.30002 SH3-containing protein SH3GLB2; KIAA1848 protein | 6.8 |
| 50 | 120809 | AA346495 | gb:EST52657 Fetal heart II Homo sapiens cDNA 3' end similar to EST containing O family repeat, | 4.4 |
| | 120938 | AA386260 | Hs.104632 EST | 4.4 |
| | 120977 | AA398155 | Hs.97600 ESTs | 4.4 |
| | 120984 | BE262951 | Hs.99052 ESTs | 5.6 |
| | 120985 | AI219896 | Hs.97592 ESTs | 1.2 |
| 55 | 121011 | AA398360 | Hs.97608 EST | 3.1 |
| | 121026 | AI439713 | Hs.165295 ESTs | 3.5 |
| | 121081 | AA398721 | Hs.186749 ESTs, Highly similar to I37550 mismatch repair protein MSH2 [H.sapiens] | 5.4 |
| | 121133 | AA363307 | Hs.97032 ESTs | 3.7 |
| | 121176 | AL121523 | Hs.97774 ESTs | 1.7 |
| 60 | 121223 | AI002110 | Hs.97169 ESTs, Weakly similar to dJ667H12.2.1 [H.sapiens] | 2.9 |
| | 121320 | AA403008 | Hs.301927 c6.1A | 1.9 |
| | 121340 | AW956981 | Hs.97910 Homo sapiens cDNA FLJ13383 fis, clone PLACE1001024 | 3.5 |
| | 121408 | AA406137 | Hs.98019 EST | 6.0 |
| | 121439 | AA410190 | Hs.98076 ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens] | 7.4 |
| 65 | 121450 | AA406430 | Hs.105362 Homo sapiens, clone MGC:18257, mRNA, complete cds | 6.9 |
| | 121452 | AW971063 | Hs.292882 ESTs | 1.8 |
| | 121455 | H58306 | Hs.15165 retinoic acid induced 14 | 10.5 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 121457 | W07404 | Hs.144502 | hypothetical protein FLJ22055 | 3.4 |
| | 121496 | AA442224 | Hs.97900 | ESTs | 14.4 |
| | 121505 | AA494172 | Hs.194417 | ESTs | 13.1 |
| | 121508 | AA402515 | Hs.97887 | ESTs | 28.0 |
| 5 | 121513 | AA416653 | Hs.181510 | ESTs | 6.2 |
| | 121514 | AA412112 | | gb:z169b02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727563 3', mRNA sequence | 2.6 |
| | 121549 | AA412477 | Hs.98142 | EST | 7.4 |
| | 121558 | AA412497 | | gb:z195g12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730150 3' similar to contains | 2.8 |
| | 121577 | AA411970 | Hs.98096 | EST | 3.5 |
| 10 | 121581 | AA416568 | | gb:zu05c10.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence | 6.1 |
| | 121589 | AD001528 | Hs.89718 | spermine synthase | 3.9 |
| | 121594 | AA626010 | Hs.98247 | ESTs | 2.2 |
| | 121622 | AA416931 | Hs.126065 | ESTs | 4.2 |
| | 121655 | AA421537 | Hs.178072 | Homo sapiens mRNA; cDNA DKFZp434B1023 (from clone DKFZp434B1023) | 7.8 |
| 15 | 121682 | AA418160 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743 | 2.0 |
| | 121690 | AV660305 | Hs.110286 | ESTs | 4.7 |
| | 121706 | U55184 | Hs.154145 | hypothetical protein FLJ11585 | 12.7 |
| | 121714 | AA419225 | Hs.98269 | Homo sapiens cDNA FLJ11953 fis, clone HEMBB1000883 | 8.1 |
| | 121729 | AI949597 | Hs.98325 | ESTs | 1.8 |
| 20 | 121731 | AA421041 | Hs.180744 | ESTs | 4.0 |
| | 121744 | AA398784 | Hs.97514 | ESTs | 7.1 |
| | 121748 | BE536911 | Hs.234545 | hypothetical protein NUF2R | 19.5 |
| | 121773 | AB033022 | Hs.158654 | KIAA1196 protein | 7.9 |
| | 121775 | AA421773 | Hs.161008 | ESTs | 1.7 |
| 25 | 121776 | AA292579 | Hs.125133 | hypothetical protein FLJ22501 | 6.6 |
| | 121786 | AI810774 | Hs.98376 | ESTs | 10.5 |
| | 121832 | AW340797 | Hs.98434 | ESTs | 5.8 |
| | 121836 | AA328348 | Hs.218289 | ESTs | 3.8 |
| | 121839 | AA425691 | Hs.191606 | ESTs, Highly similar to KIAA1048 protein [H.sapiens] | 5.0 |
| 30 | 121842 | AF027406 | Hs.104865 | serine/threonine kinase 23 | 2.7 |
| | 121847 | AA446628 | Hs.2799 | cartilage linking protein 1 | 2.3 |
| | 121871 | AW972668 | Hs.293044 | ESTs | 2.9 |
| | 121882 | AA426376 | Hs.98459 | ESTs | 5.0 |
| | 121911 | AA427950 | | gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773499 3' | 7.2 |
| 35 | 121915 | AA428179 | Hs.223405 | ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens] | 2.5 |
| | 121935 | AA428647 | Hs.98611 | EST | 2.3 |
| | 121983 | AA298760 | Hs.180191 | hypothetical protein FLJ14904 | 3.4 |
| | 121985 | AI862570 | Hs.299214 | Homo sapiens, clone IMAGE:2822295, mRNA, partial cds | 11.4 |
| | 121995 | AA210863 | Hs.3532 | nemo-like kinase | 3.8 |
| 40 | 121999 | AA430211 | Hs.98668 | EST | 6.4 |
| | 122009 | AW292763 | Hs.160822 | Homo sapiens cDNA: FLJ20863 fis, clone ADKA01804 | 2.2 |
| | 122013 | AA431085 | Hs.98706 | ESTs | 6.5 |
| | 122036 | W92142 | Hs.271963 | ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION | 13.1 |
| | 122050 | AI453076 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 | 9.1 |
| 45 | 122060 | AA431738 | Hs.98750 | EST | 13.1 |
| | 122114 | AW161023 | Hs.104921 | ESTs | 1.5 |
| | 122188 | AA398838 | | gb:z180d01.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence | 3.3 |
| | 122204 | AA435936 | Hs.98842 | EST | 5.6 |
| | 122246 | AA329550 | Hs.29417 | HCF-binding transcription factor Zhangfei | 5.1 |
| 50 | 122257 | AA436819 | Hs.98899 | ESTs | 5.6 |
| | 122302 | AA441801 | Hs.104947 | ESTs | 5.8 |
| | 122341 | AW601969 | Hs.99010 | hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 | 2.0 |
| | 122356 | AA443794 | Hs.98390 | ESTs | 7.3 |
| | 122369 | AA443985 | Hs.303222 | ESTs | 12.2 |
| 55 | 122371 | AA868555 | Hs.178222 | ESTs | 5.0 |
| | 122372 | AA446008 | Hs.336677 | EST | 7.6 |
| | 122378 | AB032948 | Hs.21356 | hypothetical protein DKFZp762K2015 | 2.5 |
| | 122405 | AA446572 | Hs.303223 | EST | 2.8 |
| | 122412 | AA446869 | Hs.119316 | ESTs | 7.3 |
| 60 | 122415 | AA446918 | Hs.99088 | EST | 1.9 |
| | 122418 | AA446966 | Hs.99090 | ESTs, Moderately similar to similar to KIAA0766 [H.sapiens] | 6.8 |
| | 122440 | AW505139 | Hs.9460 | Homo sapiens mRNA; cDNA DKFZp547C244 (from clone DKFZp547C244) | 2.6 |
| | 122446 | AA447603 | Hs.99123 | EST | 1.8 |
| | 122448 | AA447626 | Hs.99127 | EST | 3.5 |
| 65 | 122458 | AI266159 | Hs.104980 | ESTs | 1.5 |
| | 122460 | AW418788 | Hs.99148 | ESTs, Weakly similar to S43569 R01H10.6 protein - Caenorhabditis elegans [C.elegans] | 9.7 |
| | 122464 | AA448158 | Hs.99152 | EST | 4.8 |

| | | | | | | |
|----|--------|----------|-----------|--|-------|--|
| | 122490 | AA448349 | Hs.238151 | EST | 6.1 | |
| | 122492 | AA448417 | Hs.104990 | ESTs | 5.4 | |
| | 122502 | AA204969 | Hs.234863 | Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492 | 1.3 | |
| 5 | 122510 | AA449232 | Hs.99195 | ESTs | 11.2 | |
| | 122530 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma 2 subunit | 10.1 | |
| | 122547 | AA779725 | Hs.164589 | ESTs | 2.5 | |
| | 122555 | AA194055 | Hs.293858 | ESTs | 1.9 | |
| | 122570 | AA452578 | Hs.262907 | ESTs | 9.5 | |
| | 122572 | AA452601 | Hs.99287 | EST | 11.0 | |
| 10 | 122586 | AK001910 | Hs.99303 | Homo sapiens cDNA FLJ11048 fis, clone PLACE1004516 | 3.4 | |
| | 122587 | AB040893 | Hs.6968 | KIAA1460 protein | 2.0 | |
| | 122598 | AI028173 | Hs.99329 | ESTs | 1.7 | |
| | 122599 | AL355841 | Hs.99330 | hypothetical protein FLJ23588 | 4.4 | |
| 15 | 122602 | AA411925 | Hs.301960 | ESTs | 4.6 | |
| | 122607 | AA453518 | Hs.98023 | ESTs | 61.5 | |
| | 122614 | AA453630 | Hs.99339 | EST | 10.7 | |
| | 122616 | AA453638 | Hs.161873 | ESTs | 107.3 | |
| | 122617 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 121.4 | |
| | 122618 | AA453641 | | gb:zx48e06.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence | 31.1 | |
| 20 | 122622 | AA453987 | Hs.144802 | ESTs | 5.6 | |
| | 122717 | AA456859 | Hs.178358 | ESTs | 8.5 | |
| | 122762 | AI376875 | Hs.105119 | ESTs | 10.4 | |
| | 122829 | AW204530 | Hs.99500 | ESTs | 81.8 | |
| | 122834 | AA461492 | Hs.99545 | Homo sapiens cDNA FLJ10658 fis, clone NT2RP2006052 | 3.6 | |
| 25 | 122836 | AA460581 | Hs.290996 | ESTs | 4.5 | |
| | 122837 | AA461509 | Hs.293565 | ESTs, Weakly similar to putative p150 [H.sapiens] | 2.7 | |
| | 122838 | AA460584 | Hs.334386 | ESTs | 75.3 | |
| | 122854 | AA600235 | Hs.9625 | NIMA (never in mitosis gene a)-related kinase 6 | 7.7 | |
| | 122856 | AI929374 | Hs.75367 | Src-like-adaptor | 5.8 | |
| 30 | 122861 | AA335721 | Hs.119394 | ESTs | 1.3 | |
| | 122866 | BE539656 | Hs.283705 | ESTs | 4.1 | |
| | 122868 | AF005216 | Hs.115541 | Janus kinase 2 (a protein tyrosine kinase) | 5.3 | |
| | 122870 | AW576312 | Hs.318722 | Homo sapiens cDNA: FLJ21766 fis, clone COLF7179 | 9.9 | |
| | 122872 | AW081394 | Hs.97103 | ESTs | 5.3 | |
| 35 | 122879 | AA769410 | Hs.128654 | ESTs | 13.9 | |
| | 122907 | AA470074 | Hs.169896 | ESTs | 11.5 | |
| | 122916 | AA470140 | Hs.229170 | EST | 1.7 | |
| | 122981 | AA478951 | Hs.105629 | ESTs | 5.0 | |
| 40 | 123013 | AW968324 | Hs.17384 | ESTs | 15.4 | |
| | 123016 | AW338067 | Hs.323231 | Homo sapiens cDNA FLJ11946 fis, clone HEMBB1000709 | 2.8 | |
| | 123034 | AL359571 | Hs.44054 | neirin (GSK3B interacting protein) | 8.7 | |
| | 123072 | AI382600 | Hs.104308 | ESTs, Weakly similar to KIAA1395 protein [H.sapiens] | 8.8 | |
| | 123082 | AA485360 | Hs.105661 | ESTs | 3.9 | |
| | 123088 | AI343652 | Hs.105667 | ESTs | 3.8 | |
| 45 | 123110 | AA486256 | Hs.193510 | EST | 7.4 | |
| | 123114 | BE304942 | Hs.265848 | myomegalin | 2.8 | |
| | 123131 | T52027 | Hs.271795 | ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] | 2.4 | |
| | 123132 | AI061582 | Hs.324179 | Homo sapiens cDNA FLJ12371 fis, clone MAMMA1002434 | 15.6 | |
| | 123136 | AW451999 | Hs.194024 | ESTs | 5.1 | |
| 50 | 123149 | AI734179 | Hs.105676 | ESTs | 23.8 | |
| | 123152 | AW601773 | Hs.270259 | ESTs | 5.2 | |
| | 123258 | AA490929 | Hs.105274 | ESTs, Weakly similar to RMS1_HUMAN REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens] | 9.3 | |
| | 123315 | AA496369 | | gb:zv37d10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755827 3' similar to | 4.1 | |
| | 123369 | AA504757 | Hs.105738 | ESTs | 6.9 | |
| 55 | 123394 | AA731404 | Hs.105510 | ESTs | 3.6 | |
| | 123433 | AW450922 | Hs.112478 | ESTs | 3.7 | |
| | 123466 | AA599042 | Hs.112503 | EST | 7.4 | |
| | 123470 | AW303285 | Hs.303632 | Human DNA sequence from clone RP11-110H4 on chromosome 5 Contains a pseudogene similar to | 3.5 | |
| | 123471 | AB021644 | Hs.197219 | zinc finger protein 14 (KOX 6) | 5.2 | |
| 60 | 123475 | BE439553 | Hs.250528 | Homo sapiens, clone IMAGE:4098694, mRNA, partial cds | 1.7 | |
| | 123482 | N95059 | Hs.55098 | ESTs | 1.6 | |
| | 123486 | BE019072 | Hs.334802 | Homo sapiens cDNA FLJ14680 fis, clone NT2RP2004242, weakly similar to | 2.4 | |
| | 123508 | AW380388 | Hs.155546 | KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 | 2.2 | |
| | 123615 | AA609170 | | gb:af12a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence | 7.8 | |
| 65 | 123619 | AA602964 | | gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, mRNA sequence | 2.8 | |
| | 123658 | AA609364 | | gb:zu71d09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743441 3' similar to contains Alu. | 1.7 | |
| | 123674 | AI269609 | Hs.105187 | kinesin protein 9 gene | 5.7 | |

| | | | | | |
|----|--------|-----------|-----------|--|-------|
| | 123735 | NM_013241 | Hs.95231 | FH1/FH2 domain-containing protein | 10.0 |
| | 123738 | AA609891 | Hs.112777 | EST | 5.2 |
| | 123753 | AA609955 | Hs.234961 | Huntingtin interacting protein E | 30.6 |
| 5 | 123804 | AA620464 | Hs.261915 | EST, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens] | 2.1 |
| | 123811 | AA620586 | | gb:ae60g05.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:951320 3' | 2.7 |
| | 123951 | AB012922 | Hs.173043 | metastasis-associated 1-like 1 | 6.2 |
| | 123983 | AJ272267 | Hs.146178 | choline dehydrogenase | 4.4 |
| | 124001 | L42542 | Hs.75447 | raIA binding protein 1 | 7.0 |
| | 124006 | AI147155 | Hs.270016 | ESTs | 8.1 |
| 10 | 124070 | AI950314 | Hs.154762 | HIV-1 rev binding protein 2 | 3.7 |
| | 124074 | H05635 | Hs.294030 | topoisomerase-related function protein 4-2 | 1.2 |
| | 124178 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 3.1 |
| | 124203 | AA372796 | Hs.269339 | ESTs, Weakly similar to AF161356 1 HSPC093 [H.sapiens] | 5.7 |
| | 124352 | AA640891 | Hs.102406 | ESTs | 3.1 |
| 15 | 124375 | D87454 | Hs.192966 | KIAA0265 protein | 3.5 |
| | 124385 | AI267847 | | gb:ac49a10.x1 Stanley Frontal NB pool 2 Homo sapiens cDNA clone similar to contains | 57.1 |
| | 124390 | AA317338 | Hs.7535 | COBW-like protein | 2.8 |
| | 124391 | AF155099 | Hs.279780 | NY-REN-18 antigen | 7.1 |
| 20 | 124417 | N34059 | | gb:yv28h09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3' similar to contains | 3.3 |
| | 124428 | H13540 | Hs.82202 | ribosomal protein L17 | 2.9 |
| | 124440 | AA532519 | Hs.129043 | Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2. Contains part of a | 7.8 |
| | 124466 | R10084 | Hs.113319 | kinesin heavy chain member 2 | 2.6 |
| | 124482 | N53935 | | gb:yv59d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3', mRNA sequence | 7.9 |
| | 124498 | H79433 | Hs.268997 | ESTs | 7.8 |
| 25 | 124515 | AA669097 | Hs.109370 | ESTs | 3.3 |
| | 124608 | N71076 | Hs.102800 | ESTs, Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] | 4.5 |
| | 124631 | NM_014053 | Hs.270594 | FLVCR protein | 3.2 |
| | 124634 | AI765123 | Hs.143671 | Homo sapiens cDNA FLJ13533 fis, clone PLACE1006371 | 5.8 |
| | 124637 | AA160474 | Hs.75798 | hypothetical protein | 9.3 |
| 30 | 124642 | AW968856 | Hs.278569 | sorting nexin 17 | 3.5 |
| | 124649 | N92593 | Hs.313054 | ESTs | 6.1 |
| | 124656 | AW297702 | Hs.102915 | ESTs | 8.3 |
| | 124661 | R48170 | Hs.78436 | EphB1 | 5.6 |
| 35 | 124683 | AA381661 | Hs.119878 | ESTs, Weakly similar to M3K9_HUMAN MITOGEN-ACTIVATED PROTEIN KINASE KINASE | 7.9 |
| | 124712 | R09166 | Hs.191148 | ESTs | 5.7 |
| | 124735 | R22952 | Hs.268685 | ESTs | 11.3 |
| | 124761 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, partial cds | 9.0 |
| | 124768 | AW368528 | Hs.100855 | ESTs | 8.1 |
| 40 | 124775 | R41772 | Hs.100878 | ESTs | 4.9 |
| | 124777 | R41933 | Hs.140237 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE | 2.8 |
| | 124788 | R43543 | Hs.100912 | Homo sapiens cDNA: FLJ22726 fis, clone HSI15005 | 5.1 |
| | 124809 | AL355722 | Hs.106875 | Homo sapiens EST from clone 35214, full insert | 4.2 |
| | 124811 | R46068 | Hs.288912 | hypothetical protein FLJ22604 | 14.2 |
| 45 | 124812 | R47948 | Hs.188732 | ESTs | 7.9 |
| | 124822 | AA418160 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743 | 6.6 |
| | 124825 | AA501669 | Hs.336693 | ESTs | 2.3 |
| | 124833 | AW975868 | Hs.294100 | ESTs | 2.7 |
| | 124857 | R63652 | Hs.137190 | ESTs | 2.3 |
| 50 | 124860 | R65763 | Hs.101477 | EST | 23.9 |
| | 124863 | AI382555 | Hs.127950 | bromodomain-containing 1 | 2.0 |
| | 124876 | AF135422 | Hs.27059 | GDP-mannose pyrophosphorylase A | 4.4 |
| | 124878 | BE397530 | Hs.288057 | hypothetical protein FLJ22242 | 2.7 |
| | 124902 | H37941 | Hs.101883 | ESTs | 5.7 |
| | 124903 | AW296713 | Hs.221441 | ESTs | 32.4 |
| 55 | 124930 | AI076343 | Hs.173939 | ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens] | 22.8 |
| | 124942 | R99978 | Hs.268892 | ESTs, Moderately similar to B34087 hypothetical protein [H.sapiens] | 6.1 |
| | 124958 | AI078645 | Hs.431 | murine leukemia viral (bmi-1) oncogene homolog | 1.9 |
| | 124980 | T40841 | Hs.98681 | ESTs | 4.5 |
| 60 | 125002 | T59338 | Hs.269463 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION | 4.9 |
| | 125047 | T79815 | Hs.279793 | ESTs | 5.0 |
| | 125051 | T79956 | Hs.100588 | EST | 135.3 |
| | 125056 | T81310 | Hs.100592 | ESTs | 5.4 |
| | 125101 | AI472068 | Hs.286236 | KIAA1856 protein | 5.6 |
| 65 | 125113 | T96595 | Hs.302270 | ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS F WARNING ENTRY !!! [H.sapiens] | 1.8 |
| | 125115 | T97341 | | gb:ye57e05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121856 3' similar to | 9.6 |
| | 125125 | AI222382 | Hs.240767 | Human DNA sequence from clone RP1-12G14 on chromosome 6q24.1-25.2. Contains the 5' end of the gene | 1.5 |
| | 125147 | W38150 | | Empirically selected from AFFX single probeset | 1.7 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 125161 | W44657 | Hs.144232 | EST | 10.7 |
| | 125249 | AA630863 | Hs.131375 | ESTs, Moderately similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens] | 1.3 |
| | 125255 | AF098162 | Hs.118631 | timeless (Drosophila) homolog | 9.4 |
| | 125279 | AW401809 | Hs.4779 | KIAA1150 protein | 1.5 |
| 5 | 125280 | AI123705 | Hs.106932 | ESTs | 8.0 |
| | 125298 | AW972542 | Hs.289008 | Homo sapiens cDNA: FLJ21814 fis, clone HEP01068 | 1.5 |
| | 125660 | AW292171 | Hs.23978 | scaffold attachment factor B | 5.9 |
| | 125827 | NM_003403 | Hs.97496 | YY1 transcription factor | 1.2 |
| | 125891 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 6.4 |
| 10 | 126005 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (survivin) | 14.3 |
| | 126202 | AA157632 | Hs.272630 | vacuolar proton pump delta polypeptide | 2.4 |
| | 126695 | AA643322 | Hs.172028 | a disintegrin and metalloproteinase domain 10 | 9.1 |
| | 127050 | AW411066 | Hs.274351 | CGI-89 protein | 17.0 |
| | 127274 | AW966158 | Hs.58582 | Homo sapiens cDNA FLJ12789 fis, clone NT2RP2001947 | 12.8 |
| 15 | 128355 | AW293012 | Hs.161623 | ESTs | 7.3 |
| | 128493 | D87466 | Hs.240112 | KIAA0276 protein | 3.1 |
| | 128493 | D87466 | Hs.240112 | KIAA0276 protein | 1.3 |
| | 128522 | BE173977 | Hs.10098 | putative nucleolar RNA helicase | 9.4 |
| | 128527 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | 1.5 |
| 20 | 128528 | R39234 | Hs.251699 | ESTs, Weakly similar to IDN4-GGTR14 [H.sapiens] | 2.8 |
| | 128595 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family member | 12.1 |
| | 128599 | NM_015366 | Hs.102336 | Rho GTPase activating protein 8 | 2.3 |
| | 128604 | AI879099 | Hs.102397 | GIOT-3 for gonadotropin inducible transcription repressor-3 | 1.3 |
| | 128608 | BE267994 | Hs.102419 | zinc finger protein | 7.1 |
| 25 | 128625 | AB037841 | Hs.102652 | hypothetical protein ASH1 | 1.3 |
| | 128629 | AL096748 | Hs.102708 | DKFZP434A043 protein | 3.2 |
| | 128639 | AW582962 | Hs.102897 | CGI-47 protein | 2.0 |
| | 128656 | AA458542 | Hs.10326 | coatamer protein complex, subunit epsilon | 1.4 |
| | 128656 | AA458542 | Hs.10326 | coatamer protein complex, subunit epsilon | 1.3 |
| 30 | 128658 | BE397354 | Hs.324830 | diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2 | 2.4 |
| | 128670 | AA975486 | Hs.103441 | Homo sapiens, Similar to RIKEN cDNA 1700010L19 gene, clone MGC:16214, mRNA, complete cds | 7.1 |
| | 128691 | W27939 | Hs.103834 | hypothetical protein MGC5576 | 7.7 |
| | 128696 | BE081143 | Hs.225977 | nuclear receptor coactivator 3 | 3.8 |
| | 128700 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cys-X-Cys), member 11 | 1.6 |
| 35 | 128714 | T85231 | Hs.179661 | tubulin, beta 5 | 7.6 |
| | 128717 | AK001564 | Hs.104222 | hypothetical protein FLJ10702 | 5.5 |
| | 128733 | BE147740 | Hs.104558 | ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens] | 2.7 |
| | 128737 | AF292100 | Hs.104613 | RP42 homolog | 2.8 |
| | 128742 | AA307211 | Hs.251531 | proteasome (prosome, macropain) subunit, alpha type, 4 | 4.4 |
| 40 | 128746 | AI470163 | Hs.323342 | actin related protein 2/3 complex, subunit 4 (20 kD) | 2.2 |
| | 128747 | AB027249 | Hs.104741 | PDZ-binding kinase; T-cell originated protein kinase | 2.8 |
| | 128772 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 5.3 |
| | 128781 | N71826 | Hs.105465 | small nuclear ribonucleoprotein polypeptide F | 53.9 |
| | 128797 | NM_002975 | Hs.105927 | stem cell growth factor; lymphocyte secreted C-type lectin | 13.3 |
| 45 | 128806 | AW630942 | Hs.106061 | RD RNA-binding protein | 2.6 |
| | 128814 | AW248431 | Hs.256526 | nuclear prelamin A recognition factor | 2.2 |
| | 128830 | BE281170 | Hs.106357 | valosin-containing protein | 5.9 |
| | 128835 | AK001731 | Hs.106390 | Homo sapiens mRNA; cDNA DKFZp586H0924 (from clone DKFZp586H0924) | 1.6 |
| | 128854 | BE159181 | Hs.168232 | hypothetical protein FLJ13855 | 2.2 |
| 50 | 128854 | BE159181 | Hs.168232 | hypothetical protein FLJ13855 | 1.9 |
| | 128868 | AA419008 | Hs.106730 | chromosome 22 open reading frame 3 | 3.0 |
| | 128868 | AA419008 | Hs.106730 | chromosome 22 open reading frame 3 | 2.2 |
| | 128871 | AF189723 | Hs.106778 | ATPase, Ca++ transporting, type 2C, member 1 | 1.5 |
| | 128891 | F34856 | Hs.292457 | Homo sapiens, clone MGC:16362, mRNA, complete cds | 13.3 |
| 55 | 128906 | R57988 | Hs.10706 | epithelial protein lost in neoplasm beta | 4.7 |
| | 128920 | AA622037 | Hs.166468 | programmed cell death 5 | 1.4 |
| | 128925 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321 | 1.9 |
| | 128946 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | 7.2 |
| | 128949 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase domain 12 (meltin alpha) (ADAM-12) | 2.4 |
| 60 | 128958 | AW139032 | Hs.107376 | hypothetical protein DKFZp434N035 | 1.3 |
| | 128959 | AI580127 | Hs.107381 | hypothetical protein FLJ11200 | 10.9 |
| | 128965 | AW150697 | Hs.107418 | ESTs | 1.4 |
| | 128970 | AI375672 | Hs.165028 | ESTs | 1.3 |
| | 128975 | BE560779 | Hs.284233 | NICE-5 protein | 14.0 |
| 65 | 128979 | AW271217 | Hs.281434 | Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838 | 1.6 |
| | 128995 | AI816224 | Hs.107747 | DKFZP566C243 protein | 1.9 |
| | 129019 | AI950087 | | gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone 3', mRNA sequence | 2.9 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 129021 | AL044675 | Hs.173081 | KIAA0530 protein | 3.8 |
| | 129021 | AL044675 | Hs.173081 | KIAA0530 protein | 2.5 |
| | 129032 | R80088 | Hs.108104 | ubiquitin-conjugating enzyme E2L 3 | 3.4 |
| | 129076 | AW296806 | Hs.326234 | ESTs, Highly similar to T46422 hypothetical protein DKFZp434M2023.1 [H.sapiens] | 5.0 |
| 5 | 129078 | AI351010 | Hs.102267 | lysosomal | 2.1 |
| | 129088 | AA744610 | Hs.194431 | palladin | 17.1 |
| | 129095 | L12350 | Hs.108623 | thrombospondin 2 | 2.7 |
| | 129096 | AA463189 | Hs.288906 | WW Domain-Containing Gene | 20.9 |
| | 129097 | BE243933 | Hs.108642 | zinc finger protein 22 (KOX 15) | 3.0 |
| 10 | 129099 | AF146074 | Hs.108660 | ATP-binding cassette, sub-family C (CFTR/MRP), member 5 | 5.8 |
| | 129136 | W93048 | Hs.250723 | hypothetical protein MGC2747 | 5.9 |
| | 129149 | AA356620 | Hs.108947 | KIAA0050 gene product | 6.3 |
| | 129172 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 1.8 |
| | 129192 | AA286914 | Hs.183299 | ESTs | 2.1 |
| 15 | 129194 | AA150797 | Hs.109276 | latexin protein | 3.2 |
| | 129198 | N57532 | Hs.109315 | KIAA1415 protein | 5.8 |
| | 129207 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mimecan) | 8.0 |
| | 129228 | U40714 | Hs.239307 | tyrosyl-tRNA synthetase | 2.9 |
| | 129229 | AF013758 | Hs.109643 | polyadenylate binding protein-interacting protein 1 | 3.2 |
| 20 | 129254 | AA252468 | Hs.1098 | DKFZp434J1813 protein | 2.6 |
| | 129255 | AI961727 | Hs.109804 | H1 histone family, member X | 7.3 |
| | 129288 | W26392 | Hs.110080 | ESTs, Weakly similar to S13495 pregnancy zone protein [H.sapiens] | 9.6 |
| | 129296 | AI051967 | Hs.110122 | ESTs | 1.2 |
| | 129323 | AA287239 | Hs.5518 | Homo sapiens cDNA FLJ11311 fis, clone PLACE1010102 | 5.1 |
| 25 | 129340 | H75334 | Hs.11050 | F-box only protein 9 | 4.6 |
| | 129347 | BE614192 | Hs.279869 | melanoma-associated antigen recognised by cytotoxic T lymphocytes | 7.6 |
| | 129362 | U30246 | Hs.110736 | solute carrier family 12 (sodium/potassium/chloride transporters), member 2 | 6.7 |
| | 129366 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 8.6 |
| | 129370 | AI686379 | Hs.110796 | SAR1 protein | 1.4 |
| 30 | 129372 | NM_016039 | Hs.110803 | CGI-99 protein | 2.0 |
| | 129403 | AF149785 | Hs.111126 | pituitary tumor-transforming 1 interacting protein | 7.4 |
| | 129404 | AI267700 | Hs.317584 | ESTs | 5.0 |
| | 129404 | AI267700 | Hs.317584 | ESTs | 2.5 |
| | 129423 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 10.2 |
| 35 | 129449 | AI096988 | Hs.111554 | ADP-ribosylation factor-like 7 | 8.0 |
| | 129453 | AW974265 | Hs.111632 | Lsm3 protein | 3.2 |
| | 129482 | AA188185 | Hs.289043 | spindlin | 6.7 |
| | 129482 | AA188185 | Hs.289043 | spindlin | 3.6 |
| | 129513 | AW843633 | Hs.306163 | hypothetical protein AL110115 | 7.1 |
| 40 | 129515 | AF255303 | Hs.112227 | membrane-associated nucleic acid binding protein | 2.5 |
| | 129527 | AA769221 | Hs.270847 | delta-tubulin | 3.2 |
| | 129559 | W01296 | Hs.11360 | hypothetical protein FLJ14784 | 7.5 |
| | 129560 | AA317841 | Hs.7845 | hypothetical protein MGC2752 | 6.8 |
| | 129570 | AI923097 | Hs.11441 | chromosome 1 open reading frame 8 | 2.0 |
| 45 | 129575 | F08282 | Hs.278428 | progesterin induced protein | 1.6 |
| | 129587 | H14718 | Hs.11506 | Human clone 23589 mRNA sequence | 6.8 |
| | 129588 | BE408300 | Hs.301862 | postmeiotic segregation increased 2-like 9 | 1.4 |
| | 129591 | N57423 | Hs.179898 | HSPC055 protein | 7.3 |
| | 129594 | AW403724 | Hs.36989 | coagulation factor VII (serum prothrombin conversion accelerator) | 9.0 |
| 50 | 129596 | AF035537 | Hs.115521 | REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta | 1.6 |
| | 129628 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (melanoma, p16, Inhibits CDK4) | 2.2 |
| | 129628 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 1.4 |
| | 129629 | AK000398 | Hs.11747 | hypothetical protein FLJ20391 | 3.8 |
| | 129649 | AD000092 | Hs.16488 | calreticulin | 3.3 |
| 55 | 129675 | NM_015556 | Hs.172180 | KIAA0440 protein | 13.4 |
| | 129680 | U03749 | | gb:Human chromogranin A (CHGA) gene, promoter an | 14.1 |
| | 129689 | AW748482 | Hs.77873 | B7 homolog 3 | 2.6 |
| | 129702 | AI304966 | Hs.12035 | ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] | 7.4 |
| | 129720 | AA156214 | Hs.12152 | APMCF1 protein | 2.0 |
| 60 | 129721 | NM_001415 | Hs.211539 | eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD) | 1.7 |
| | 129726 | H15474 | Hs.132898 | fatty acid desaturase 1 | 8.3 |
| | 129778 | AK001676 | Hs.12457 | hypothetical protein FLJ10814 | 1.8 |
| | 129779 | AA394090 | Hs.12460 | Homo sapiens clone 23870 mRNA sequence | 5.4 |
| | 129800 | AF052112 | Hs.12540 | lysosomal | 1.7 |
| 65 | 129806 | AB023148 | Hs.173373 | KIAA0931 protein | 1.2 |
| | 129815 | BE565817 | Hs.26498 | hypothetical protein FLJ21657 | 3.1 |
| | 129840 | NM_006590 | Hs.12820 | SnRNP assembly defective 1 homolog | 1.8 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 129861 | AL049999 | Hs.85963 | DKFZP564M182 protein | 2.2 |
| | 129864 | AI393237 | Hs.129914 | runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) | 1.7 |
| | 129869 | AI222069 | Hs.13015 | hypothetical protein similar to mouse Dnaj1 | 2.7 |
| | 129922 | AF042379 | Hs.13386 | gamma-tubulin complex protein 2 | 4.5 |
| 5 | 129945 | BE514376 | Hs.165998 | PAI-1 mRNA-binding protein | 1.8 |
| | 129953 | AA412195 | Hs.13740 | ESTs | 2.5 |
| | 129972 | AW753185 | Hs.180628 | dynamitin 1-like | 1.8 |
| | 129983 | U09848 | Hs.132390 | zinc finger protein 36 (KOX 18) | 1.3 |
| | 129989 | AB015856 | Hs.247433 | activating transcription factor 6 | 4.0 |
| 10 | 130010 | AA301116 | Hs.142838 | nucleolar phosphoprotein Nopp34 | 1.6 |
| | 130081 | AA287325 | Hs.14713 | ESTs | 4.0 |
| | 130082 | S73265 | Hs.1473 | gastrin-releasing peptide | 1.8 |
| | 130097 | AL046962 | Hs.14845 | forkhead box O3A | 2.8 |
| | 130100 | AL135561 | Hs.14891 | hypothetical protein FLJ21047 | 2.3 |
| 15 | 130111 | X53002 | Hs.149846 | integrin, beta 5 | 2.3 |
| | 130112 | AA916785 | Hs.180610 | splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) | 3.0 |
| | 130112 | AA916785 | Hs.180610 | splicing factor proline/glutamine rich (| 2.1 |
| | 130128 | L76937 | Hs.150477 | Werner syndrome | 1.8 |
| | 130135 | AA311426 | Hs.21635 | tubulin, gamma 1 | 6.1 |
| 20 | 130211 | NM_003358 | Hs.23703 | ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens] | 1.6 |
| | 130212 | D80001 | Hs.152629 | KIAA0179 protein | 1.3 |
| | 130236 | R85367 | Hs.51957 | splicing factor, arginine/serine-rich 2, interacting protein | 2.0 |
| | 130241 | AL035588 | Hs.153203 | MyoD family inhibitor | 3.2 |
| | 130242 | X79201 | Hs.153221 | synovial sarcoma, translocated to X chromosome | 5.4 |
| 25 | 130249 | D81983 | Hs.322852 | GAS2-related on chromosome 22 | 4.8 |
| | 130263 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related kinase 2 | 1.4 |
| | 130287 | AA479005 | Hs.154036 | tumor suppressing subtransferable candidate 3 | 2.6 |
| | 130310 | AB011121 | Hs.154248 | amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 | 6.3 |
| | 130353 | Z19084 | Hs.172210 | MUF1 protein | 6.2 |
| 30 | 130356 | AF127577 | Hs.155017 | nuclear receptor interacting protein 1 | 2.4 |
| | 130357 | AI224442 | Hs.155020 | putative methyltransferase | 3.4 |
| | 130359 | NM_013449 | Hs.277401 | bromodomain adjacent to zinc finger domain, 2A | 8.5 |
| | 130367 | AL135301 | Hs.8768 | hypothetical protein FLJ10849 | 1.4 |
| | 130372 | AI077464 | Hs.5011 | RNA binding motif protein 9 | 3.3 |
| 35 | 130393 | N89487 | Hs.155291 | KIAA0005 gene product | 1.8 |
| | 130399 | AW374106 | Hs.155356 | hypothetical protein MGC2840 similar to a putative glucosyltransferase | 3.4 |
| | 130407 | BE385099 | Hs.334727 | hypothetical protein MGC3017 | 2.3 |
| | 130409 | NM_001197 | Hs.155419 | BCL2-interacting killer (apoptosis-inducing) | 2.7 |
| | 130419 | AF037448 | Hs.155489 | NS1-associated protein 1 | 1.8 |
| 40 | 130441 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic polypeptide | 2.3 |
| | 130448 | BE513202 | Hs.15589 | PPAR binding protein | 3.9 |
| | 130455 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acetyltransferase) | 33.6 |
| | 130456 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 4.6 |
| | 130471 | AL121438 | Hs.183706 | adducin 1 (alpha) | 2.7 |
| 45 | 130485 | BE245851 | Hs.180779 | H2B histone family, member B | 5.0 |
| | 130487 | U49844 | Hs.77613 | ataxia telangiectasia and Rad3 related | 4.3 |
| | 130498 | L38951 | Hs.180446 | karyopherin (importin) beta 1 | 1.6 |
| | 130503 | BE208491 | Hs.295112 | KIAA0618 gene product | 16.1 |
| | 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) | 6.1 |
| 50 | 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 5.3 |
| | 130526 | AW876523 | Hs.15929 | hypothetical protein FLJ12910 | 2.1 |
| | 130542 | U64675 | Hs.179825 | RAN binding protein 2-like 1 | 7.8 |
| | 130544 | AA321238 | Hs.4310 | eukaryotic translation initiation factor 1A | 1.5 |
| | 130553 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 14.4 |
| 55 | 130556 | AI907018 | Hs.15977 | Empirically selected from AFFX single probeset | 4.7 |
| | 130567 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 7.9 |
| | 130568 | AA232119 | Hs.16085 | putative G-protein coupled receptor | 3.3 |
| | 130574 | AF083208 | Hs.16178 | apoptosis antagonizing transcription factor | 1.2 |
| | 130586 | AB007891 | Hs.16349 | KIAA0431 protein | 5.6 |
| 60 | 130598 | AL042210 | Hs.16493 | hypothetical protein DKFZp762N2316; KIAA1803 protein | 1.4 |
| | 130601 | AA609738 | Hs.16525 | ESTs | 1.5 |
| | 130614 | AI354355 | Hs.16697 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) | 1.3 |
| | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transaminase 1 | 12.1 |
| | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 2.4 |
| 65 | 130618 | AA383439 | Hs.16758 | Spir-1 protein | 15.9 |
| | 130667 | BE246961 | Hs.17639 | Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, partial cds | 13.9 |
| | 130674 | AL048842 | Hs.194019 | attractin | 1.5 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 130675 | AA442233 | Hs.17731 | hypothetical protein FLJ12892 | 5.4 |
| | 130692 | AA652501 | Hs.13561 | hypothetical protein MGC4692 | 5.0 |
| | 130693 | R68537 | Hs.17962 | ESTs | 2.0 |
| | 130712 | AJ271881 | Hs.279762 | bromodomain-containing 7 | 1.8 |
| 5 | 130714 | AI348274 | Hs.18212 | DNA segment on chromosome X (unique) 9879 expressed sequence | 2.0 |
| | 130730 | AB007920 | Hs.18586 | KIAA0451 gene product | 3.7 |
| | 130744 | H59696 | Hs.18747 | POP7 (processing of precursor, <i>S. cerevisiae</i>) homolog | 3.1 |
| | 130751 | AF052105 | Hs.18879 | chromosome 12 open reading frame | 1.4 |
| | 130757 | AL036067 | Hs.18925 | protein x 0001 | 5.7 |
| 10 | 130768 | AF258627 | Hs.211562 | ATP-binding cassette, sub-family A (ABC1), member 1 | 5.1 |
| | 130789 | AK000355 | Hs.8899 | sirtuin (silent mating type information regulation 2, <i>S.cerevisiae</i> , homolog) 5 | 5.2 |
| | 130815 | AB018298 | Hs.19822 | SEC24 (<i>S. cerevisiae</i>) related gene family, member D | 1.5 |
| | 130836 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding protein, R binder family) | 15.7 |
| | 130841 | AL157468 | Hs.325825 | Homo sapiens cDNA FLJ20848 fis, clone ADKA01732 | 2.8 |
| 15 | 130843 | AA447492 | Hs.20183 | ESTs, Weakly similar to AF164793 1 protein x 013 [H.sapiens] | 1.5 |
| | 130844 | U76248 | Hs.20191 | seven in absentia (<i>Drosophila</i>) homolog 2 | 3.4 |
| | 130855 | AJ243706 | Hs.143323 | putative DNA/chromatin binding motif | 1.7 |
| | 130861 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 1.9 |
| | 130879 | NM_003416 | Hs.2076 | zinc finger protein 7 (KOX 4, clone HF.16) | 1.4 |
| 20 | 130880 | BE514434 | Hs.20830 | kinesin-like 2 | 2.1 |
| | 130892 | AL120837 | Hs.20993 | high-glucose-regulated protein 8 | 2.4 |
| | 130898 | AB033078 | Hs.186613 | sphingosine-1-phosphate lyase 1 | 1.7 |
| | 130911 | BE409769 | Hs.21189 | DnaJ (Hsp40) homolog, subfamily A, member 2 | 1.8 |
| | 130919 | N79110 | Hs.21276 | collagen, type IV, alpha 3 (Goodpasture antigen) binding protein | 2.3 |
| 25 | 130944 | BE382657 | Hs.21486 | signal transducer and activator of transcription 1, 91kD | 5.4 |
| | 130971 | N39842 | Hs.301444 | KIAA1673 | 2.2 |
| | 130992 | BE398091 | Hs.74316 | desmoplakin (DPI, DPII) | 1.8 |
| | 130993 | T97401 | Hs.21929 | ESTs | 1.6 |
| | 131005 | AV658308 | Hs.2210 | thyroid hormone receptor interactor 3 | 1.6 |
| 30 | 131028 | AI879165 | Hs.2227 | CCAAT/enhancer binding protein (C/EBP), gamma | 1.2 |
| | 131042 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 1.6 |
| | 131046 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cys-X-Cys), member 10 | 7.4 |
| | 131046 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 3.0 |
| | 131047 | H23230 | Hs.22481 | ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens] | 1.7 |
| 35 | 131060 | AA194422 | Hs.22564 | myosin VI | 5.1 |
| | 131060 | AA194422 | Hs.22564 | myosin VI | 2.5 |
| | 131070 | N53344 | Hs.22607 | ESTs | 7.1 |
| | 131076 | AA749230 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (| 2.0 |
| | 131076 | AA749230 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosam | 1.9 |
| 40 | 131099 | AL133353 | Hs.226581 | COX15 (yeast) homolog, cytochrome c oxidase assembly protein | 7.0 |
| | 131174 | NM_006540 | Hs.29131 | nuclear receptor coactivator 2 | 1.9 |
| | 131185 | BE280074 | Hs.23960 | cyclin B1 | 5.8 |
| | 131206 | AW138839 | Hs.24210 | ESTs | 2.0 |
| | 131213 | AA885699 | Hs.24332 | CGI-26 protein | 7.0 |
| 45 | 131225 | H62087 | Hs.31659 | thyroid hormone receptor-associated protein, 95-kD subunit | 7.5 |
| | 131231 | N47468 | Hs.59757 | zinc finger protein 281 | 2.9 |
| | 131233 | D89053 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain 3 | 3.5 |
| | 131243 | AW383256 | Hs.24752 | spectrin SH3 domain binding protein 1 | 2.8 |
| | 131245 | AL080080 | Hs.24766 | thioredoxin domain-containing | 2.8 |
| 50 | 131247 | AL043100 | Hs.326190 | fatty acid amide hydrolase | 5.6 |
| | 131281 | AA251716 | Hs.25227 | ESTs | 5.7 |
| | 131283 | X80038 | Hs.339713 | Homo sapiens clone F19374 APO E-C2 gene cluster | 1.3 |
| | 131305 | AV656017 | Hs.184325 | CGI-76 protein | 5.0 |
| | 131320 | AA505691 | Hs.145696 | splicing factor (CC1.3) | 1.8 |
| 55 | 131339 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nlbrin) | 2.6 |
| | 131339 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nlbrin) | 2.6 |
| | 131375 | AW293165 | Hs.143134 | ESTs | 5.4 |
| | 131390 | BE269388 | Hs.182698 | mitochondrial ribosomal protein L20 | 5.3 |
| | 131410 | BE259110 | Hs.279836 | HSPC166 protein | 2.2 |
| 60 | 131412 | NM_012247 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selenium donor protein | 2.0 |
| | 131429 | AL046302 | Hs.26750 | hypothetical protein FLJ21908 | 1.4 |
| | 131458 | BE297567 | Hs.27047 | hypothetical protein FLJ20392 | 1.7 |
| | 131475 | AA992841 | Hs.27263 | KIAA1458 protein | 2.0 |
| | 131501 | AV661958 | Hs.8207 | GK001 protein | 2.6 |
| 65 | 131501 | AV661958 | Hs.8207 | GK001 protein | 1.6 |
| | 131511 | AA732153 | Hs.27865 | Homo sapiens cDNA: FLJ21333 fis, clone COL02535 | 2.0 |
| | 131528 | AU076408 | Hs.28309 | UDP-glucose dehydrogenase | 1.6 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 131532 | BE268278 | Hs.28393 | hypothetical protein MGC2592 | 7.4 |
| | 131543 | AW966881 | Hs.41639 | programmed cell death 2 | 2.2 |
| | 131544 | AL355715 | Hs.28555 | programmed cell death 9 (PDCD9) | 2.1 |
| | 131562 | NM_003512 | Hs.28777 | H2A histone family, member L | 1.7 |
| 5 | 131564 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405 | 5.1 |
| | 131564 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 1.8 |
| | 131569 | AL389951 | Hs.271623 | nucleoporin 50kD | 5.0 |
| | 131618 | BE393822 | Hs.29645 | Homo sapiens mRNA; cDNA DKFZp761C029 (from clone DKFZp761C029); partial cds | 1.8 |
| | 131622 | R78195 | Hs.29692 | Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213 | 1.3 |
| 10 | 131623 | AB037791 | Hs.29716 | hypothetical protein FLJ10980 | 2.2 |
| | 131623 | AB037791 | Hs.29716 | hypothetical protein FLJ10980 | 1.9 |
| | 131643 | AW410601 | Hs.30026 | HSPC182 protein | 2.9 |
| | 131653 | AW960597 | Hs.30164 | ESTs | 1.3 |
| | 131656 | AI218918 | Hs.30209 | KIAA0854 protein | 2.8 |
| 15 | 131669 | X52486 | Hs.3041 | uracil-DNA glycosylase 2 | 2.8 |
| | 131692 | BE559681 | Hs.30736 | KIAA0124 protein | 5.6 |
| | 131714 | AA642831 | Hs.31016 | putative DNA binding protein | 2.9 |
| | 131722 | D13757 | Hs.311 | phosphoribosyl pyrophosphate amidotransferase | 3.4 |
| | 131737 | AK001641 | Hs.31323 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein | 3.8 |
| 20 | 131760 | X76732 | Hs.3164 | nucleobindin 2 | 2.9 |
| | 131760 | X76732 | Hs.3164 | nucleobindin 2 | 2.8 |
| | 131763 | AI878932 | Hs.317 | topoisomerase (DNA) I | 3.4 |
| | 131772 | AA382590 | Hs.170980 | KIAA0948 protein | 25.5 |
| | 131774 | BE267158 | Hs.169474 | DKFZP586J0119 protein | 5.5 |
| 25 | 131787 | D87077 | Hs.196275 | KIAA0240 protein | 2.4 |
| | 131793 | AW966127 | Hs.32246 | Homo sapiens cDNA FLJ14656 fis, clone NT2RP2002439 | 7.9 |
| | 131795 | BE501849 | Hs.32317 | high-mobility group 20B | 1.4 |
| | 131798 | X86098 | Hs.301449 | adenovirus 5 E1A binding protein | 4.1 |
| | 131817 | U20536 | Hs.3280 | caspase 6, apoptosis-related cysteine protease | 4.2 |
| 30 | 131824 | U28838 | Hs.32935 | TATA box binding protein (TBP)-associated factor, RNA polymerase III, GTF3B subunit 2 | 3.5 |
| | 131850 | AI251317 | Hs.33184 | ESTs | 5.1 |
| | 131878 | AA083764 | Hs.6101 | hypothetical protein MGC3178 | 5.8 |
| | 131885 | BE502341 | Hs.3402 | ESTs | 13.7 |
| | 131885 | BE502341 | Hs.3402 | ESTs | 2.4 |
| 35 | 131887 | W17064 | Hs.332848 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 | 3.2 |
| | 131900 | AA099014 | Hs.231029 | Homo sapiens, clone MGC:15961, mRNA, complete cds | 8.7 |
| | 131900 | AA099014 | Hs.231029 | Homo sapiens, clone MGC:15961, mRNA, com | 2.0 |
| | 131904 | AF078866 | Hs.284296 | Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 | 5.5 |
| | 131905 | AA179298 | Hs.3439 | stomatin-like 2 | 11.3 |
| 40 | 131913 | AW207440 | Hs.185973 | degenerative spermatocyte (homolog Drosophila; lipid desaturase) | 1.7 |
| | 131916 | AA025976 | Hs.34569 | ESTs | 5.2 |
| | 131925 | AF151048 | Hs.183180 | anaphase promoting complex subunit 11 (yeast APC11 homolog) | 2.7 |
| | 131929 | BE541211 | Hs.34804 | Homo sapiens cDNA FLJ11472 fis, clone HEMBA1001711 | 5.3 |
| | 131941 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 2.3 |
| 45 | 131950 | AA355113 | Hs.35380 | x 001 protein | 1.5 |
| | 131962 | AK000046 | Hs.267448 | hypothetical protein FLJ20039 | 2.3 |
| | 131965 | W79283 | Hs.35962 | ESTs | 1.4 |
| | 131971 | BE567100 | Hs.154938 | hypothetical protein MDS025 | 3.5 |
| | 131977 | U90441 | Hs.3622 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II | 6.5 |
| 50 | 131985 | AA503020 | Hs.36563 | hypothetical protein FLJ22418 | 2.4 |
| | 131991 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 (yeast homolog), beta | 2.1 |
| | 132019 | H56995 | Hs.37372 | Homo sapiens DNA binding peptide mRNA, partial cds | 3.2 |
| | 132031 | AF193844 | Hs.3758 | COP9 complex subunit 7a | 5.8 |
| | 132062 | BE266155 | Hs.3832 | clathrin-associated protein AP47 | 1.5 |
| 55 | 132084 | NM_002267 | Hs.3886 | karyopherin alpha 3 (importin alpha 4) | 3.7 |
| | 132103 | BE171921 | Hs.3991 | ESTs | 1.4 |
| | 132105 | AV646076 | Hs.39959 | ESTs | 5.8 |
| | 132116 | AW960474 | Hs.40289 | ESTs | 1.7 |
| | 132176 | AA857025 | Hs.8878 | kinesin-like 1 | 3.3 |
| 60 | 132180 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 14.7 |
| | 132192 | AA206153 | Hs.4209 | mitochondrial ribosomal protein L37 | 5.5 |
| | 132194 | R42432 | Hs.4212 | ESTs | 4.4 |
| | 132203 | NM_004782 | Hs.194714 | synaptosomal-associated protein, 29kD | 2.2 |
| | 132207 | BE206939 | Hs.42287 | E2F transcription factor 6 | 2.2 |
| 65 | 132235 | AV658411 | Hs.42656 | KIAA1681 protein | 7.8 |
| | 132240 | AB018324 | Hs.42676 | KIAA0781 protein | 1.5 |
| | 132252 | AI566004 | Hs.141269 | Homo sapiens cDNA: FLJ21550 fis, clone COL06258 | 1.3 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 132266 | AA301228 | Hs.43299 | hypothetical protein FLJ12890 | 5.7 |
| | 132273 | AA227710 | Hs.43658 | DKFZP586L151 protein | 4.2 |
| | 132276 | AA653507 | Hs.285711 | hypothetical protein FLJ13089 | 2.1 |
| 5 | 132288 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glucose transporter), member 10 | 1.5 |
| | 132294 | AB023191 | Hs.44131 | KIAA0974 protein | 10.0 |
| | 132298 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 1.9 |
| | 132299 | AW405882 | Hs.44205 | cortistatin | 9.2 |
| | 132325 | N37065 | Hs.44856 | hypothetical protein FLJ12116 | 2.0 |
| | 132348 | AW067708 | Hs.170311 | heterogeneous nuclear ribonucleoprotein D-like | 6.5 |
| 10 | 132370 | AW572805 | Hs.46645 | ESTs | 3.8 |
| | 132374 | AF155582 | Hs.46744 | core1 UDP-galactose:N-acetylgalactosamine- α -R beta 1,3-galactosyltransferase | 1.5 |
| | 132376 | AI279892 | Hs.46801 | sorting nexin 14 | 12.5 |
| | 132384 | AA312135 | Hs.46967 | HSPCO34 protein | 28.3 |
| | 132393 | AL135094 | Hs.47334 | hypothetical protein FLJ14495 | 1.9 |
| 15 | 132450 | AA100012 | Hs.48827 | hypothetical protein FLJ12085 | 1.9 |
| | 132452 | AW973521 | Hs.247324 | mitochondrial ribosomal protein S14 | 6.1 |
| | 132456 | AB011084 | Hs.48924 | KIAA0512 gene product; ALEX2 | 1.7 |
| | 132465 | AW169847 | Hs.49169 | KIAA1634 protein | 8.6 |
| | 132470 | AI224456 | Hs.4934 | H.sapiens polyA site DNA | 5.2 |
| 20 | 132484 | X16660 | Hs.119007 | RAB4, member RAS oncogene family | 1.4 |
| | 132518 | AW885606 | Hs.5064 | ESTs | 6.1 |
| | 132528 | T78736 | Hs.50758 | SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 | 3.3 |
| | 132530 | AA306105 | Hs.50785 | SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 | 2.0 |
| | 132532 | AA454132 | Hs.5080 | mitochondrial ribosomal protein L16 | 2.9 |
| 25 | 132534 | BE388673 | Hs.5086 | hypothetical protein MGC10433 | 2.2 |
| | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 7.3 |
| | 132571 | AW674699 | Hs.5169 | suppressor of G2 allele of SKP1, S. cerevisiae, homolog of | 1.7 |
| | 132574 | AW631437 | Hs.5184 | TH1 drosophila homolog | 7.1 |
| | 132596 | AK001484 | Hs.5298 | CGI-45 protein | 2.2 |
| 30 | 132611 | AA345547 | Hs.53263 | hypothetical protein FLJ13287 | 2.2 |
| | 132612 | H12751 | Hs.5327 | PRO1914 protein | 6.8 |
| | 132616 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 14.0 |
| | 132638 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 9928 expressed sequence | 11.4 |
| | 132648 | U51127 | Hs.54434 | hypothetical protein MGC1715 | 1.9 |
| 35 | 132668 | AB018319 | Hs.5460 | KIAA0776 protein | 2.6 |
| | 132692 | AW191962 | Hs.249239 | collagen, type VIII, alpha 2 | 2.0 |
| | 132715 | F11875 | Hs.5534 | Homo sapiens cDNA FLJ12961 fis, clone NT2RP2005645 | 1.5 |
| | 132718 | NM_004600 | Hs.554 | Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro) | 3.0 |
| 40 | 132724 | AI142265 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 2.4 |
| | 132731 | AI189075 | Hs.301872 | hypothetical protein MGC4840 | 12.4 |
| | 132744 | AA010233 | Hs.55921 | glutamyl-prolyl-HRNA synthetase | 14.6 |
| | 132760 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblastoma cells | 2.7 |
| | 132771 | Y10275 | Hs.56407 | phosphoserine phosphatase | 3.0 |
| | 132773 | AA459713 | Hs.295901 | KIAA0493 protein | 2.3 |
| 45 | 132784 | AI142133 | Hs.56845 | GDP dissociation inhibitor 2 | 1.8 |
| | 132798 | AI026701 | Hs.5716 | KIAA0310 gene product | 3.7 |
| | 132807 | U07418 | Hs.57301 | mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) | 1.8 |
| | 132810 | AB007944 | Hs.5737 | KIAA0475 gene product | 5.9 |
| 50 | 132813 | BE313625 | Hs.57435 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | 8.7 |
| | 132815 | AI815189 | Hs.57475 | sex comb on midleg homolog 1 | 6.4 |
| | 132817 | N27852 | Hs.57553 | tousled-like kinase 2 | 3.6 |
| | 132821 | AJ251595 | Hs.169610 | CD44 antigen (homing function and Indian blood group system) | 2.8 |
| | 132833 | U78525 | Hs.57783 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) | 14.6 |
| | 132842 | NM_004850 | Hs.279771 | Homo sapiens clone PP1596 unknown mRNA | 1.6 |
| 55 | 132844 | F12200 | Hs.5811 | chromosome 21 open reading frame 59 | 2.5 |
| | 132851 | U09716 | Hs.287912 | lectin, mannose-binding, 1 | 1.4 |
| | 132863 | BE268048 | Hs.236494 | RAB10, member RAS oncogene family | 4.2 |
| | 132869 | AW963217 | Hs.203961 | ESTs, Moderately similar to AF116721 89 PRO2168 [H.sapiens] | 2.8 |
| | 132873 | AW007683 | Hs.58598 | KIAA1266 protein | 2.0 |
| 60 | 132875 | NM_004850 | Hs.58617 | Rho-associated, coiled-coil containing protein kinase 2 | 1.6 |
| | 132891 | BE267143 | Hs.59271 | U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol) | 1.4 |
| | 132897 | AW503667 | Hs.59545 | ring finger protein 15 | 5.4 |
| | 132902 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 6.1 |
| | 132912 | AW732760 | Hs.167578 | Homo sapiens cDNA FLJ11095 fis, clone PLACE1005374 | 7.1 |
| 65 | 132913 | W78714 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921 | 2.8 |
| | 132940 | T79136 | Hs.127243 | Homo sapiens mRNA for KIAA1724 protein, partial cds | 6.1 |
| | 132941 | AI817165 | Hs.6120 | hypothetical protein FLJ13222 | 10.3 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 132942 | AA554458 | Hs.197751 | KIAA0666 protein | 1.8 |
| | 132952 | AI658580 | Hs.61426 | Homo sapiens mesenchymal stem cell protein DSC96 mRNA, partial cds | 2.2 |
| | 132962 | AA576635 | Hs.6153 | CGI-48 protein | 4.9 |
| 5 | 132972 | AA034365 | Hs.288924 | Homo sapiens cDNA FLJ11392 fis, clone HEMBA1000575 | 2.7 |
| | 132973 | AA035446 | Hs.323277 | ESTs | 5.3 |
| | 132977 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 3.2 |
| | 132980 | AA040696 | Hs.62016 | ESTs | 1.3 |
| | 132994 | AA112748 | Hs.279905 | clone HQ0310 PRO0310p1 | 3.0 |
| 10 | 133012 | AA847843 | Hs.62711 | Homo sapiens, clone IMAGE:3351295, mRNA | 10.3 |
| | 133015 | AJ002744 | Hs.246315 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 7 (GalNAc-T7) | 2.1 |
| | 133016 | AI439688 | Hs.6289 | hypothetical protein FLJ20886 | 1.3 |
| | 133053 | AI065016 | Hs.6390 | Homo sapiens clone FLB3344 PRO0845 mRNA, complete cds | 6.0 |
| | 133062 | AW500374 | Hs.64056 | PRO0149 protein | 5.3 |
| 15 | 133069 | BE247441 | Hs.6430 | protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein | 4.9 |
| | 133091 | AK001628 | Hs.64691 | KIAA0483 protein | 3.5 |
| | 133110 | AA808177 | Hs.65228 | ESTs | 13.1 |
| | 133134 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 1.3 |
| | 133145 | H94227 | Hs.6592 | Homo sapiens, clone IMAGE:2961368, mRNA, partial cds | 2.2 |
| 20 | 133152 | Z11695 | Hs.324473 | mitogen-activated protein kinase 1 | 1.3 |
| | 133174 | AA431620 | Hs.324178 | hypothetical protein MGC2745 | 17.1 |
| | 133175 | AW955632 | Hs.66666 | ESTs, Weakly similar to S19560 proline-rich protein MP4 - mouse [M.musculus] | 1.8 |
| | 133177 | X97795 | Hs.66718 | RAD54 (S.cerevisiae)-like | 4.9 |
| | 133197 | AI275243 | Hs.180201 | hypothetical protein FLJ20671 | 3.1 |
| 25 | 133208 | AI801777 | Hs.6774 | ESTs | 4.4 |
| | 133226 | AW954569 | Hs.296287 | Homo sapiens, Similar to bromodomain-containing 4, clone IMAGE:3542455, mRNA, partial cds | 1.7 |
| | 133228 | AI492924 | Hs.6831 | golgi phosphoprotein 1 | 6.0 |
| | 133240 | AK001489 | Hs.242894 | ADP-ribosylation factor-like 1 | 1.5 |
| | 133254 | AI567421 | Hs.273330 | Homo sapiens, clone IMAGE:3544662, mRNA, partial cds | 1.4 |
| 30 | 133266 | AI160873 | Hs.69233 | zinc finger protein | 5.6 |
| | 133268 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTEIN D2 [H.sapiens] | 1.9 |
| | 133285 | M76477 | Hs.289082 | GM2 ganglioside activator protein | 4.7 |
| | 133291 | BE297855 | Hs.69855 | NRAS-related gene | 5.0 |
| | 133314 | AA102670 | Hs.70725 | gamma-aminobutyric acid (GABA) A receptor, pi | 2.7 |
| 35 | 133321 | T79526 | Hs.179516 | integral type I protein | 9.3 |
| | 133327 | AL390127 | Hs.7104 | Kruppel-like factor 13 | 4.4 |
| | 133347 | BE257758 | Hs.71475 | acid cluster protein 33 | 1.8 |
| | 133360 | AI016521 | Hs.71816 | v-akt murine thymoma viral oncogene homolog 1 | 5.5 |
| | 133366 | AA292811 | Hs.72050 | non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase) | 2.7 |
| 40 | 133367 | AF231919 | Hs.18759 | KIAA0539 gene product | 1.7 |
| | 133370 | AF245505 | Hs.72157 | DKFZP564I1922 protein | 1.8 |
| | 133383 | BE313555 | Hs.7252 | KIAA1224 protein | 1.7 |
| | 133390 | AI950382 | Hs.72660 | phosphatidylserine receptor | 1.3 |
| | 133391 | AW103364 | Hs.727 | inhibin, beta A (activin A, activin AB alpha polypeptide) | 16.1 |
| 45 | 133394 | AA305127 | Hs.237225 | hypothetical protein HT023 | 12.2 |
| | 133437 | AL031591 | Hs.7370 | phosphatidylinositol transfer protein, beta | 10.4 |
| | 133452 | NM_002759 | Hs.274382 | protein kinase, interferon-inducible double stranded RNA dependent | 1.2 |
| | 133453 | AI659306 | Hs.73826 | protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) | 1.7 |
| | 133500 | AW964804 | Hs.74280 | hypothetical protein FLJ22237 | 11.1 |
| 50 | 133529 | W45623 | Hs.74571 | ADP-ribosylation factor 1 | 2.8 |
| | 133540 | AL037159 | Hs.74619 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 | 2.9 |
| | 133543 | AU077073 | Hs.108327 | damage-specific DNA binding protein 1 (127kD) | 2.5 |
| | 133578 | AU077050 | Hs.75066 | translin | 1.5 |
| | 133579 | X75346 | Hs.75074 | mitogen-activated protein kinase-activated protein kinase 2 | 2.1 |
| 55 | 133582 | BE391579 | Hs.75087 | Fas-activated serine/threonine kinase | 1.3 |
| | 133594 | AW160781 | Hs.172589 | nuclear phosphoprotein similar to S. cerevisiae PWP1 | 2.2 |
| | 133595 | AA393273 | Hs.75133 | transcription factor 6-like 1 (mitochondrial transcription factor 1-like) | 1.5 |
| | 133599 | NM_002885 | Hs.75151 | RAP1, GTPase activating protein 1 | 5.7 |
| | 133621 | NM_004893 | Hs.75258 | H2A histone family, member Y | 25.5 |
| 60 | 133627 | NM_002047 | Hs.75280 | glycyl-tRNA synthetase | 15.8 |
| | 133631 | NM_000401 | Hs.75334 | exostoses (multiple) 2 | 3.3 |
| | 133649 | U25849 | Hs.75393 | acid phosphatase 1, soluble | 1.6 |
| | 133690 | AV661185 | Hs.75574 | mitochondrial ribosomal protein L19 | 4.1 |
| | 133720 | L27841 | Hs.75737 | pericentriolar material 1 | 1.5 |
| 65 | 133722 | AW969976 | Hs.279009 | matrix Gla protein | 6.3 |
| | 133751 | AW402048 | Hs.334787 | Homo sapiens, Similar to likely ortholog of yeast ARV1, clone IMAGE:3506392, mRNA | 3.9 |
| | 133757 | T52946 | Hs.196209 | RAE1 (RNA export 1, S.pombe) homolog | 1.7 |
| | 133760 | BE271766 | Hs.181357 | laminin receptor 1 (67kD, ribosomal protein SA) | 1.8 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 133765 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteoblast) | 1.5 |
| | 133780 | AA557660 | Hs.76152 | decorin | 3.5 |
| | 133784 | BE622743 | Hs.301064 | arfaptin 1 | 6.8 |
| | 133791 | M34338 | Hs.76244 | spermidine synthase | 2.6 |
| 5 | 133797 | AL133921 | Hs.76272 | retinoblastoma-binding protein 2 | 1.4 |
| | 133822 | D50525 | Hs.699 | peptidylprolyl isomerase B (cyclophilin B) | 8.0 |
| | 133842 | AW797468 | Hs.285013 | putative human HLA class II associated protein I | 13.5 |
| | 133845 | AA147026 | Hs.76704 | ESTs | 2.2 |
| | 133850 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 1.8 |
| 10 | 133859 | U86782 | Hs.178761 | 26S proteasome-associated pad1 homolog | 2.0 |
| | 133865 | AB011155 | Hs.170290 | discs, large (Drosophila) homolog 5 | 2.8 |
| | 133867 | AW340125 | Hs.76989 | KIAA0097 gene product | 6.7 |
| | 133868 | AB012193 | Hs.183874 | cullin 4A | 2.5 |
| | 133881 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin) | 3.0 |
| 15 | 133922 | U30825 | Hs.77608 | splicing factor, arginine/serine-rich 9 | 1.4 |
| | 133924 | D86326 | Hs.325948 | vesicle docking protein p115 | 5.4 |
| | 133929 | NM_006306 | Hs.211602 | SMC1 (structural maintenance of chromosomes 1, yeast)-like 1 | 4.9 |
| | 133936 | L17128 | Hs.77719 | gamma-glutamyl carboxylase | 3.7 |
| | 133941 | BE244332 | Hs.77770 | adaptor-related protein complex 3, mu 2 subunit | 12.1 |
| 20 | 133959 | X81789 | Hs.77897 | splicing factor 3a, subunit 3, 60kD | 9.7 |
| | 133976 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor gene activator) | 3.1 |
| | 133989 | AL040328 | Hs.78202 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin | 1.3 |
| | 133997 | AI824113 | Hs.78281 | regulator of G-protein signalling 12 | 9.7 |
| | 134010 | AB016092 | Hs.197114 | RNA binding protein; AT-rich element binding factor | 2.4 |
| 25 | 134015 | D31764 | Hs.278569 | sorting nexin 17 | 2.5 |
| | 134070 | NM_003590 | Hs.78946 | cullin 3 | 1.3 |
| | 134110 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | 4.2 |
| | 134129 | NM_014742 | Hs.79305 | KIAA0255 gene product | 2.2 |
| | 134134 | H86504 | Hs.173328 | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform | 5.0 |
| 30 | 134200 | BE559598 | Hs.197803 | KIAA0160 protein | 3.2 |
| | 134206 | AF107463 | Hs.79968 | splicing factor 30, survival of motor neuron-related | 2.5 |
| | 134208 | NM_000288 | Hs.79993 | peroxisomal biogenesis factor 7 | 2.1 |
| | 134219 | NM_000402 | Hs.80206 | glucose-6-phosphate dehydrogenase | 9.1 |
| | 134234 | BE300078 | Hs.80449 | Homo sapiens, clone IMAGE:3535294, mRNA, partial cds | 2.8 |
| 35 | 134275 | AI878910 | Hs.3688 | cisplatin resistance-associated overexpressed protein | 1.8 |
| | 134292 | AI906291 | Hs.81234 | immunoglobulin superfamily, member 3 | 2.0 |
| | 134301 | AW502505 | Hs.81360 | Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 | 2.5 |
| | 134305 | U61397 | Hs.81424 | ubiquitin-like 1 (sentrin) | 2.8 |
| | 134324 | AB029023 | Hs.179946 | KIAA1100 protein | 10.4 |
| 40 | 134326 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (versican) | 1.9 |
| | 134329 | N92036 | Hs.81848 | RAD21 (S. pombe) homolog | 2.6 |
| | 134337 | NM_004922 | Hs.81964 | SEC24 (S. cerevisiae) related gene family, member C | 2.3 |
| | 134348 | AW291946 | Hs.82065 | interleukin 6 signal transducer (gp130, oncostatin M receptor) | 13.0 |
| | 134367 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, | 8.8 |
| 45 | 134376 | X06560 | Hs.82396 | 2',5'-oligoadenylate synthetase 1 (40-46 kD) | 1.5 |
| | 134379 | AW362124 | Hs.323193 | hypothetical protein MGC3222 | 8.1 |
| | 134384 | AI589941 | Hs.8254 | Homo sapiens, Similar to tumor differentially expressed 1, clone IMAGE:3639252, mRNA, partial cds | 2.6 |
| | 134391 | AA417383 | Hs.82582 | integrin, beta-like 1 (with EGF-like repeat domains) | 4.1 |
| | 134395 | AA456539 | Hs.8262 | lysosomal | 1.7 |
| 50 | 134403 | AA334551 | Hs.82767 | sperm specific antigen 2 | 2.6 |
| | 134405 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 1.3 |
| | 134411 | BE272095 | Hs.167791 | reticulocalbin 1, EF-hand calcium binding domain | 3.2 |
| | 134415 | AI750762 | Hs.82911 | protein tyrosine phosphatase type IVA, member 2 | 1.9 |
| | 134421 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 10.3 |
| 55 | 134424 | Z44190 | Hs.83023 | peroxisomal biogenesis factor 11B | 2.4 |
| | 134446 | AA112036 | Hs.83419 | KIAA0252 protein | 1.2 |
| | 134447 | M58603 | Hs.83428 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | 1.6 |
| | 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 2.1 |
| | 134480 | NM_005000 | Hs.83916 | Empirically selected from AFFX single probeset | 5.3 |
| 60 | 134485 | X82153 | Hs.83942 | cathepsin K (pseudosclerosis) | 2.5 |
| | 134498 | AW246273 | Hs.84131 | threonyl-tRNA synthetase | 2.1 |
| | 134513 | AA425473 | Hs.84429 | KIAA0971 protein | 3.8 |
| | 134516 | AK001571 | Hs.273357 | hypothetical protein FLJ10709 | 2.4 |
| | 134520 | BE091005 | Hs.74861 | activated RNA polymerase II transcription cofactor 4 | 6.7 |
| 65 | 134529 | AW411479 | Hs.848 | FK506-binding protein 4 (59kD) | 2.3 |
| | 134577 | BE244323 | Hs.85951 | exportin, tRNA (nuclear export receptor for tRNAs) | 5.5 |
| | 134582 | AA927177 | Hs.86041 | CGG triplet repeat binding protein 1 | 5.8 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 134612 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 2.2 |
| | 134624 | AF035119 | Hs.8700 | deleted in liver cancer 1 | 2.0 |
| | 134632 | X78520 | Hs.174139 | chloride channel 3 | 2.3 |
| | 134654 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 1.4 |
| 5 | 134664 | AA256106 | Hs.87507 | ESTs | 72.9 |
| | 134666 | BE391929 | Hs.8752 | transmembrane protein 4 | 8.5 |
| | 134687 | U62317 | Hs.88251 | arylsulfatase A | 6.0 |
| | 134692 | NM_003474 | Hs.8850 | a disintegrin and metalloproteinase domain 12 (meltrin alpha) | 4.3 |
| | 134705 | BE161887 | Hs.88799 | anaphase-promoting complex subunit 10 | 2.3 |
| 10 | 134714 | Y14768 | Hs.890 | lysosomal | 6.7 |
| | 134719 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alpha) | 2.3 |
| | 134722 | AF129536 | Hs.284226 | F-box only protein 6 | 2.9 |
| | 134724 | AF045239 | Hs.321576 | ring finger protein 22 | 6.6 |
| | 134746 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell receptor | 2.3 |
| 15 | 134751 | AW630803 | Hs.89497 | lamin B1 | 6.2 |
| | 134790 | BE002798 | Hs.287850 | integral membrane protein 1 | 1.9 |
| | 134806 | AD001528 | Hs.89718 | spermine synthase | 1.8 |
| | 134834 | AW451370 | Hs.8991 | adaptor-related protein complex 1, gamma 2 subunit | 1.4 |
| | 134850 | AI701162 | Hs.90207 | hypothetical protein MGC11138 | 1.4 |
| 20 | 134853 | BE268326 | Hs.90280 | 5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase | 5.6 |
| | 134859 | D26488 | Hs.90315 | KIAA0007 protein | 2.8 |
| | 134880 | AI879195 | Hs.90606 | 15 kDa selenoprotein | 1.7 |
| | 134910 | AA532963 | Hs.9100 | Homo sapiens cDNA FLJ13100 fis, clone NT2RP3002255 | 1.7 |
| | 134925 | AW885909 | Hs.6975 | PRO1073 protein | 2.1 |
| 25 | 134955 | AW401361 | Hs.91773 | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform | 1.3 |
| | 134971 | AI097346 | Hs.286049 | phosphoserine aminotransferase | 2.1 |
| | 134975 | R50333 | Hs.92186 | Leman coiled-coil protein | 2.3 |
| | 135011 | AB037835 | Hs.92991 | KIAA1414 protein | 1.6 |
| | 135022 | NM_000408 | Hs.93201 | glycerol-3-phosphate dehydrogenase 2 (mitochondrial) | 3.9 |
| 30 | 135032 | AW301984 | Hs.173685 | hypothetical protein FLJ12619 | 6.2 |
| | 135077 | AW503733 | Hs.9414 | KIAA1488 protein | 2.0 |
| | 135083 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase small subunit 2 homolog | 1.3 |
| | 135095 | AF027219 | Hs.9443 | zinc finger protein 202 | 7.1 |
| | 135096 | AA081258 | Hs.132390 | zinc finger protein 36 (KOX 18) | 3.2 |
| 35 | 135153 | AI093155 | Hs.95420 | JM27 protein | 2.5 |
| | 135181 | BE250865 | Hs.279529 | px19-like protein | 1.4 |
| | 135199 | AA477514 | Hs.96247 | translin-associated factor X | 5.0 |
| | 135207 | N26427 | Hs.9634 | ESTs, Highly similar to C10_HUMAN PUTATIVE C10 PROTEIN [H.sapiens] | 6.1 |
| | 135214 | T78802 | Hs.96560 | hypothetical protein FLJ11656 | 4.6 |
| 40 | 135243 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 5.6 |
| | 135245 | AI028767 | Hs.262603 | ESTs | 3.5 |
| | 135257 | AW291023 | Hs.97255 | ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens] | 1.2 |
| | 135263 | AI088775 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 2.6 |
| | 135274 | AA448460 | Hs.112017 | GE36 gene | 5.3 |
| 45 | 135294 | AA150320 | Hs.9800 | protein kinase Njmu-R1 | 9.1 |
| | 135295 | AI090838 | Hs.98006 | ESTs | 2.4 |
| | 135307 | AI743770 | Hs.98368 | ESTs, Weakly similar to KIAA0822 protein [H.sapiens] | 13.3 |
| | 135321 | AI652069 | Hs.98614 | ribosome binding protein 1 (dog 180kD homolog) | 2.6 |
| | 135354 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE proteins) | 8.3 |
| 50 | 135361 | AA373452 | Hs.167700 | Homo sapiens cDNA FLJ10174 fis, clone HEMBA1003959 | 1.5 |
| | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 4.9 |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar | 2.0 |
| | 134975 | R50333 | Hs.92186 | Leman coiled-coil protein | 2.6 |
| | 135011 | AB037835 | Hs.92991 | KIAA1414 protein | 1.4 |
| 55 | 135022 | NM_000408 | Hs.93201 | glycerol-3-phosphate dehydrogenase 2 (mi | 1.6 |
| | 135032 | AW301984 | Hs.173685 | hypothetical protein FLJ12619 | 1.4 |
| | 135077 | AW503733 | Hs.9414 | KIAA1488 protein | 1.8 |
| | 135083 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase s | 2.5 |
| | 135095 | AF027219 | Hs.9443 | zinc finger protein 202 | 1.5 |
| 60 | 135096 | AA081258 | Hs.132390 | zinc finger protein 36 (KOX 18) | 2.1 |
| | 135153 | AI093155 | Hs.95420 | JM27 protein | 4.4 |
| | 135181 | BE250865 | Hs.279529 | px19-like protein | 14.9 |
| | 135199 | AA477514 | Hs.96247 | translin-associated factor X | 1.3 |
| | 135207 | N26427 | Hs.9634 | ESTs, Highly similar to C10_HUMAN PUTATI | 1.7 |
| 65 | 135214 | T78802 | Hs.96560 | hypothetical protein FLJ11656 | 6.1 |
| | 135243 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 2.7 |
| | 135245 | AI028767 | Hs.262603 | ESTs | 12.2 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 135257 | AW291023 | Hs.97255 | ESTs, Weakly similar to A46010 X-linked | 7.6 |
| | 135263 | AI088775 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 1.8 |
| | 135274 | AA448460 | Hs.112017 | GE36 gene | 4.1 |
| | 135294 | AA150320 | Hs.9800 | protein kinase Njmu-R1 | 1.2 |
| 5 | 135295 | AI090838 | Hs.98006 | ESTs | 4.8 |
| | 135307 | AI743770 | Hs.98368 | ESTs, Weakly similar to KIAA0822 protein | 5.8 |
| | 135321 | AI652069 | Hs.98614 | ribosome binding protein 1 (dog 180kD ho | 12.3 |
| | 135354 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 5.7 |
| | 135361 | AA373452 | Hs.167700 | Homo sapiens cDNA FLJ10174 fis, clone HE | 7.9 |
| 10 | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 1.9 |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 13.9 |
| | 302256 | AA857131 | Hs.171595 | HIV TAT specific factor 1 | 5.3 |
| | 302276 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 2.2 |
| | 303135 | AW592789 | Hs.279474 | HSPC070 protein | 1.4 |
| 15 | 303686 | AK000714 | Hs.109441 | MSTP033 protein | 5.2 |
| | 310085 | R43191 | Hs.101248 | Homo sapiens clone IMAGE:32553, mRNA seq | 2.3 |
| | 315518 | AA808229 | Hs.167771 | ESTs | 2.8 |
| | 317781 | NM_007057 | Hs.42650 | ZW10 Interactor | 2.0 |
| | 320836 | AI268997 | Hs.197289 | rab3 GTPase-activating protein, non-cata | 5.5 |
| 20 | 321114 | AA902256 | Hs.78979 | Golgi apparatus protein 1 | 1.4 |
| | 322221 | N24236 | Hs.179662 | nucleosome assembly protein 1-like 1 | 1.3 |
| | 322474 | AF118083 | Hs.29494 | PRO1912 protein | 2.9 |
| | 322556 | BE041451 | Hs.177507 | hypothetical protein | 1.6 |
| | 323541 | AF292100 | Hs.104613 | RP42 homolog | 1.8 |
| 25 | 407827 | BE278431 | Hs.40323 | BUB3 (budding uninhibited by benzimidazo | 1.6 |
| | 408196 | AL034548 | Hs.43627 | SRY (sex determining region Y)-box 22 | 6.1 |
| | 408813 | AI580090 | Hs.48295 | RNA helicase family | 5.6 |
| | 409176 | R73727 | Hs.101617 | ESTs, Weakly similar to T32527 hypotheti | 2.6 |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 2.4 |
| 30 | 414108 | AI267592 | Hs.75761 | SFRS protein kinase 1 | 1.5 |
| | 414846 | AW304454 | Hs.77495 | UBX domain-containing 1 | 4.2 |
| | 416980 | AA381133 | Hs.80684 | high-mobility group (nonhistone chromoso | 23.6 |
| | 417378 | R57256 | Hs.82037 | TATA box binding protein (TBP)-associate | 5.8 |
| | 418283 | S79895 | Hs.83942 | cathepsin K (pseudodysostosis) | 1.3 |
| 35 | 418467 | NM_006910 | Hs.85273 | retinoblastoma-binding protein 6 | 1.6 |
| | 420269 | U72937 | Hs.96264 | alpha thalassemia/mental retardation syn | 2.3 |
| | 420802 | U22376 | Hs.1334 | v-myb avian myeloblastosis viral oncogen | 1.6 |
| | 421225 | AA463798 | Hs.102696 | MCT-1 protein | 3.5 |
| | 421642 | AF172066 | Hs.106346 | retinoic acid repressible protein | 4.9 |
| 40 | 421828 | AW891965 | Hs.279789 | histone deacetylase 3 | 3.1 |
| | 421983 | AI252640 | Hs.110364 | peptidylprolyl isomerase C (cyclophilin | 1.9 |
| | 422052 | AA302744 | Hs.104518 | ESTs | 2.4 |
| | 422055 | NM_014320 | Hs.111029 | putative heme-binding protein | 4.1 |
| | 423750 | AF165883 | Hs.298229 | prefoldin 2 | 7.0 |
| 45 | 424001 | W67883 | Hs.137476 | paternally expressed 10 (PEG10; KIAA105 | 4.9 |
| | 425182 | AF041259 | Hs.155040 | zinc finger protein 217 | 3.4 |
| | 425284 | AF155568 | Hs.155489 | NS1-associated protein 1 | 2.1 |
| | 426372 | BE304680 | Hs.169531 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 7.5 |
| | 428049 | AW183765 | Hs.182238 | GW128 protein | 1.7 |
| 50 | 428477 | AW500533 | Hs.11482 | splicing factor, arginine/serine-rich 11 | 2.4 |
| | 437562 | AB001636 | Hs.5683 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 3.8 |
| | 438449 | AK001333 | Hs.6216 | Homo sapiens hepatocellular carcinoma-as | 5.6 |
| | 441560 | F13386 | Hs.7888 | Homo sapiens clone 23736 mRNA sequence | 2.0 |
| | 445580 | AF167572 | Hs.12912 | skb1 (S. pombe) homolog | 7.5 |
| 55 | 446999 | AA151520 | Hs.334822 | hypothetical protein MGC4485 | 2.2 |
| | 447111 | AI017574 | Hs.17409 | cysteine-rich protein 1 (intestinal) | 2.8 |
| | 447778 | BE620592 | Hs.71190 | ESTs, Weakly similar to S16506 hypotheti | 1.7 |
| | 448873 | NM_003677 | Hs.22393 | density-regulated protein | 5.9 |
| | 449687 | W68520 | Hs.331328 | Intermediate filament protein syncoilin | 5.6 |
| 60 | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 1.4 |
| | 450703 | AA011202 | Hs.184771 | nuclear factor I/C (CCAAT-binding transc | 4.7 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 2.9 |
| | 452511 | BE408178 | Hs.285165 | Homo sapiens cDNA FLJ20845 fis, clone AD | 12.1 |
| | 453157 | AF077036 | Hs.31989 | DKFZP586G1722 protein | 4.7 |
| 65 | 453658 | BE541906 | Hs.87819 | Homo sapiens, clone MGC:2492, mRNA, comp | 1.3 |
| | 100833 | AF135168 | Hs.108802 | N-ethylmaleimide-sensitive factor | 3.2 |
| | 102481 | U50360 | | gb:Human calcium, calmodulin-dependent p | 6.2 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 102827 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 7.9 |
| | 103549 | BE270465 | Hs.78793 | protein kinase C, zeta | 2.0 |
| | 104331 | AB040450 | Hs.279862 | cdk inhibitor p21 binding protein | 5.3 |
| | 110018 | AW579842 | Hs.104557 | hypothetical protein FLJ10697 | 2.0 |
| 5 | 115008 | AK001827 | Hs.87889 | helicase-mol | 5.7 |
| | 119075 | M10905 | Hs.287820 | fibronectin 1 | 1.3 |
| | 119615 | AL034423 | Hs.75875 | ubiquitin-conjugating enzyme E2 variant | 2.9 |
| | 125006 | BE065136 | Hs.145696 | splicing factor (CC1.3) | 1.7 |
| | 127609 | X80031 | Hs.530 | collagen, type IV, alpha 3 (Goodpasture | 2.4 |
| 10 | 129209 | R62676 | Hs.17820 | Rho-associated, coiled-coil containing p | 5.2 |
| | 129917 | M30773 | Hs.278540 | protein phosphatase 3 (formerly 2B), reg | 4.5 |
| | 130182 | BE267033 | Hs.192853 | ubiquitin-conjugating enzyme E2G 2 (homo | 11.0 |
| | 130365 | W56119 | Hs.155103 | eukaryotic translation initiation factor | 3.3 |
| | 131135 | NM_016569 | Hs.267182 | TBX3-Iso protein | 1.3 |
| 15 | 131853 | AI681917 | Hs.3321 | ESTs, Highly similar to IRX1_HUMAN IROQU | 3.2 |
| | 131881 | AW361018 | Hs.3383 | upstream regulatory element binding prot | 14.3 |
| | 132726 | N52298 | Hs.55608 | hypothetical protein MGC955 | 3.0 |
| | 135193 | X95525 | Hs.96103 | TATA box binding protein (TBP)-associate | 2.7 |
| | 409487 | H19886 | | gb:yn57a05.r1 Soares adult brain N2b5H | 2.3 |
| 20 | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone HE | 7.4 |

TABLE 4A

Table 4A shows the accession numbers for those pkeys lacking unigeneID's for Table 4. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accessions |
|--------|-------------------------|--|
| 123615 | 30686_-15 | AA609170 |
| 123619 | 371681_1 | AA602964 AA609200 |
| 101445 | 1650_-5 | M21259 |
| 124385 | 656394_1 | AI267847 N27351 |
| 124417 | 1642364_1 | N34059 N46979 |
| 124482 | 1657509_1 | N53935 N53950 |
| 102481 | 31281_-28 | U50360 |
| 103349 | 11052_-2 | X89059 |
| 110856 | 19346_14 | AA992380 N33063 N21418 H79958 R21911 H79957 103797 109699_1 AA080912 AA075318 AA083403 AA076594 AA078992 AA084926 AA081881 AA113913 AA113892 AA083821 AA134801 AA082953 AA070343 AA062835 AA075419 AA063293 AA071252 AA078900 AA062836 AW974305 |
| 120280 | 160212_1 | AA190577 AA181657 |
| 113248 | 328626_1 | T63857 AW971220 AA493469 T63699 |
| 120472 | 44573_2 | AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 |
| 129019 | 44573_2 | AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 |
| 120695 | 9683_3 | AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468 |
| 122188 | 275673_1 | AA398838 AA435847 |
| 121581 | 283769_1 | AA416568 AA442889 AA417233 AA442223 |
| 122618 | 305217_1 | AA453641 AA454061 |
| 109026 | 150431_1 | AA157811 AA836869 |
| 123658 | genbank_AA609364 | AA609364 |
| 123811 | genbank_AA620586 | AA620586 |
| 125115 | genbank_T97341 | T97341 |
| 125147 | NOT_FOUND_entrez_W38150 | W38150 |
| 118737 | 382979_1 | AA199686 N73861 |
| 120274 | genbank_AA177051 | AA177051 |
| 113196 | genbank_T57317 | T57317 |
| 120504 | genbank_AA256837 | AA256837 |
| 120639 | genbank_AA286942 | AA286942 |

120809 genbank_AA346495 AA346495
 113702 genbank_T97307 T97307
 129680 23162_1 U03749 NM_001275 J03483 J03915 AI214509 AW245744 AL046455 AA318960 AI741505 AA843875 AI829382 AI560122
 5 AI858999 D55958 AI684005 D53170 AA854091 AI025609 D53119 D54729 D55504 D55377 D55313 AW512244 AA846441
 AW043898 AI969102 AA405741 AI091983 AA788784 AA706586 AA854361 AW470949 AA843095 AA772028 AI148432
 AI038109 AA782478 AA910064 AI220384 AA781296 AA843881 AA854064 AA843125 AA843419 AA319036 AA319054
 AI273831 W32275 AI584185 C05724 AA789023 AI686818 D54392 AI022485 AA431410 AA854232 W39212 W15214 AA894441
 AI803081 AI167381 AW245389 AA319430 AA335156 AI042646 AA327030 AA725170 T27943 AA889304 AA976699 AI687001
 AI621107 AI865540 AA772107 C06286 AA319661 AA405992
 10 101045 entrez_J05614 J05614
 117247 genbank N21032
 110501 genbank H55748
 103392 entrez_X94563 X94563
 105032 genbank AA127818
 15 119513 NOT_FOUND_entrez W37933
 105445 genbank AA252395
 121514 genbank AA412112
 121558 genbank AA412497
 121911 genbank AA427950
 20 123315 714071_1 AA496369 AA496646
 114911 genbank AA236672
 409487 1134778_1 H19886 AW402806 T10231

TABLE 5: Figure 5 from BRCA 001 US

Table 5 shows genes upregulated in tumor tissue compared to normal breast tissue.

5

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal breast tissue

10

| Pkey | ExAccn | UnigenelD | UnigeneTitle | R1 |
|--------|-----------|-----------|--|------|
| 100114 | X02308 | Hs.82962 | thymidylate synthetase | 2.9 |
| 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fascin) | 7.5 |
| 100154 | H60720 | Hs.81892 | KIAA0101 gene product | 9.2 |
| 100335 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrolase | 2.7 |
| 100666 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 5.7 |
| 100667 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 9 |
| 100668 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 7.6 |
| 100678 | AW502935 | Hs.740 | PTK2 protein tyrosine kinase 2 | 53.2 |
| 100988 | AK000405 | Hs.76480 | ubiquitin-like 4 | 11.4 |
| 101031 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B) | 8.2 |
| 101045 | J05614 | | gb:Human proliferating cell nuclear anti | 5 |
| 101332 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 3.4 |
| 101352 | AI494299 | Hs.16297 | COX17 (yeast) homolog, cytochrome c oxid | 6.3 |
| 101580 | NM_012151 | Hs.83363 | coagulation factor VIII-associated (Intr | 5.7 |
| 101592 | AF064853 | Hs.91299 | guanine nucleotide binding protein (| 5.6 |
| 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 14.4 |
| 101806 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 8.9 |
| 101810 | NM_000318 | Hs.180612 | peroxisomal membrane protein 3 (35kD, Ze | 3.2 |
| 101983 | AI904232 | Hs.75323 | prohibitin | 8.4 |
| 102107 | BE258602 | Hs.182366 | heat shock protein 75 | 1.4 |
| 102165 | BE313280 | Hs.159627 | death associated protein 3 | 4.6 |
| 102198 | AW950852 | Hs.74598 | polymerase (DNA directed), delta 2, regu | 4.3 |
| 102217 | AA829978 | Hs.301613 | JTV1 gene | 6.7 |
| 102220 | U24389 | Hs.65436 | lysosomal | 4.3 |
| 102302 | AA306342 | Hs.69171 | protein kinase C-like 2 | 2.7 |
| 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 2 |
| 102374 | U33635 | Hs.90572 | PTK7 protein tyrosine kinase 7 | 6.2 |
| 102455 | U48705 | Hs.75562 | discoidin domain receptor family, member | 6.9 |
| 102568 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 5.3 |
| 102618 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 5.8 |
| 102687 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 4.3 |
| 102689 | U96132 | Hs.171280 | hydroxyacyl-Coenzyme A dehydrogenase, ty | 6 |
| 102704 | AU077058 | Hs.54089 | BRCA1 associated RING domain 1 | 1.9 |
| 102705 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 2.3 |
| 102801 | BE252241 | Hs.38041 | pyridoxal (pyridoxine, vitamin B6) kinas | 6.4 |
| 102827 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 5.6 |
| 103060 | NM_005940 | Hs.155324 | matrix metalloproteinase 11 (MMP11; stro | 4.5 |
| 103080 | AU077231 | Hs.82932 | cyclin D1 (PRAD1; parathyroid adenomas | 3.1 |
| 103178 | AA205475 | Hs.275865 | ribosomal protein S18 | 9.9 |
| 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 8.8 |
| 103238 | AI369285 | Hs.75189 | death-associated protein | 5.6 |
| 103547 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, | 9.7 |
| 103549 | BE270465 | Hs.78793 | protein kinase C, zeta | 7.9 |
| 103886 | AK001278 | Hs.105737 | hypothetical protein FLJ10416 similar to | 6.5 |
| 104325 | BE379766 | Hs.150675 | polymerase (RNA) II (DNA directed) polyp | 6.3 |
| 104827 | AW052006 | Hs.8551 | PRP4/STK/WD splicing factor | 10.9 |
| 104846 | AI250789 | Hs.32478 | ESTs | 5.6 |
| 104854 | AA041276 | Hs.154729 | 3-phosphoinositide dependent protein kin | 12.3 |
| 104867 | AA278898 | Hs.225979 | hypothetical protein similar to small G | 2 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 104896 | AW015318 | Hs.23165 | ESTs | 17.7 |
| | 104909 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 5 |
| | 104916 | AW958157 | Hs.155489 | NS1-associated protein 1 | 1.7 |
| | 104919 | AA026880 | Hs.25252 | prolactin receptor | 1.4 |
| 5 | 104974 | Y12059 | Hs.278675 | bromodomain-containing 4 | 1.4 |
| | 104978 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 7.2 |
| | 105012 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.3 |
| | 105039 | AA907305 | Hs.36475 | ESTs | 2.5 |
| | 105079 | AA151342 | Hs.12677 | CGI-147 protein | 9.5 |
| 10 | 105088 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PL | 2.2 |
| | 105393 | AF167570 | Hs.256583 | interleukin enhancer binding factor 3, 9 | 5.4 |
| | 105547 | AA262640 | Hs.27445 | unknown | 9.3 |
| | 105564 | BE616694 | Hs.288042 | hypothetical protein FLJ14299 | 1.4 |
| | 105658 | AA985190 | Hs.246875 | hypothetical protein FLJ20059 | 9.4 |
| 15 | 105746 | AW151952 | Hs.46679 | hypothetical protein FLJ20739 | 1.5 |
| | 105858 | AF151066 | Hs.281428 | hypothetical protein | 2.9 |
| | 105930 | AF016371 | Hs.9880 | peptidyl prolyl isomerase H (cyclophilin | 5.2 |
| | 106094 | AA533491 | Hs.23317 | hypothetical protein FLJ14681 | 6.8 |
| | 106350 | AK001404 | Hs.194698 | cyclin B2 | 5.7 |
| 20 | 106359 | AW390282 | Hs.31130 | transmembrane 7 superfamily member 2 | 6.3 |
| | 106610 | AA458882 | Hs.79732 | fibulin 1 | 7.9 |
| | 106624 | NM_003595 | Hs.26350 | tyrosylprotein sulfotransferase 2 | 7.7 |
| | 106713 | BE614802 | Hs.184352 | hypothetical protein FLJ12549 | 4.5 |
| | 106829 | AW95893 | Hs.27099 | hypothetical protein FLJ23293 similar to | 16.2 |
| 25 | 106846 | AB037744 | Hs.34892 | KIAA1323 protein | 2.2 |
| | 106873 | N49809 | Hs.11197 | Homo sapiens, clone IMAGE:3343149, mRNA, | 16.8 |
| | 106973 | BE156256 | Hs.11923 | hypothetical protein | 6.6 |
| | 107029 | AF264750 | Hs.288971 | myeloid/lymphoid or mixed-lineage leukem | 1.8 |
| | 107197 | W15477 | Hs.64639 | glioma pathogenesis-related protein | 6.1 |
| 30 | 107859 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 8.4 |
| | 107901 | L42612 | Hs.335952 | keratin 6B | 2.5 |
| | 107922 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 2.2 |
| | 107974 | AW956103 | Hs.61712 | pyruvate dehydrogenase kinase, isoenzyme | 6.7 |
| | 108274 | AF129535 | Hs.272027 | F-box only protein 5 | 7.1 |
| 35 | 108647 | BE546947 | Hs.44276 | homeo box C10 | 9.8 |
| | 108695 | AB029000 | Hs.70823 | KIAA1077 protein | 7.2 |
| | 108894 | AK001431 | Hs.5105 | hypothetical protein FLJ10569 | 4 |
| | 109011 | AA156542 | Hs.72127 | ESTs | 1.4 |
| | 109068 | AA164293 | Hs.72545 | ESTs | 2.9 |
| 40 | 109273 | AA375752 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 2.9 |
| | 109468 | NM_015310 | Hs.6763 | KIAA0942 protein | 3.2 |
| | 110240 | A1668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 4.2 |
| | 110330 | A1288666 | Hs.16621 | DKFZP434I116 protein | 6.2 |
| | 110501 | H55748 | | gb:yq94a01.s1 Soares fetal liver spleen | 6.1 |
| 45 | 110742 | AW190338 | Hs.28029 | hypothetical protein MGC11256 | 7.6 |
| | 110762 | BE044245 | Hs.30011 | hypothetical protein MGC2963 | 9.3 |
| | 110856 | AA992380 | | gb:ot37g06.s1 Soares_testis_NHT Homo sap | 2.3 |
| | 110958 | NM_005864 | Hs.24587 | signal transduction protein (SH3 contain | 6.7 |
| | 111125 | N63823 | Hs.269115 | ESTs, Moderately similar to Z195_HUMAN Z | 3.6 |
| 50 | 111179 | AK000136 | Hs.10760 | asporin (LRR class 1) | 7.1 |
| | 111239 | N90956 | Hs.17230 | hypothetical protein FLJ22087 | 7.9 |
| | 111285 | AA778711 | Hs.4310 | eukaryotic translation initiation factor | 6.9 |
| | 111392 | W46342 | Hs.325081 | Homo sapiens, clone IMAGE:3659680, mRNA, | 8.4 |
| | 111937 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (fr | 10.6 |
| 55 | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 14.6 |
| | 112995 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYK | 5.6 |
| | 113777 | BE266947 | Hs.10590 | zinc finger protein 313 | 13.4 |
| | 113791 | A1269096 | Hs.135578 | chitinase, di-N-acetyl- | 1.3 |
| | 113811 | BE207480 | Hs.6994 | Homo sapiens cDNA: FLJ22044 fis, clone H | 3.1 |
| 60 | 113834 | T26483 | Hs.6059 | EGF-containing fibulin-like extracellular | 11.3 |
| | 113868 | W57902 | Hs.90744 | proteasome (prosome, macropain) 26S subu | 2.7 |
| | 113870 | AL079314 | Hs.16537 | hypothetical protein, similar to (U06944 | 6.1 |
| | 113923 | AW953484 | Hs.3849 | hypothetical protein FLJ22041 similar to | 1.9 |
| | 114275 | AW515443 | Hs.306117 | KIAA0306 protein | 15.8 |
| 65 | 114895 | AA236177 | Hs.76591 | KIAA0887 protein | 7.1 |
| | 114965 | AI733881 | Hs.72472 | BMP-R1B | 2.3 |
| | 115061 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 11.8 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 115278 | AK002163 | Hs.301724 | hypothetical protein FLJ11301 | 1.5 |
| | 115291 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 6.2 |
| | 115652 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 10.6 |
| 5 | 115693 | AF231023 | Hs.55173 | cadherin, EGF LAG seven-pass G-type rece | 6.8 |
| | 115941 | AI867451 | Hs.46679 | hypothetical protein FLJ20739 | 5.5 |
| | 115968 | AB037753 | Hs.62767 | KIAA1332 protein | 9.8 |
| | 116011 | AL359053 | Hs.57664 | Homo sapiens mRNA full length insert cDN | 2.4 |
| | 116417 | AW499664 | Hs.12484 | Human clone 23826 mRNA sequence | 7.4 |
| | 116470 | AI272141 | Hs.83484 | SRV (sex determining region Y)-box 4 | 2.1 |
| 10 | 116637 | AK001043 | Hs.92033 | integrin-linked kinase-associated serine | 2.7 |
| | 117132 | AI393666 | Hs.42315 | p10-binding protein | 5.2 |
| | 117881 | AF161470 | Hs.260622 | butyrate-induced transcript 1 | 5.7 |
| | 118528 | AI949952 | Hs.49397 | ESTs | 7.4 |
| | 119075 | M10905 | Hs.287820 | fibronectin 1 | 5.7 |
| 15 | 119265 | BE539706 | Hs.285363 | ESTs | 1.4 |
| | 119349 | T65004 | Hs.163561 | ESTs | 8.4 |
| | 119403 | AL117554 | Hs.119908 | nucleolar protein NOP5/NOP58 | 6.7 |
| | 119789 | BE393948 | Hs.50915 | kallikrein 5 (KLK5; KLK-L2; stratum com | 9.2 |
| 20 | 120206 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 45.7 |
| | 120253 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 38.9 |
| | 120297 | AA191384 | Hs.104072 | ESTs, Weakly similar to Z195_HUMAN ZINC | 15.2 |
| | 120325 | AA195651 | Hs.104106 | ESTs | 6.4 |
| | 120327 | AK000292 | Hs.278732 | hypothetical protein FLJ20285 | 16.1 |
| | 120349 | AW969481 | Hs.55189 | hypothetical protein | 16.8 |
| 25 | 120356 | AF000545 | Hs.296433 | putative purinergic receptor | 28.1 |
| | 120371 | AA219305 | Hs.104196 | EST | 12.4 |
| | 120383 | AL109963 | Hs.123122 | FSH primary response (LRPR1, rat) homolo | 9.7 |
| | 120386 | AW969665 | Hs.154848 | hypothetical protein DKFZp434D0127 | 32.6 |
| 30 | 120389 | AW967985 | Hs.325572 | ESTs, Moderately similar to ALU7_HUMAN A | 21.7 |
| | 120396 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 12.5 |
| | 120418 | AW966893 | Hs.26613 | Homo sapiens mRNA; cDNA DKFZp586F1323 (f | 11.4 |
| | 120472 | AI950087 | | gb:zwq05c02.x1 NCI_CGAP_Kid12 Homo sapien | 19.4 |
| | 120484 | AA253170 | Hs.96473 | EST | 10.4 |
| 35 | 120570 | AA280679 | Hs.271445 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 14.4 |
| | 120582 | BE244830 | Hs.284228 | ZNF135-like protein | 10.2 |
| | 120596 | AA282074 | Hs.237323 | N-acetylglucosamine-phosphate mutase | 7.5 |
| | 120624 | AW407987 | Hs.173518 | M-phase phosphoprotein homolog | 52 |
| | 120695 | AA976503 | | gb:oaq30a04.s1 NCI_CGAP_GC4 Homo sapiens | 46.8 |
| 40 | 120713 | AW449855 | Hs.96557 | Homo sapiens cDNA FLJ12727 fis, clone NT | 5.9 |
| | 120750 | AI191410 | Hs.96693 | ESTs, Moderately similar to 2109260A B c | 7 |
| | 120774 | AI608909 | Hs.193985 | ESTs | 7.8 |
| | 120807 | AA346385 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 6.8 |
| | 120809 | AA346495 | | gb:EST52657 Fetal heart II Homo sapiens | 4.4 |
| 45 | 120984 | BE262951 | Hs.99052 | ESTs | 5.6 |
| | 121081 | AA398721 | Hs.186749 | ESTs, Highly similar to I37550 mismatch | 5.4 |
| | 121408 | AA406137 | Hs.98019 | EST | 6 |
| | 121505 | AA494172 | Hs.194417 | ESTs | 13.1 |
| | 121508 | AA402515 | Hs.97887 | ESTs | 28 |
| | 121513 | AA416653 | Hs.181510 | ESTs | 6.2 |
| 50 | 121549 | AA412477 | Hs.98142 | EST | 7.4 |
| | 121558 | AA412497 | | gb:zt95g12.s1 Soares_testis_NHT Homo sap | 2.8 |
| | 121655 | AA421537 | Hs.178072 | Homo sapiens mRNA; cDNA DKFZp434B1023 (f | 7.8 |
| | 121744 | AA398784 | Hs.97514 | ESTs | 7.1 |
| 55 | 121748 | BE536911 | Hs.234545 | hypothetical protein NUF2R | 19.5 |
| | 121773 | AB033022 | Hs.158654 | KIAA1196 protein | 7.9 |
| | 121832 | AW340797 | Hs.98434 | ESTs | 5.8 |
| | 121839 | AA425691 | Hs.191606 | ESTs, Highly similar to KIAA1048 protein | 5 |
| | 121882 | AA426376 | Hs.98459 | ESTs | 5 |
| 60 | 121911 | AA427950 | | gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_ | 7.2 |
| | 121999 | AA430211 | Hs.98668 | EST | 6.4 |
| | 122013 | AA431085 | Hs.98706 | ESTs | 6.5 |
| | 122036 | W92142 | Hs.271963 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 13.1 |
| | 122356 | AA443794 | Hs.98390 | ESTs | 7.3 |
| 65 | 122371 | AA868555 | Hs.178222 | ESTs | 5 |
| | 122372 | AA446008 | Hs.336677 | EST | 7.6 |
| | 122460 | AW418788 | Hs.99148 | ESTs, Weakly similar to S43569 R01H10.6 | 9.7 |
| | 122490 | AA448349 | Hs.238151 | EST | 6.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-------|
| | 122492 | AA448417 | Hs.104990 | ESTs | 5.4 |
| | 122510 | AA449232 | Hs.99195 | ESTs | 11.2 |
| | 122530 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 10.1 |
| | 122572 | AA452601 | Hs.99287 | EST | 11 |
| 5 | 122607 | AA453518 | Hs.98023 | ESTs | 61.5 |
| | 122614 | AA453630 | Hs.99339 | EST | 10.7 |
| | 122616 | AA453638 | Hs.161873 | ESTs | 107.3 |
| | 122618 | AA453641 | | gb:zx48e06.s1 Soares_testis_NHT Homo sap | 31.1 |
| | 122622 | AA453987 | Hs.144802 | ESTs | 5.6 |
| 10 | 122717 | AA456859 | Hs.178358 | ESTs | 8.5 |
| | 122829 | AW204530 | Hs.99500 | ESTs | 81.8 |
| | 122838 | AA460584 | Hs.334386 | ESTs | 75.3 |
| | 122856 | AI929374 | Hs.75367 | Src-like-adaptor | 5.8 |
| | 122868 | AF005216 | Hs.115541 | Janus kinase 2 (a protein tyrosine kinas | 5.3 |
| 15 | 122907 | AA470074 | Hs.169896 | ESTs | 11.5 |
| | 123016 | AW338067 | Hs.323231 | Homo sapiens cDNA FLJ11946 fis, clone HE | 2.8 |
| | 123034 | AL359571 | Hs.44064 | ninein (GSK3B interacting protein) | 8.7 |
| | 123136 | AW451999 | Hs.194024 | ESTs | 5.1 |
| | 123152 | AW601773 | Hs.270259 | ESTs | 5.2 |
| 20 | 123394 | AA731404 | Hs.105510 | ESTs | 3.6 |
| | 123466 | AA599042 | Hs.112503 | EST | 7.4 |
| | 123486 | BE019072 | Hs.334802 | Homo sapiens cDNA FLJ14680 fis, clone NT | 2.4 |
| | 123615 | AA609170 | | gb:af12a12.s1 Soares_testis_NHT Homo sap | 7.8 |
| | 123735 | NM_013241 | Hs.95231 | FH1/FH2 domain-containing protein | 10 |
| 25 | 123753 | AA609955 | Hs.234961 | Huntingtin Interacting protein E | 30.6 |
| | 124006 | AI147155 | Hs.270016 | ESTs | 8.1 |
| | 124385 | AI267847 | | gb:aq49a10.x1 Stanley Frontal NB pool 2 | 57.1 |
| | 124440 | AA532519 | Hs.129043 | Human DNA sequence from clone 989H11 on | 7.8 |
| | 124656 | AW297702 | Hs.102915 | ESTs | 8.3 |
| 30 | 124683 | AA381661 | Hs.119878 | ESTs, Weakly similar to M3K9_HUMAN MITOG | 7.9 |
| | 124735 | R22952 | Hs.268685 | ESTs | 11.3 |
| | 124761 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 9 |
| | 124768 | AW368528 | Hs.100855 | ESTs | 8.1 |
| | 124788 | R43543 | Hs.100912 | Homo sapiens cDNA: FLJ22726 fis, clone H | 5.1 |
| 35 | 124811 | R46068 | Hs.288912 | hypothetical protein FLJ22604 | 14.2 |
| | 124812 | R47948 | Hs.188732 | ESTs | 7.9 |
| | 124822 | AA418160 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PL | 6.6 |
| | 124860 | R65763 | Hs.101477 | EST | 23.9 |
| | 124903 | AW296713 | Hs.221441 | ESTs | 32.4 |
| 40 | 124930 | AI076343 | Hs.173939 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 22.8 |
| | 124942 | R99978 | Hs.268892 | ESTs, Moderately similar to B34087 hypot | 6.1 |
| | 125051 | T79956 | Hs.100588 | EST | 135.3 |
| | 125056 | T81310 | Hs.100592 | ESTs | 5.4 |
| | 125101 | AI472068 | Hs.286236 | KIAA1856 protein | 5.6 |
| 45 | 125115 | T97341 | | gb:ye57e05.s1 Soares fetal liver spleen | 9.6 |
| | 125280 | AI123705 | Hs.106932 | ESTs | 8 |
| | 127274 | AW966158 | Hs.58582 | Homo sapiens cDNA FLJ12789 fis, clone NT | 12.8 |
| | 128528 | R39234 | Hs.251699 | ESTs, Weakly similar to IDN4-GGTR14 [H.s | 2.8 |
| | 128670 | AA975486 | Hs.103441 | Homo sapiens, Similar to RIKEN cDNA 1700 | 7.1 |
| 50 | 128691 | W27939 | Hs.103834 | hypothetical protein MGC5576 | 7.7 |
| | 128772 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 5.3 |
| | 128781 | N71826 | Hs.105465 | small nuclear ribonucleoprotein polypept | 53.9 |
| | 128797 | NM_002975 | Hs.105927 | stem cell growth factor; lymphocyte secr | 13.3 |
| | 128868 | AA419008 | Hs.106730 | chromosome 22 open reading frame 3 | 3 |
| 55 | 128891 | F34856 | Hs.292457 | Homo sapiens, clone MGC:16362, mRNA, com | 13.3 |
| | 128946 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | 7.2 |
| | 128975 | BE560779 | Hs.284233 | NICE-5 protein | 14 |
| | 128995 | AI816224 | Hs.107747 | DKFZP566C243 protein | 1.9 |
| | 129019 | AI950087 | | gb:wx05c02.x1 NCI_CGAP_Kld12 Homo sapien | 2.9 |
| 60 | 129076 | AW296806 | Hs.326234 | ESTs, Highly similar to T46422 hypotheti | 5 |
| | 129088 | AA744610 | Hs.194431 | palladin | 17.1 |
| | 129096 | AA463189 | Hs.288906 | WW Domain-Containing Gene | 20.9 |
| | 129198 | N57532 | Hs.109315 | KIAA1415 protein | 5.8 |
| | 129347 | BE614192 | Hs.279869 | melanoma-associated antigen recognised b | 7.6 |
| 65 | 129362 | U30246 | Hs.110736 | solute carrier family 12 (sodium/potassi | 6.7 |
| | 129372 | NM_016039 | Hs.110803 | CGI-99 protein | 2 |
| | 129404 | AI267700 | Hs.317584 | ESTs | 5 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 129482 | AA188185 | Hs.289043 | spindlin | 6.7 |
| | 129559 | W01296 | Hs.11360 | hypothetical protein FLJ14784 | 7.5 |
| | 129587 | H14718 | Hs.11506 | Human clone 23589 mRNA sequence | 6.8 |
| 5 | 129629 | AK000398 | Hs.11747 | hypothetical protein FLJ20391 | 3.8 |
| | 129649 | AD000092 | Hs.16488 | calreticulin | 3.3 |
| | 129680 | U03749 | | gbtHuman chromogranin A (CHGA) gene, pro | 14.1 |
| | 129689 | AW748482 | Hs.77873 | B7 homolog 3 | 2.6 |
| | 129702 | AI304966 | Hs.12035 | ESTs, Weakly similar to I38022 hypotheti | 7.4 |
| | 129720 | AA156214 | Hs.12152 | APMCF1 protein | 2 |
| 10 | 130010 | AA301116 | Hs.142838 | nucleolar phosphoprotein Nopp34 | 1.6 |
| | 130097 | AL046962 | Hs.14845 | forkhead box O3A | 2.8 |
| | 130135 | AA311426 | Hs.21635 | tubulin, gamma 1 | 6.1 |
| | 130211 | NM_003358 | Hs.23703 | ESTs, Moderately similar to CEGT_HUMAN C | 1.6 |
| | 130242 | X79201 | Hs.153221 | synovial sarcoma, translocated to X chro | 5.4 |
| 15 | 130359 | NM_013449 | Hs.277401 | bromodomain adjacent to zinc finger doma | 8.5 |
| | 130365 | W56119 | Hs.155103 | eukaryotic translation initiation factor | 11 |
| | 130448 | BE513202 | Hs.15589 | PPAR binding protein | 3.9 |
| | 130455 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 33.6 |
| | 130471 | AL121438 | Hs.183706 | adducin 1 (alpha) | 2.7 |
| 20 | 130503 | BE208491 | Hs.295112 | KIAA0618 gene product | 16.1 |
| | 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 6.1 |
| | 130542 | U64675 | Hs.179825 | RAN binding protein 2-like 1 | 7.8 |
| | 130553 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 14.4 |
| | 130556 | AI907018 | Hs.15977 | Empirically selected from AFFX single pr | 4.7 |
| 25 | 130567 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 7.9 |
| | 130574 | AF083208 | Hs.16178 | apoptosis antagonizing transcription fac | 1.2 |
| | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 12.1 |
| | 130667 | BE246961 | Hs.17639 | Homo sapiens ubiquitin protein ligase (U | 13.9 |
| | 130693 | R68537 | Hs.17962 | ESTs | 2 |
| 30 | 130744 | H59696 | Hs.18747 | POP7 (processing of precursor, S. cerevi | 3.1 |
| | 130757 | AL036067 | Hs.18925 | protein x 0001 | 5.7 |
| | 130880 | BE514434 | Hs.20830 | kinesin-like 2 | 2.1 |
| | 130944 | BE382657 | Hs.21486 | signal transducer and activator of trans | 5.4 |
| | 131046 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 7.4 |
| 35 | 131060 | AA194422 | Hs.22564 | myosin VI | 5.1 |
| | 131099 | AL133353 | Hs.226581 | COX15 (yeast) homolog, cytochrome c oxid | 7 |
| | 131135 | NM_016569 | Hs.267182 | TBX3-iso protein | 3.3 |
| | 131185 | BE280074 | Hs.23960 | cyclin B1 | 5.8 |
| | 131225 | H62087 | Hs.31659 | thyroid hormone receptor-associated prot | 7.5 |
| 40 | 131245 | AL080080 | Hs.24766 | thioredoxin domain-containing | 2.8 |
| | 131283 | X80038 | Hs.339713 | Homo sapiens clone F19374 APO E-C2 gene | 1.3 |
| | 131569 | AL389951 | Hs.271623 | nucleoporin 50kD | 5 |
| | 131643 | AW410601 | Hs.30026 | HSPC182 protein | 2.9 |
| | 131714 | AA642831 | Hs.31016 | putative DNA binding protein | 2.9 |
| 45 | 131722 | D13757 | Hs.311 | phosphoribosyl pyrophosphate amidotransf | 3.4 |
| | 131760 | X76732 | Hs.3164 | nucleobindin 2 | 2.9 |
| | 131793 | AW966127 | Hs.32246 | Homo sapiens cDNA FLJ14656 fls, clone NT | 7.9 |
| | 131885 | BE502341 | Hs.3402 | ESTs | 13.7 |
| 50 | 131900 | AA099014 | Hs.231029 | Homo sapiens, clone MGC:15961, mRNA, com | 8.7 |
| | 131905 | AA179298 | Hs.3439 | stomatin-like 2 | 11.3 |
| | 131941 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 2.3 |
| | 131971 | BE567100 | Hs.154938 | hypothetical protein MDS025 | 3.5 |
| | 132180 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 14.7 |
| 55 | 132203 | NM_004782 | Hs.194714 | synaptosomal-associated protein, 29kD | 7.8 |
| | 132273 | AA227710 | Hs.43658 | DKFZP586L151 protein | 10 |
| | 132288 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glu | 9.2 |
| | 132294 | AB023191 | Hs.44131 | KIAA0974 protein | 2 |
| | 132348 | AW067708 | Hs.170311 | heterogeneous nuclear ribonucleoprotein | 12.5 |
| | 132370 | AW572805 | Hs.46645 | ESTs | 28.3 |
| 60 | 132384 | AA312135 | Hs.46967 | HSPC034 protein | 6.1 |
| | 132450 | AA100012 | Hs.48827 | hypothetical protein FLJ12085 | 8.6 |
| | 132465 | AW169847 | Hs.49169 | KIAA1634 protein | 6.1 |
| | 132532 | AA454132 | Hs.5080 | mitochondrial ribosomal protein L16 | 7.1 |
| | 132574 | AW631437 | Hs.5184 | TH1 drosophila homolog | 14 |
| 65 | 132638 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 12.4 |
| | 132718 | NM_004600 | Hs.554 | Sjogren syndrome antigen A2 (60kD, ribon | 3.7 |
| | 132726 | N52298 | Hs.55608 | hypothetical protein MGC955 | 14.3 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 132731 | AI189075 | Hs.301872 | hypothetical protein MGC4840 | 5.9 |
| | 132744 | AA010233 | Hs.55921 | glutamyl-prolyl-IRNA synthetase | 6.4 |
| | 132773 | AA459713 | Hs.295901 | KIAA0493 protein | 14.6 |
| | 132798 | AI026701 | Hs.5716 | KIAA0310 gene product | 2.5 |
| 5 | 132810 | AB007944 | Hs.5737 | KIAA0475 gene product | 4.2 |
| | 132833 | U78525 | Hs.57783 | eukaryotic translation initiation factor | 6.1 |
| | 132842 | NM_016154 | Hs.279771 | Homo sapiens clone PP1596 unknown mRNA | 7.1 |
| | 132851 | U09716 | Hs.287912 | lectin, mannose-binding, 1 | 6.1 |
| | 132891 | BE267143 | Hs.59271 | U2(RNU2) small nuclear RNA auxiliary fac | 2.7 |
| 10 | 132941 | AI817165 | Hs.6120 | hypothetical protein FLJ13222 | 2.1 |
| | 132972 | AA034365 | Hs.288924 | Homo sapiens cDNA FLJ11392 fis, clone HE | 3.5 |
| | 132980 | AA040696 | Hs.62016 | ESTs | 1.3 |
| | 132994 | AA112748 | Hs.279905 | clone HQ0310 PRO0310p1 | 17.1 |
| | 133016 | AI439688 | Hs.6289 | hypothetical protein FLJ20886 | 4.4 |
| 15 | 133177 | X97795 | Hs.66718 | RAD54 (S.cerevisiae)-like | 4.4 |
| | 133208 | AI801777 | Hs.6774 | ESTs | 5.5 |
| | 133254 | AI567421 | Hs.273330 | Homo sapiens, clone IMAGE:3544662, mRNA, | 1.3 |
| | 133266 | AI160873 | Hs.69233 | zinc finger protein | 16.1 |
| | 133268 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKH | 12.2 |
| 20 | 133285 | M76477 | Hs.289082 | GM2 ganglioside activator protein | 10.4 |
| | 133390 | AI950382 | Hs.72660 | phosphatidylserine receptor | 5.7 |
| | 133391 | AW103364 | Hs.727 | inhibin, beta A (activin A, activin AB a | 25.5 |
| | 133540 | AL037159 | Hs.74619 | proteasome (prosome, macropain) 26S subu | 1.7 |
| | 133594 | AW160781 | Hs.172589 | nuclear phosphoprotein similar to S. cer | 2.6 |
| 25 | 133621 | NM_004893 | Hs.75258 | H2A histone family, member Y | 13.5 |
| | 133720 | L27841 | Hs.75737 | pericentriolar material 1 | 6.7 |
| | 133760 | BE271766 | Hs.181357 | laminin receptor 1 (67kD, ribosomal prot | 5.4 |
| | 133784 | BE622743 | Hs.301064 | arfaplin 1 | 12.1 |
| | 133791 | M34338 | Hs.76244 | spermidine synthase | 9.7 |
| 30 | 133797 | AL133921 | Hs.76272 | retinoblastoma-binding protein 2 | 1.3 |
| | 133822 | D50525 | Hs.699 | peptidylprolyl isomerase B (cyclophilin | 9.7 |
| | 133850 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 4.2 |
| | 133865 | AB011155 | Hs.170290 | discs, large (Drosophila) homolog 5 | 5 |
| | 133881 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 9.1 |
| 35 | 133924 | D86326 | Hs.325948 | vesicle docking protein p115 | 1.8 |
| | 133959 | X81789 | Hs.77897 | splicing factor 3a, subunit 3, 60kD | 10.4 |
| | 133989 | AL040328 | Hs.78202 | SWI/SNF related, matrix associated, acti | 2.6 |
| | 133997 | AI824113 | Hs.78281 | regulator of G-protein signalling 12 | 13 |
| | 134234 | BE300078 | Hs.80449 | Homo sapiens, clone IMAGE:3535294, mRNA, | 10.3 |
| 40 | 134348 | AW291946 | Hs.82065 | interleukin 6 signal transducer (gp130, | 6.7 |
| | 134376 | X06560 | Hs.82396 | 2',5'-oligoadenylate synthetase 1 (40-46 | 5.5 |
| | 134379 | AW362124 | Hs.323193 | hypothetical protein MGC3222 | 5.8 |
| | 134405 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 72.9 |
| | 134421 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 6.7 |
| 45 | 134480 | NM_005000 | Hs.83916 | Empirically selected from AFFX single pr | 6.2 |
| | 134516 | AK001571 | Hs.273357 | hypothetical protein FLJ10709 | 1.4 |
| | 134529 | AW411479 | Hs.848 | FK506-binding protein 4 (59kD) | 2.8 |
| | 134751 | AW630803 | Hs.89497 | lamin B1 | 6.1 |
| | 134790 | BE002798 | Hs.287850 | integral membrane protein 1 | 1.2 |
| 50 | 134806 | AD001528 | Hs.89718 | spermine synthase | 2.6 |
| | 134850 | AI701162 | Hs.90207 | hypothetical protein MGC11138 | 9.1 |
| | 134859 | D26488 | Hs.90315 | KIAA0007 protein | 13.3 |
| | 134971 | AI097346 | Hs.286049 | phosphoserine aminotransferase | 2 |
| | 135181 | BE250865 | Hs.279529 | px19-like protein | 14.9 |
| 55 | 135207 | N26427 | Hs.9634 | ESTs, Highly similar to C10_HUMAN PUTATI | 1.7 |
| | 135245 | AI028767 | Hs.262603 | ESTs | 12.2 |
| | 135257 | AW291023 | Hs.97255 | ESTs, Weakly similar to A46010 X-linked | 7.6 |
| | 135307 | AI743770 | Hs.98368 | ESTs, Weakly similar to KIAA0822 protein | 5.8 |
| | 135321 | AI652069 | Hs.98614 | ribosome binding protein 1 (dog 180kD ho | 12.3 |
| 60 | 135354 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 5.7 |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 13.9 |
| | 302276 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c | 5.3 |
| | 317781 | NM_007057 | Hs.42650 | ZW10 Interactor | 2.8 |
| | 321114 | AA902256 | Hs.78979 | Golgi apparatus protein 1 | 5.5 |
| 65 | 322556 | BE041451 | Hs.177507 | hypothetical protein | 2.9 |
| | 420802 | U22376 | Hs.1334 | v-myb avian myeloblastosis viral oncogen | 2.3 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 (PEG10; KIAA105 | 7 |

| | | | | | |
|---|--------|----------|-----------|--|------|
| 5 | 425182 | AF041259 | Hs.155040 | zinc finger protein 217 | 2.3 |
| | 446999 | AA151520 | Hs.334822 | hypothetical protein MGC4485 | 7.5 |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.6 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 4.7 |
| | 453157 | AF077036 | Hs.31989 | DKFZP586G1722 protein | 12.1 |

TABLE 5A

Table 5A shows the accession numbers for those pkeys lacking unigeneID's for Table 5. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

| | | |
|----|-------------|--|
| 10 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |
| 15 | Pkey | CAT number Accessions |
| | 123615 | 30686_-15 AA609170 |
| | 124385 | 656394_1 AI267847 N27351 |
| | 110856 | 19346_14 AA992380 N33063 N21418 H79958 R21911 H79957 |
| 20 | 120472 | 44573_2 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 |
| 30 | 129019 | 44573_2 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 |
| 35 | | 120695 9683_3 AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468 |
| 40 | 122618 | 305217_1 AA453641 AA454061 |
| | 125115 | genbank_T97341 T97341 |
| | 120809 | genbank_AA346495 AA346495 |
| 45 | 129680 | 23162_1 U03749 NM_001275 J03483 J03915 AI214509 AW245744 AL046455 AA318960 AI741505 AA843875 AI829382 AI560122 AI858999 D55958 AI684005 D53170 AA854091 AI025609 D53119 D54729 D55504 D55377 D55313 AW512244 AA846441 AW043898 AI969102 AA405741 AI091983 AA788784 AA706586 AA854361 AW470949 AA843095 AA772028 AI148432 AI038109 AA782478 AA910064 AI220384 AA781296 AA843881 AA854064 AA843125 AA843419 AA319036 AA319054 AI273831 W32275 AI584185 C05724 AA789023 AI686818 D54392 AI022485 AA431410 AA854232 W39212 W15214 AA894441 AI803081 AI167381 AW245389 AA319430 AA335156 AI042646 AA327030 AA725170 T27943 AA889304 AA976699 AI687001 AI621107 AI865540 AA772107 C06286 AA319661 AA405992 |
| 50 | 101045 | entrez_J05614 J05614 |
| | 110501 | genbank_H55748 H55748 |
| | 121558 | genbank_AA412497 AA412497 |
| 55 | 121911 | genbank_AA427950 AA427950 |

TABLE 6: Figure 6 from BRCA 001 US

Table 6 shows genes upregulated in tumor tissue compared to normal breast tissue.

5

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal breast tissue

10

15

| Pkey | ExAccn | UnigeneID | UnigeneTitle | R1 |
|--------|-----------|-----------|--|-------|
| 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fasciclin | 7.5 |
| 100678 | AW502935 | Hs.740 | PTK2 protein tyrosine kinase 2 | 53.2 |
| 101806 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 8.9 |
| 102455 | U48705 | Hs.75562 | discoidin domain receptor family, member | 6.9 |
| 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 8.8 |
| 105743 | BE246502 | Hs.9598 | sema domain, immunoglobulin domain (Ig), | 2.6 |
| 105746 | AW151952 | Hs.46679 | hypothetical protein FLJ20739 | 1.5 |
| 106373 | AW503807 | Hs.21907 | histone acetyltransferase | 1.8 |
| 110240 | AI668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 4.2 |
| 119260 | AK001724 | Hs.102950 | coat protein gamma-cop | 3.2 |
| 120206 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 45.7 |
| 120253 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 38.9 |
| 120297 | AA191384 | Hs.104072 | ESTs, Weakly similar to Z195_HUMAN ZINC | 15.2 |
| 120624 | AW407987 | Hs.173518 | M-phase phosphoprotein homolog | 52 |
| 120695 | AA976503 | Hs.173518 | gb:oc30a04.s1 NCI_CGAP_GC4 Homo sapiens | 46.8 |
| 120807 | AA346385 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 6.8 |
| 121508 | AA402515 | Hs.97887 | ESTs | 28 |
| 122607 | AA453518 | Hs.98023 | ESTs | 61.5 |
| 122616 | AA453638 | Hs.161873 | ESTs | 107.3 |
| 122618 | AA453641 | Hs.161873 | gb:zx48e06.s1 Soares_testis_NHT Homo sap | 31.1 |
| 122829 | AW204530 | Hs.99500 | ESTs | 81.8 |
| 122838 | AA460584 | Hs.334386 | ESTs | 75.3 |
| 123753 | AA609955 | Hs.234961 | Huntingtin interacting protein E | 30.6 |
| 124385 | AI267847 | Hs.101477 | gb:aq49a10.x1 Stanley Frontal NB pool 2 | 57.1 |
| 124860 | R65763 | Hs.101477 | EST | 23.9 |
| 124930 | AI076343 | Hs.173939 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 22.8 |
| 125051 | T79956 | Hs.100588 | EST | 135.3 |
| 128781 | N71826 | Hs.105465 | small nuclear ribonucleoprotein polypept | 53.9 |
| 129096 | AA463189 | Hs.288906 | WW Domain-Containing Gene | 20.9 |
| 129347 | BE614192 | Hs.279869 | melanoma-associated antigen recognised b | 7.6 |
| 129689 | AW748482 | Hs.77873 | B7 homolog 3 | 2.6 |
| 130503 | BE208491 | Hs.295112 | KIAA0618 gene product | 16.1 |
| 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 6.1 |
| 131046 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 7.4 |
| 131643 | AW410601 | Hs.30026 | HSPC182 protein | 2.9 |
| 131925 | AF151048 | Hs.183180 | anaphase promoting complex subunit 11 (y | 2.7 |
| 132180 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 14.7 |
| 132370 | AW572805 | Hs.46645 | ESTs | 28.3 |
| 132994 | AA112748 | Hs.279905 | clone HQ0310 PRO0310p1 | 17.1 |
| 133016 | AI439688 | Hs.6289 | hypothetical protein FLJ20886 | 4.4 |
| 133266 | AI160873 | Hs.69233 | zinc finger protein | 16.1 |
| 133391 | AW103364 | Hs.727 | Inhibin, beta A (activin A, activin AB a | 25.5 |
| 134169 | AI690916 | Hs.178137 | transducer of ERBB2, 1 | 1.2 |
| 134219 | NM_000402 | Hs.80206 | glucose-6-phosphate dehydrogenase | 1.9 |
| 134405 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 72.9 |
| 134529 | AW411479 | Hs.848 | FK506-binding protein 4 (59kD) | 2.8 |
| 134975 | R50333 | Hs.92186 | Leman coiled-coil protein | 2.6 |
| 135181 | BE250865 | Hs.279529 | px19-like protein | 14.9 |
| 322556 | BE041451 | Hs.177507 | hypothetical protein | 2.9 |

60

TABLE 6A

Table 6A shows the accession numbers for those pkeys lacking unigeneID's for Table 6. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accessions |
|------|------------|------------|
|------|------------|------------|

| | | |
|--------|----------|-----------------|
| 124385 | 656394_1 | AI267847 N27351 |
|--------|----------|-----------------|

| | | |
|--------|--------|---|
| 120695 | 9683_3 | AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468 |
|--------|--------|---|

| | | |
|--------|----------|-------------------|
| 122618 | 305217_1 | AA453641 AA454061 |
|--------|----------|-------------------|

TABLE 7: Figure 7 from BRCA 001-1 US

5 Table 7 shows genes upregulated in tumor tissue compared to normal breast tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

| | | | | | |
|----|------------------|--|-----------|--|--------------------|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal breast tissue | | | |
| 15 | ORF struct info: | Structural characterization of open reading frame for the sequence of the gene | | | |
| | Pkey | ExAccn | UnigeneID | UnigeneTitle | R1 ORF struct info |
| 20 | 100113 | NM_001269 | Hs.84746 | chromosome condensation 1 | 2.3 TM |
| | 100114 | X02308 | Hs.82962 | thymidylate synthetase | 2.9 other |
| | 100131 | D12485 | Hs.11951 | ectonucleotide pyrophosphatase/phosphodi | 1.9 other |
| | 100146 | BE185499 | Hs.2471 | KIAA0020 gene product | 1.9 TM |
| | 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fasciclin | 7.6 other |
| 25 | 100154 | H60720 | Hs.81892 | KIAA0101 gene product | 9.2 other |
| | 100163 | W44671 | Hs.124 | gene predicted from cDNA with a complete | 1.6 other |
| | 100220 | AW015534 | Hs.217493 | annexin A2 | 2 other |
| | 100265 | D38521 | Hs.112396 | KIAA0077 protein | 1.5 other |
| | 100271 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 13.5 other |
| 30 | 100275 | BE242802 | Hs.154797 | KIAA0090 protein | 5.1 other |
| | 100323 | D50920 | Hs.23106 | KIAA0130 gene product | 1.9 TM |
| | 100335 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.7 other |
| | 100364 | NM_004341 | Hs.154868 | carbamoyl-phosphate synthetase 2, aspart | 2 other |
| | 100372 | NM_014791 | Hs.184339 | KIAA0175 gene product | 2.6 other |
| 35 | 100393 | D84145 | Hs.39913 | novel RGD-containing protein | 3.2 other |
| | 100400 | AW954324 | Hs.75790 | phosphatidylinositol glycan, class C | 1.5 other |
| | 100418 | D86978 | Hs.84790 | KIAA0225 protein | 2 other |
| | 100482 | M65028 | Hs.81361 | heterogeneous nuclear ribonucleoprotein | 2.9 other |
| | 100518 | NM_004415 | Hs.74316 | desmoplakin (DPI, DPL) | 1.9 other |
| 40 | 100666 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 5.7 other |
| | 100667 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 9 ? |
| | 100668 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 7.7 other |
| | 100678 | AW502935 | Hs.740 | PTK2 protein tyrosine kinase 2 | 53.2 other |
| | 100783 | AF078847 | Hs.191356 | general transcription factor IIH, polype | 6 other |
| 45 | 100892 | BE245294 | Hs.180789 | S164 protein | 1.7 ? |
| | 100945 | AF002225 | Hs.180686 | ubiquitin protein ligase E3A (human papi | 1.5 other |
| | 100969 | AA157634 | Hs.79172 | solute carrier family 25 (mitochondrial | 6.3 other |
| | 100988 | AK000405 | Hs.76480 | ubiquitin-like 4 | 11.4 ? |
| | 100999 | H38765 | Hs.80706 | diaphorase (NADH/NADPH) (cytochrome b-5 | 1.6 other |
| 50 | 101031 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 8.4 other |
| | 101045 | J05614 | | gb:Human proliferating cell nuclear anti | 5 ? |
| | 101077 | N99692 | Hs.75227 | Empirically selected from AFFX single pr | 2.6 other |
| | 101093 | L06419 | Hs.75093 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.4 ? |
| | 101186 | AA020956 | Hs.179881 | core-binding factor, beta subunit | 2 TM |
| 55 | 101216 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 1.8 other |
| | 101228 | AA333387 | Hs.82916 | chaperonin containing TCP1, subunit 6A (| 1.7 TM |
| | 101247 | AA132666 | Hs.78802 | glycogen synthase kinase 3 beta | 1.9 other |
| | 101249 | L18964 | Hs.1904 | protein kinase C, iota | 1.5 other |
| | 101332 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 5.3 other |
| 60 | 101352 | AI494299 | Hs.16297 | COX17 (yeast) homolog, cytochrome c oxid | 4.2 other |
| | 101396 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 1.9 TM |
| | 101445 | M21259 | | gb:Human Alu repeats in the region 5' to | 1.6 TM |
| | 101470 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 2.5 other |
| | 101478 | NM_002890 | Hs.758 | RAS p21 protein activator (GTPase activa | 5.5 other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 101483 | M24486 | Hs.76768 | procollagen-proline, 2-oxoglutarate 4-di | 2.1 | other |
| | 101540 | J04977 | Hs.84981 | X-ray repair complementing defective rep | 1.6 | other |
| | 101573 | AW248421 | Hs.250758 | proteasome (prosome, macropain) 26S subu | 5.7 | other |
| | 101580 | NM_012151 | Hs.83363 | coagulation factor VIII-associated (intr | 1.8 | other |
| 5 | 101592 | AF064853 | Hs.91299 | guanine nucleotide binding protein (G pr | 5.6 | ? |
| | 101621 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 2.4 | other |
| | 101702 | AW504089 | Hs.179574 | protein phosphatase 2 (formerly 2A), reg | 1.3 | other |
| | 101734 | M74099 | Hs.147049 | cut (Drosophila)-like 1 (CCAAT displacem | 2.1 | ? |
| | 101759 | M80244 | Hs.184601 | solute carrier family 7 (cationic amino | 5 | TM |
| 10 | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 14.4 | SS, |
| | 101782 | AA306495 | Hs.1869 | phosphoglucosyltransferase 1 | 5.2 | other |
| | 101805 | AW409747 | Hs.75612 | stress-induced-phosphoprotein 1 (Hsp70/H | 8.6 | other |
| | 101806 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 8.9 | SS, TM |
| | 101810 | NM_000318 | Hs.180612 | peroxisomal membrane protein 3 (35kD, Ze | 3.2 | TM |
| 15 | 101879 | AA176374 | Hs.243886 | nuclear autoantigenic sperm protein (his | 1.6 | other |
| | 101911 | AA441787 | Hs.119689 | glycoprotein hormones, alpha polypeptide | 31.3 | ? |
| | 101920 | AF182645 | Hs.8024 | IK cytokine, down-regulator of HLA II | 1.8 | other |
| | 101973 | U41514 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 2.4 | other |
| | 102009 | BE245149 | Hs.82643 | protein tyrosine kinase 9 | 1.3 | other |
| 20 | 102036 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 2 | ? |
| | 102083 | T35901 | Hs.75117 | interleukin enhancer binding factor 2, 4 | 1.6 | other |
| | 102107 | BE258602 | Hs.182366 | heat shock protein 75 | 1.4 | other |
| | 102123 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 1.8 | other |
| | 102165 | BE313280 | Hs.159627 | death associated protein 3 | 4.6 | ? |
| 25 | 102198 | AW950852 | Hs.74598 | polymerase (DNA directed), delta 2, regu | 4.4 | ? |
| | 102217 | AA829978 | Hs.301613 | JTV1 gene | 6.7 | other |
| | 102220 | U24389 | Hs.65436 | lysosomal | 4.4 | TM |
| | 102234 | AW163390 | Hs.278554 | heterochromatin-like protein 1 | 1.9 | TM |
| | 102260 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, impor | 4.4 | other |
| 30 | 102302 | AA306342 | Hs.69171 | protein kinase C-like 2 | 2.7 | ? |
| | 102330 | BE298063 | Hs.77254 | chromobox homolog 1 (Drosophila HP1 beta | 1.5 | other |
| | 102339 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 2.3 | TM |
| | 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 2 | TM |
| | 102349 | AU077055 | Hs.289107 | baculoviral IAP repeat-containing 2 | 3.2 | other |
| 35 | 102369 | U39840 | Hs.299867 | hepatocyte nuclear factor 3, alpha | 2 | other |
| | 102374 | U33635 | Hs.90572 | PTK7 protein tyrosine kinase 7 | 6.2 | other |
| | 102391 | AA296874 | Hs.77494 | deoxyguanosine kinase | 1.5 | TM |
| | 102455 | U48705 | Hs.75562 | discoilin domain receptor family, member | 7 | other |
| | 102465 | NM_001359 | Hs.81548 | 2,4-dienoyl CoA reductase 1, mitochondri | 1.8 | SS, |
| 40 | 102488 | U50939 | Hs.61828 | amyloid beta precursor protein-binding p | 1.5 | ? |
| | 102489 | AL080116 | Hs.74420 | origin recognition complex, subunit 3 (y | 3.3 | other |
| | 102494 | AI188137 | Hs.75193 | COP9 homolog | 2.1 | other |
| | 102501 | AF217197 | Hs.74562 | siah binding protein 1; FBP interacting | 3.2 | other |
| | 102522 | BE250944 | Hs.183556 | solute carrier family 1 (neutral amino a | 2.8 | ? |
| 45 | 102532 | AF040253 | Hs.70186 | suppressor of Ty (S.cerevisiae) 5 homolo | 5.7 | ? |
| | 102564 | U59423 | Hs.79067 | MAD (mothers against decapentaplegic, Dr | 2.3 | other |
| | 102568 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 5.3 | other |
| | 102580 | U60808 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 2.1 | other |
| | 102581 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 1.6 | ? |
| 50 | 102582 | U61232 | Hs.32675 | tubulin-specific chaperone e | 2.1 | other |
| | 102617 | AW161453 | Hs.198767 | COP9 (constitutive photomorphogenic, Ara | 1.8 | other |
| | 102618 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 5.8 | other |
| | 102627 | AL021918 | Hs.158174 | zinc finger protein 184 (Kruppel-like) | 1.3 | other |
| | 102663 | NM_002270 | Hs.168075 | karyopherin (importin) beta 2 | 1.8 | TM |
| 55 | 102676 | BE262989 | Hs.12045 | putative protein | 2.3 | other |
| | 102687 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 4.4 | ? |
| | 102689 | U96132 | Hs.171280 | hydroxyacyl-Coenzyme A dehydrogenase, ty | 6 | ? |
| | 102696 | BE540274 | Hs.239 | forkhead box M1 | 4.2 | other |
| | 102704 | AU077058 | Hs.54089 | BRCA1 associated RING domain 1 | 1.9 | other |
| 60 | 102705 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 2.3 | SS, TM |
| | 102750 | AB014460 | Hs.66196 | nth (E.coli endonuclease III)-like 1 | 1.2 | TM |
| | 102801 | BE252241 | Hs.38041 | pyridoxal (pyridoxine, vitamin B6) kinas | 6.5 | other |
| | 102812 | U90549 | Hs.236774 | high-mobility group (nonhistone chromoso | 1.6 | other |
| | 102827 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 5.6 | TM |
| 65 | 102844 | AV653790 | Hs.324275 | WW domain-containing protein 1 | 1.3 | TM |
| | 102868 | X02419 | Hs.77274 | plasminogen activator, urokinase | 4.4 | other |
| | 102925 | BE440142 | Hs.2943 | signal recognition particle 19kD | 1.9 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 102935 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 2.4 | ? |
| | 102968 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase | 2.7 | other |
| | 102983 | BE387202 | Hs.118638 | non-metastatic cells 1, protein (NM23A) | 3.1 | other |
| | 102985 | U95742 | Hs.2707 | G1 to S phase transition 1 | 5.2 | ? |
| 5 | 103023 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 1.6 | other |
| | 103038 | AA926960 | Hs.334883 | CDC28 protein kinase 1 | 2.5 | TM |
| | 103060 | NM_005940 | Hs.155324 | matrix metalloproteinase 11 (MMP11; stro | 4.5 | other |
| | 103080 | AU077231 | Hs.82932 | cyclin D1 (PRAD1: parathyroid adenomatos | 3.1 | other |
| | 103089 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 2.4 | other |
| 10 | 103177 | BE244377 | Hs.48876 | farnesyl-diphosphate farnesyltransferase | 3.5 | other |
| | 103178 | AA205475 | Hs.275865 | ribosomal protein S18 | 9.9 | ? |
| | 103179 | NM_001777 | Hs.82685 | CD47 antigen (Rh-related antigen, integr | 1.3 | other |
| | 103181 | X69636 | Hs.334731 | Homo sapiens, clone IMAGE:3448306, mRNA, | 2 | other |
| | 103185 | NM_006825 | Hs.74368 | transmembrane protein (63kD), endoplasmic | 1.6 | other |
| 15 | 103191 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), cata | 2.5 | other |
| | 103193 | NM_004766 | Hs.75724 | coatomer protein complex, subunit beta 2 | 2.2 | TM |
| | 103194 | NM_004939 | Hs.78580 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 6.3 | TM |
| | 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 8.8 | TM |
| | 103223 | BE275607 | Hs.1708 | chaperonin containing TCP1, subunit 3 (g | 3 | other |
| 20 | 103232 | X75962 | Hs.129780 | tumor necrosis factor receptor superfamily | 1.8 | other |
| | 103238 | AI369285 | Hs.75189 | death-associated protein | 5.6 | TM |
| | 103297 | NM_001545 | Hs.9078 | immature colon carcinoma transcript 1 | 1.9 | ? |
| | 103330 | AI803447 | Hs.77496 | small nuclear ribonucleoprotein polypept | 2.5 | other |
| | 103349 | X89059 | | gbt.H.sapiens mRNA for unknown protein ex | 1.6 | other |
| 25 | 103376 | AL036166 | Hs.323378 | coated vesicle membrane protein | 1.8 | other |
| | 103391 | X94453 | Hs.114366 | pyrroline-5-carboxylate synthetase (glut | 2.3 | other |
| | 103392 | X94563 | | gbt.H.sapiens dbi/acbp gene exon 1 & 2. | 4 | TM |
| | 103430 | BE564090 | Hs.20716 | translocase of inner mitochondrial membr | 1.3 | other |
| | 103491 | AF264750 | Hs.288971 | myeloid/lymphoid or mixed-lineage leukem | 5.7 | ? |
| 30 | 103505 | AL031224 | Hs.33102 | transcription factor AP-2 beta (activati | 5.1 | other |
| | 103547 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, | 9.7 | ? |
| | 103588 | NM_006218 | Hs.85701 | phosphoinositide-3-kinase, catalytic, al | 2 | other |
| | 103613 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 1.3 | ? |
| | 103621 | BE379766 | Hs.150675 | polymerase (RNA) II (DNA directed) polyp | 2 | other |
| 35 | 103622 | AA609685 | Hs.278672 | membrane component, chromosome 11, surfa | 2.3 | TM |
| | 103727 | AI878883 | Hs.296381 | growth factor receptor-bound protein 2 | 1.3 | other |
| | 103754 | AI015709 | Hs.172089 | Homo sapiens mRNA; cDNA DKFZp586I2022 (f | 1.3 | other |
| | 103780 | AA094752 | Hs.169992 | hypothetical 43.2 Kd protein | 7.6 | ? |
| | 103795 | H26531 | Hs.7367 | Homo sapiens BTB domain protein (BDPL) m | 1.3 | SS, TM |
| 40 | 103797 | AA080912 | | gb:zn04d03.r1 Stratagene hNT neuron (937 | 1.6 | other |
| | 103813 | AI042582 | Hs.181271 | CGI-120 protein | 1.6 | other |
| | 103855 | W02363 | Hs.302267 | hypothetical protein FLJ10330 | 1.6 | other |
| | 103886 | AK001278 | Hs.105737 | hypothetical protein FLJ10416 similar to | 6.6 | TM |
| | 104052 | NM_002407 | Hs.97644 | mammaglobin 2 | 2.9 | other |
| 45 | 104079 | AA251242 | Hs.103238 | ESTs | 1.4 | other |
| | 104174 | AA478984 | Hs.6451 | PRO0659 protein | 5.6 | TM |
| | 104227 | AB002343 | Hs.98938 | protocadherin alpha 9 | 1.6 | other |
| | 104275 | AI751970 | Hs.101067 | GCN5 (general control of amino-acid synt | 5.4 | other |
| | 104325 | BE379766 | Hs.150675 | polymerase (RNA) II (DNA directed) polyp | 6.4 | other |
| 50 | 104370 | AA324597 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 1.6 | other |
| | 104423 | R83113 | Hs.1432 | protein kinase C substrate 80K-H | 5.2 | other |
| | 104482 | AB037762 | Hs.44268 | myelin gene expression factor 2 | 1.2 | other |
| | 104667 | AI239923 | Hs.30098 | ESTs | 1.4 | other |
| | 104757 | AI694413 | Hs.332649 | olfactory receptor, family 2, subfamily | 2.4 | other |
| 55 | 104804 | AI858702 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapien | 1.4 | other |
| | 104806 | AB023175 | Hs.22982 | KIAA0958 protein | 2.4 | other |
| | 104827 | AW052006 | Hs.8551 | PRP4/STK/WD splicing factor | 10.9 | other |
| | 104846 | AI250789 | Hs.32478 | ESTs | 5.7 | other |
| | 104854 | AA041276 | Hs.154729 | 3-phosphoinositide dependent protein kin | 12.3 | ? |
| 60 | 104867 | AA278898 | Hs.225979 | hypothetical protein similar to small G | 2.1 | other |
| | 104871 | T78044 | Hs.28893 | Homo sapiens mRNA; cDNA DKFZp564O2364 (f | 1.4 | other |
| | 104896 | AW015318 | Hs.23165 | ESTs | 17.7 | other |
| | 104909 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 5.1 | TM |
| | 104916 | AW958157 | Hs.155489 | NS1-associated protein 1 | 1.8 | other |
| 65 | 104919 | AA026880 | Hs.25252 | prolactin receptor | 1.5 | other |
| | 104930 | AF043467 | Hs.32893 | neurexophilin 2 | 2.3 | other |
| | 104973 | NM_015310 | Hs.6763 | KIAA0942 protein | 5.1 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 104974 | Y12059 | Hs.278675 | bromodomain-containing 4 | 1.5 | other |
| | 104975 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 2.4 | other |
| | 104978 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 7.3 | other |
| | 104979 | AA937934 | Hs.321062 | ESTs | 1.3 | other |
| 5 | 104994 | AI499930 | Hs.334885 | mitochondrial GTP binding protein | 3.6 | ? |
| | 105009 | BE379584 | Hs.34789 | dolichyl-diphosphooligosaccharide-protei | 5.6 | other |
| | 105012 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.4 | other |
| | 105028 | AI050715 | Hs.2331 | E2F transcription factor 5, p130-binding | 2.2 | other |
| | 105041 | AB037716 | Hs.26204 | KIAA1295 protein | 2.2 | other |
| 10 | 105045 | BE242899 | Hs.129951 | speckle-type POZ protein | 3.9 | ? |
| | 105079 | AA151342 | Hs.12677 | CGI-147 protein | 9.5 | TM |
| | 105087 | AA147884 | Hs.9812 | Homo sapiens cDNA FLJ14388 fis, clone HE | 5.7 | other |
| | 105088 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PL | 2.2 | other |
| | 105095 | Z78407 | Hs.27023 | vesicle transport-related protein | 2.2 | other |
| 15 | 105110 | BE387350 | Hs.33122 | KIAA1160 protein | 1.6 | other |
| | 105126 | AW975433 | Hs.36288 | ESTs | 6.4 | ? |
| | 105127 | AA045648 | Hs.301957 | nudix (nucleoside diphosphate linked moi | 2.2 | other |
| | 105141 | AA164687 | Hs.177576 | mannosyl (alpha-1,3-)-glycoprotein beta- | 2.8 | other |
| | 105158 | AW976357 | Hs.234545 | hypothetical protein NUF2R | 2 | other |
| 20 | 105169 | BE245294 | Hs.180789 | S164 protein | 1.7 | other |
| | 105186 | AA191512 | Hs.28005 | Homo sapiens cDNA FLJ11309 fis, clone PL | 4.9 | SS, TM |
| | 105254 | AA071276 | Hs.19469 | KIAA0859 protein | 2 | TM |
| | 105281 | AA263143 | Hs.24596 | RAD51-interacting protein | 2.9 | ? |
| | 105288 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DNAJ | 1.9 | TM |
| 25 | 105302 | AA700122 | Hs.3355 | sentrin-specific protease | 8.2 | ? |
| | 105331 | AW270037 | Hs.179507 | KIAA0779 protein | 1.8 | SS, |
| | 105359 | NM_016015 | Hs.8054 | CGI-68 protein | 8.4 | other |
| | 105366 | BE264645 | Hs.282093 | hypothetical protein FLJ21918 | 5.1 | other |
| | 105373 | AW887701 | Hs.32356 | hypothetical protein FLJ20628 | 2.6 | other |
| 30 | 105374 | BE242803 | Hs.262823 | hypothetical protein FLJ10326 | 2.2 | TM |
| | 105387 | AW592146 | Hs.108636 | membrane protein CH1 | 2.3 | SS, TM |
| | 105393 | AF167570 | Hs.256583 | interleukin enhancer binding factor 3, 9 | 5.5 | SS, |
| | 105399 | BE386877 | Hs.334811 | Npw38-binding protein NpwBP | 1.6 | other |
| | 105400 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 1.6 | other |
| 35 | 105445 | AA252395 | | gb:zs12g10.s1 NCL CGAP_GCB1 Homo sapiens | 5.1 | ? |
| | 105507 | BE268348 | Hs.226318 | CCR4-NOT transcription complex, subunit | 1.6 | other |
| | 105529 | AA113449 | Hs.32471 | hypothetical protein FLJ20364 | 1.3 | other |
| | 105530 | AB023179 | Hs.9059 | KIAA0962 protein | 3.5 | other |
| | 105547 | AA262640 | Hs.27445 | unknown | 9.3 | other |
| 40 | 105564 | BE616694 | Hs.288042 | hypothetical protein FLJ14299 | 1.4 | other |
| | 105596 | AA579535 | Hs.18490 | hypothetical protein FLJ20452 | 10.9 | TM |
| | 105597 | AF054284 | Hs.334826 | splicing factor 3b, subunit 1, 155kD | 2.9 | TM |
| | 105608 | AI808201 | Hs.287863 | hypothetical protein FLJ12475 | 1.7 | ? |
| 45 | 105610 | AA280072 | Hs.99872 | fetal Alzheimer antigen | 1.4 | other |
| | 105617 | AK000892 | Hs.4069 | glucocorticoid modulatory element bindin | 1.7 | TM |
| | 105620 | AW302245 | Hs.181390 | casein kinase 1, gamma 2 | 5.6 | other |
| | 105658 | AA985190 | Hs.246875 | hypothetical protein FLJ20059 | 9.4 | other |
| | 105697 | AW499988 | Hs.27801 | zinc finger protein 278 | 2 | TM |
| | 105708 | R26944 | Hs.180777 | Homo sapiens mRNA; cDNA DKFZp564M0264 (f | 1.7 | other |
| 50 | 105743 | BE246502 | Hs.9598 | sema domain, immunoglobulin domain (Ig), | 2.7 | other |
| | 105746 | AW151952 | Hs.46679 | hypothetical protein FLJ20739 | 1.5 | ? |
| | 105759 | AI123118 | Hs.15159 | chemokine-like factor, alternatively spl | 1.3 | other |
| | 105771 | AI267720 | Hs.153221 | synovial sarcoma, translocated to X chro | 1.6 | other |
| | 105820 | AA741336 | Hs.152108 | transcriptional unit N143 | 2.2 | other |
| 55 | 105826 | AA478756 | Hs.194477 | E3 ubiquitin ligase SMURF2 | 1.3 | other |
| | 105856 | AI262106 | Hs.12653 | ESTs | 2.4 | other |
| | 105858 | AF151066 | Hs.281428 | hypothetical protein | 2.9 | other |
| | 105875 | AK001708 | Hs.32271 | hypothetical protein FLJ10846 | 1.4 | other |
| | 105930 | AF016371 | Hs.9880 | peptidyl prolyl isomerase H (cyclophilin | 5.3 | other |
| 60 | 106000 | AW194426 | Hs.20726 | ESTs | 1.7 | other |
| | 106011 | AW081202 | Hs.12284 | Homo sapiens, clone IMAGE:2989556, mRNA, | 2.8 | other |
| | 106017 | AA477956 | Hs.26268 | ESTs | 1.4 | other |
| | 106073 | AL157441 | Hs.17834 | downstream neighbor of SON | 1.4 | other |
| | 106078 | AA130158 | Hs.19977 | ESTs, Moderately similar to ALU8_HUMAN A | 1.6 | ? |
| 65 | 106094 | AA533491 | Hs.23317 | hypothetical protein FLJ14681 | 6.9 | other |
| | 106140 | AB006624 | Hs.14912 | KIAA0286 protein | 1.6 | other |
| | 106271 | AA251393 | Hs.289052 | Homo sapiens, Similar to RIKEN cDNA 5430 | 10.8 | ? |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 106288 | AB037742 | Hs.24336 | KIAA1321 protein | 1.3 | other |
| | 106300 | Y10043 | Hs.19114 | high-mobility group (nonhistone chromoso | 3.7 | other |
| | 106333 | AL043114 | Hs.22410 | ESTs, Weakly similar to A54849 collagen | 5.5 | SS, |
| | 106350 | AK001404 | Hs.194698 | cyclin B2 | 5.8 | other |
| 5 | 106359 | AW390282 | Hs.31130 | transmembrane 7 superfamily member 2 | 6.4 | other |
| | 106381 | AB040916 | Hs.24106 | KIAA1483 protein | 6.6 | other |
| | 106389 | AW748420 | Hs.6236 | Homo sapiens cDNA: FLJ21487 fis, clone C | 2.2 | TM |
| | 106457 | AF119256 | Hs.27801 | zinc finger protein 278 | 2.7 | other |
| | 106470 | D63078 | Hs.186180 | Homo sapiens cDNA: FLJ23038 fis, clone L | 2.3 | other |
| 10 | 106586 | AA243837 | Hs.57787 | ESTs | 1.6 | other |
| | 106589 | AK000933 | Hs.28661 | Homo sapiens cDNA FLJ10071 fis, clone HE | 2.4 | ? |
| | 106610 | AA458882 | Hs.79732 | fibulin 1 | 8 | SS, |
| | 106624 | NM_003595 | Hs.26350 | tyrosylprotein sulfotransferase 2 | 7.8 | other |
| | 106650 | AL049951 | Hs.22370 | Homo sapiens mRNA; cDNA DKFZp564O0122 (f | 1.8 | other |
| 15 | 106669 | AV657117 | Hs.184164 | ESTs, Moderately similar to S65657 alpha | 1.3 | TM |
| | 106713 | BE614802 | Hs.184352 | hypothetical protein FLJ12549 | 4.6 | other |
| | 106717 | AA600357 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-bi | 1.3 | other |
| | 106723 | BE388094 | Hs.21857 | ESTs | 1.6 | SS, |
| | 106795 | AF174487 | Hs.293753 | Bcl-2-related ovarian killer protein-lik | 5.7 | other |
| 20 | 106829 | AW959893 | Hs.27099 | hypothetical protein FLJ23293 similar to | 16.2 | TM |
| | 106831 | BE564871 | Hs.29463 | centrin, EF-hand protein, 3 (CDC31 yeast | 1.5 | other |
| | 106846 | AB037744 | Hs.34892 | KIAA1323 protein | 2.2 | other |
| | 106852 | AF151031 | Hs.300631 | hypothetical protein | 1.3 | other |
| | 106873 | N49809 | Hs.11197 | Homo sapiens, clone IMAGE:3343149, mRNA, | 16.8 | other |
| 25 | 106886 | W79171 | Hs.9567 | GL002 protein | 1.5 | TM |
| | 106906 | AA861271 | Hs.222024 | transcription factor BMAL2 | 2.2 | other |
| | 106920 | AK001838 | Hs.296323 | serum/glucocorticoid regulated kinase | 3.4 | other |
| | 106945 | AK000511 | Hs.6294 | hypothetical protein DKFZp434L1435 simil | 6.8 | ? |
| | 106973 | BE156256 | Hs.11923 | hypothetical protein | 6.7 | other |
| 30 | 106978 | AW631480 | Hs.8688 | ESTs | 6.1 | SS, |
| | 107004 | AA146872 | Hs.300700 | hypothetical protein FLJ20727 | 1.3 | other |
| | 107029 | AF264750 | Hs.288971 | myeloid/lymphoid or mixed-lineage leukem | 1.8 | other |
| | 107071 | AW385224 | Hs.35198 | ectonucleotide pyrophosphatase/phosphodi | 1.7 | other |
| | 107113 | AK000733 | Hs.23900 | GTPase activating protein | 2.5 | other |
| 35 | 107125 | AK000512 | Hs.69388 | hypothetical protein FLJ20505 | 1.7 | other |
| | 107136 | AV661958 | Hs.8207 | GK001 protein | 4.7 | other |
| | 107146 | AK001455 | Hs.5198 | Down syndrome critical region gene 2 | 2 | other |
| | 107151 | AW378065 | Hs.8687 | ESTs | 6.4 | TM |
| | 107155 | AW391927 | Hs.7946 | KIAA1288 protein | 33.5 | other |
| 40 | 107174 | BE122762 | Hs.25338 | ESTs | 5.2 | ? |
| | 107197 | W15477 | Hs.64639 | glioma pathogenesis-related protein | 6.1 | other |
| | 107221 | AW888411 | Hs.81915 | leukemia-associated phosphoprotein p18 (| 17.4 | other |
| | 107243 | BE219716 | Hs.34727 | ESTs, Moderately similar to I38759 zinc | 7.4 | ? |
| | 107248 | AW263124 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 1.8 | other |
| 45 | 107263 | D60341 | Hs.21198 | translocase of outer mitochondrial membr | 6.7 | other |
| | 107265 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 2.5 | other |
| | 107299 | BE277457 | Hs.30661 | hypothetical protein MGC4606 | 3.2 | TM |
| | 107316 | T63174 | Hs.193700 | Homo sapiens mRNA; cDNA DKFZp586I0324 (f | 2 | TM |
| | 107354 | NM_006299 | Hs.96448 | zinc finger protein 193 | 5 | ? |
| 50 | 107392 | AW299900 | Hs.267632 | TATA element modulatory factor 1 | 1.2 | other |
| | 107481 | AA307703 | Hs.279766 | kinesin family member 4A | 1.6 | other |
| | 107529 | BE515065 | Hs.296585 | nucleolar protein (KKE/D repeat) | 3 | TM |
| | 107554 | AA001386 | Hs.59844 | ESTs | 1.4 | other |
| | 107681 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 2.3 | SS, TM |
| 55 | 107772 | AA018587 | Hs.303055 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.2 | ? |
| | 107859 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 8.4 | TM |
| | 107901 | L42612 | Hs.335952 | keratin 6B | 2.5 | other |
| | 107922 | BE153855 | Hs.61460 | lg superfamily receptor LNIR | 2.3 | other |
| | 107974 | AW956103 | Hs.61712 | pyruvate dehydrogenase kinase, isoenzyme | 6.8 | other |
| 60 | 108040 | AL121031 | Hs.159971 | SWI/SNF related, matrix associated, acti | 1.6 | other |
| | 108230 | AA054224 | Hs.59847 | ESTs | 1.3 | other |
| | 108274 | AF129535 | Hs.272027 | F-box only protein 5 | 7.2 | ? |
| | 108296 | N31256 | Hs.161623 | ESTs | 2.6 | other |
| | 108496 | AA083069 | Hs.339659 | ESTs | 3.6 | other |
| 65 | 108607 | BE300380 | Hs.69476 | Homo sapiens cDNA FLJ12758 fis, clone NT | 3.5 | other |
| | 108621 | AA101809 | Hs.182685 | ESTs | 1.7 | other |
| | 108634 | AW022410 | Hs.69507 | ESTs | 1.8 | SS, TM |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|-------|
| 5 | 108647 | BE546947 | Hs.44276 | homeo box C10 | 9.8 | other |
| | 108695 | AB029000 | Hs.70823 | KIAA1077 protein | 7.3 | other |
| | 108740 | AI089575 | Hs.9071 | progesterone membrane binding protein | 2.8 | ? |
| | 108828 | AK001693 | Hs.273344 | DKFZP564O0463 protein | 1.9 | other |
| | 108859 | AL121500 | Hs.178904 | ESTs | 1.6 | TM |
| 10 | 108872 | H06720 | Hs.111680 | endosulfine alpha | 2.2 | other |
| | 108891 | AI801235 | Hs.48480 | ESTs | 5.4 | other |
| | 108894 | AK001431 | Hs.5105 | hypothetical protein FLJ10569 | 4.1 | TM |
| | 108955 | AA149754 | Hs.195155 | Homo sapiens amino acid transport system | 5.7 | ? |
| | 108982 | AA151708 | Hs.171980 | homeo box (expressed in ES cells) 1 | 1.7 | other |
| 15 | 108987 | AA152178 | Hs.23467 | hypothetical protein FLJ10633 | 6.3 | other |
| | 109002 | AB028987 | Hs.72134 | KIAA1064 protein | 1.7 | other |
| | 109011 | AA156542 | Hs.72127 | ESTs | 1.5 | other |
| | 109026 | AA157811 | | gbzoz35d07.s1 Stratagene colon (937204) | 5.4 | other |
| | 109068 | AA164293 | Hs.72545 | ESTs | 3 | other |
| 20 | 109101 | AW608930 | Hs.52184 | hypothetical protein FLJ20618 | 1.6 | SS, |
| | 109112 | AW419196 | Hs.257924 | hypothetical protein FLJ13782 | 3.3 | TM |
| | 109124 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 1.7 | other |
| | 109139 | AJ132592 | Hs.59757 | zinc finger protein 281 | 2.7 | other |
| | 109166 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 3 | TM |
| 25 | 109198 | BE566742 | Hs.58169 | highly expressed in cancer, rich in leuc | 2.1 | other |
| | 109213 | NM_016603 | Hs.82035 | potential nuclear protein C5ORF5; GAP-li | 5.4 | other |
| | 109220 | AW958181 | Hs.189998 | ESTs | 5.8 | other |
| | 109233 | AU077281 | Hs.170285 | nucleoporin 214kD (CAIN) | 5.3 | other |
| | 109270 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DNAJ | 1.4 | other |
| 30 | 109273 | AA375752 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 3 | other |
| | 109313 | AF153201 | Hs.86276 | C2H2 (Krueppel-type) zinc finger protein | 1.3 | other |
| | 109341 | AA213506 | Hs.115099 | EST | 3 | ? |
| | 109391 | AL096858 | Hs.184245 | KIAA0929 protein Msx2 interacting nuclea | 1.5 | other |
| | 109420 | H83603 | Hs.40408 | homeo box C9 | 2.2 | SS, |
| 35 | 109426 | N30531 | Hs.42215 | protein phosphatase 1, regulatory subuni | 3.1 | TM |
| | 109429 | AI160029 | Hs.61438 | ESTs | 2 | ? |
| | 109445 | AA232103 | Hs.189915 | ESTs | 1.8 | other |
| | 109450 | AB032969 | Hs.173042 | KIAA1143 protein | 3.8 | other |
| | 109468 | NM_015310 | Hs.6763 | KIAA0942 protein | 3.3 | other |
| 40 | 109478 | AW074143 | Hs.87134 | ESTs | 2 | TM |
| | 109570 | L40027 | Hs.118890 | glycogen synthase kinase 3 alpha | 2.1 | other |
| | 109662 | F02614 | Hs.27319 | ESTs | 1.4 | other |
| | 109825 | R71264 | Hs.16798 | ESTs | 1.3 | other |
| | 110039 | H11938 | Hs.21907 | histone acetyltransferase | 2 | other |
| 45 | 110056 | AA503041 | Hs.279009 | matrix Gla protein | 2.5 | other |
| | 110085 | AA603840 | Hs.29956 | KIAA0460 protein | 1.7 | other |
| | 110110 | T07353 | Hs.7948 | ESTs | 2.9 | other |
| | 110129 | R51853 | Hs.226429 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 1.7 | SS, |
| | 110154 | NM_014521 | Hs.17667 | SH3-domain binding protein 4 | 4.3 | other |
| 50 | 110240 | AJ668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 4.3 | ? |
| | 110242 | N41744 | Hs.19978 | CGI-30 protein | 1.3 | other |
| | 110259 | H28428 | Hs.32406 | ESTs, Weakly similar to I38022 hypotheri | 2.2 | other |
| | 110312 | BE256986 | Hs.11896 | hypothetical protein FLJ12089 | 2.1 | other |
| | 110501 | H55748 | | gb:yq94a01.s1 Soares fetal liver spleen | 6.1 | ? |
| 55 | 110504 | H55915 | Hs.210859 | hypothetical protein FLJ11016 | 6.1 | TM |
| | 110525 | H57330 | Hs.37430 | EST | 6.4 | other |
| | 110568 | AK001160 | Hs.5999 | hypothetical protein FLJ10298 | 1.3 | ? |
| | 110699 | T97586 | Hs.18090 | ESTs | 1.8 | other |
| | 110705 | AB007902 | Hs.32168 | KIAA0442 protein | 1.6 | TM |
| 60 | 110742 | AW190338 | Hs.28029 | hypothetical protein MGC11256 | 7.8 | other |
| | 110761 | AL138077 | Hs.16157 | hypothetical protein FLJ12707 | 2.5 | other |
| | 110762 | BE044245 | Hs.30011 | hypothetical protein MGC2963 | 9.3 | ? |
| | 110765 | AK000322 | Hs.18457 | hypothetical protein FLJ20315 | 5.5 | SS, |
| | 110769 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 2.1 | TM |
| 65 | 110799 | AI089660 | Hs.323401 | dpy-30-like protein | 1.5 | TM |
| | 110805 | T25829 | Hs.24048 | FK506 binding protein precursor | 6.7 | TM |
| | 110813 | AA767373 | Hs.35669 | ESTs, Moderately similar to ALU1_HUMAN A | 5.7 | other |
| | 110820 | R33261 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 p | 3.4 | other |
| | 110840 | N31598 | Hs.12727 | hypothetical protein FLJ21610 | 1.7 | TM |
| | 110844 | AI740792 | Hs.167531 | methylcrotonoyl-Coenzyme A carboxylase 2 | 1.7 | other |
| | 110854 | BE612992 | Hs.27931 | hypothetical protein FLJ10607 similar to | 4.7 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 110856 | AA992380 | | gb:ot37g06.s1 Soares_testis_NHT Homo sap | 2.3 | other |
| | 110885 | BE384447 | Hs.16034 | hypothetical protein MGC13186 | 3.5 | ? |
| | 110897 | AL117430 | Hs.6880 | DKFZP434D156 protein | 2.2 | ? |
| 5 | 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 2.6 | SS, |
| | 110918 | H04360 | Hs.24283 | ESTs, Moderately similar to reduced expr | 1.9 | TM |
| | 110958 | NM_005864 | Hs.24587 | signal transduction protein (SH3 contain | 6.7 | other |
| | 110963 | AK002180 | Hs.11449 | DKFZP564O123 protein | 2 | other |
| | 110981 | AK001980 | Hs.24284 | ADP-ribosyltransferase (NAD+; poly(ADP-r | 1.3 | other |
| 10 | 110984 | AW613287 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 1.8 | ? |
| | 111125 | N63823 | Hs.269115 | ESTs, Moderately similar to Z195_HUMAN Z | 3.7 | other |
| | 111132 | AB037807 | Hs.83293 | hypothetical protein | 2.1 | TM |
| | 111164 | N46180 | Hs.122489 | Homo sapiens cDNA FLJ13289 fis, clone OV | 2.3 | other |
| | 111172 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 3.7 | other |
| | 111174 | AL050166 | Hs.26295 | Homo sapiens mRNA; cDNA DKFZp586D1122 (f | 7.5 | other |
| 15 | 111179 | AK000136 | Hs.10760 | asporin (LRR class 1) | 7.1 | other |
| | 111184 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 6.8 | other |
| | 111189 | N67603 | Hs.272130 | ESTs, Weakly similar to S65824 reverse t | 3.6 | SS, |
| | 111216 | AW139408 | Hs.152940 | ESTs | 1.5 | other |
| | 111221 | AB037782 | Hs.15119 | KIAA1361 protein | 2.6 | other |
| 20 | 111223 | AA852773 | Hs.334838 | KIAA1866 protein | 4.7 | other |
| | 111239 | N90956 | Hs.17230 | hypothetical protein FLJ22087 | 7.9 | ? |
| | 111285 | AA778711 | Hs.4310 | eukaryotic translation initiation factor | 7 | other |
| | 111299 | AB033091 | Hs.74313 | KIAA1265 protein | 5 | other |
| | 111312 | AI523913 | Hs.34504 | ESTs | 3.8 | other |
| 25 | 111318 | T99755 | Hs.334728 | ESTs | 1.2 | TM |
| | 111337 | AA837396 | Hs.263925 | LIS1-interacting protein NUDE1, rat homo | 5.1 | other |
| | 111352 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PL | 2.2 | other |
| | 111370 | AI478658 | Hs.94631 | brefeldin A-inhibited guanine nucleotide | 2.8 | ? |
| | 111384 | N94606 | Hs.288969 | HSCARG protein | 2.2 | other |
| 30 | 111389 | AK000987 | Hs.169111 | oxidation resistance 1 | 2.1 | other |
| | 111452 | R02354 | Hs.15999 | ESTs | 2.7 | TM |
| | 111486 | AI051194 | Hs.227978 | EST | 6.6 | other |
| | 111549 | W90638 | Hs.20321 | ESTs, Moderately similar to ZRF1_HUMAN Z | 1.4 | other |
| | 111585 | R10720 | Hs.20670 | EST | 1.6 | ? |
| 35 | 111627 | R52656 | Hs.21691 | ESTs | 1.6 | other |
| | 111870 | AB037834 | Hs.18685 | Homo sapiens mRNA for KIAA1413 protein, | 2.4 | other |
| | 111937 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (fr | 10.6 | other |
| | 111944 | AW083791 | Hs.21263 | suppressor of potassium transport defect | 6.6 | TM |
| | 111987 | NM_015310 | Hs.6763 | KIAA0942 protein | 5.1 | other |
| 40 | 112134 | R41823 | Hs.7413 | ESTs; calyntenin-2 | 2.8 | other |
| | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 14.6 | other |
| | 112388 | R46071 | Hs.301693 | Homo sapiens, clone IMAGE:3638994, mRNA, | 9 | other |
| | 112456 | NM_016248 | Hs.232076 | A kinase (PRKA) anchor protein 11 | 1.4 | other |
| | 112464 | AW007287 | Hs.28538 | Homo sapiens cDNA: FLJ21086 fis, clone C | 1.4 | TM |
| 45 | 112506 | AI742756 | Hs.26079 | ESTs | 3.2 | other |
| | 112513 | R68425 | Hs.13809 | hypothetical protein FLJ10648 | 2 | TM |
| | 112752 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 1.8 | other |
| | 112884 | AK000004 | Hs.5013 | Homo sapiens mRNA for FLJ00004 protein, | 6.6 | other |
| | 112923 | T10258 | Hs.5037 | EST | 1.5 | ? |
| 50 | 112936 | AW970826 | Hs.6185 | KIAA1557 protein | 3.2 | other |
| | 112958 | R61388 | Hs.6724 | ESTs | 6.1 | other |
| | 112966 | Z44718 | Hs.102548 | glucocorticoid receptor DNA binding fact | 6.5 | other |
| | 112978 | AK000272 | Hs.7099 | hypothetical protein FLJ20265 | 1.2 | other |
| | 112995 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYK | 5.6 | other |
| 55 | 112996 | BE276112 | Hs.7165 | zinc finger protein 259 | 2 | other |
| | 113047 | AI571940 | Hs.7549 | ESTs | 1.9 | other |
| | 113049 | AW965190 | Hs.7560 | Homo sapiens mRNA for KIAA1729 protein, | 2.4 | TM |
| | 113089 | T40707 | Hs.270862 | ESTs | 1.3 | SS, |
| | 113196 | T57317 | | gb:yc51a03.s1 Stratagene fetal spleen (9 | 1.7 | other |
| 60 | 113248 | T63857 | | gb:yc16e01.s1 Stratagene lung (937210) H | 2.8 | other |
| | 113254 | AK002180 | Hs.11449 | DKFZP564O123 protein | 1.3 | other |
| | 113277 | AW971049 | Hs.11774 | protein (peptidyl-prolyl cis/trans isome | 3.2 | other |
| | 113429 | AA688021 | Hs.179808 | ESTs | 1.2 | other |
| | 113499 | AI467908 | Hs.8882 | ESTs | 6 | other |
| 65 | 113547 | H59588 | Hs.15233 | ESTs | 2 | SS, |
| | 113647 | AA813887 | Hs.188173 | Homo sapiens cDNA FLJ12187 fis, clone MA | 1.3 | SS, |
| | 113702 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen | 4.4 | other |

| | | | | | | | |
|----|--------|---------------|-----------|---|------|-------|--|
| | 113759 | AW499665 | Hs.9456 | SWI/SNF related, matrix associated, acti | 1.2 | other | |
| | 113777 | BE266947 | Hs.10590 | zinc finger protein 313 | 13.4 | other | |
| | 113783 | AL359588 | Hs.7041 | hypothetical protein DKFZp762B226 | 1.7 | other | |
| 5 | 113791 | AI269096 | Hs.135578 | chitinase, di-N-acetyl- | 1.3 | other | |
| | 113808 | W44735 | Hs.9286 | Homo sapiens cDNA: FLJ21278 fis, clone C | 3.3 | other | |
| | 113811 | BE207480 | Hs.6994 | Homo sapiens cDNA: FLJ22044 fis, clone H | 3.1 | other | |
| | 113817 | H13325 | Hs.332795 | hypothetical protein DKFZp761O17121 | 3.2 | other | |
| | 113826 | AW378212 | Hs.24809 | hypothetical protein FLJ10826 | 2.3 | ? | |
| 10 | 113834 | T26483 | Hs.6059 | EGF-containing fibulin-like extracellular | 11.3 | TM | |
| | 113868 | W57902 | Hs.90744 | proteasome (prosome, macropain) 26S subu | 2.7 | other | |
| | 113870 | AL079314 | Hs.16537 | hypothetical protein, similar to (U06944 | 6.1 | other | |
| | 113885 | AW959486 | Hs.21732 | ESTs | 6.6 | other | |
| | 113923 | AW953484 | Hs.3849 | hypothetical protein FLJ22041 similar to | 1.9 | ? | |
| 15 | 113989 | W87544 | Hs.268828 | ESTs | 1.2 | other | |
| | 114022 | A1539519 | Hs.120969 | Homo sapiens cDNA FLJ11562 fis, clone HE | 5.4 | other | |
| | 114030 | A1825386 | Hs.164478 | hypothetical protein FLJ21939 similar to | 9.4 | other | |
| | 114060 | AB029551 | Hs.7910 | RING1 and YY1 binding protein | 1.8 | other | |
| | 114196 | AF017445 | Hs.150926 | fucose-1-phosphate guanylyltransferase | 1.5 | other | |
| | 114226 | AB028968 | Hs.7989 | KIAA1045 protein | 1.8 | other | |
| 20 | 114253 | BE149866 | Hs.14831 | Homo sapiens, Similar to zinc finger pro | 2.3 | other | |
| | 114262 | AL117518 | Hs.3686 | KIAA0978 protein | 1.4 | TM | |
| | 114275 | AW515443.comp | Hs.306117 | KIAA0306 protein | 15.8 | other | |
| | 114292 | A1815395 | Hs.184641 | fatty acid desaturase 2 | 1.9 | TM | |
| 25 | 114309 | AA332453 | Hs.20824 | CGI-85 protein | 2.4 | other | |
| | 114392 | AA249590 | Hs.100748 | ESTs, Weakly similar to A28996 proline-r | 1.9 | other | |
| | 114407 | BE539976 | Hs.103305 | Homo sapiens mRNA; cDNA DKFZp434B0425 (f | 1.3 | TM | |
| | 114455 | H37908 | Hs.271616 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 5.6 | other | |
| | 114463 | AL120247 | Hs.40109 | KIAA0872 protein | 5.3 | TM | |
| | 114464 | AI091713 | Hs.106597 | Homo sapiens, Similar to RIKEN cDNA 1110 | 1.3 | other | |
| 30 | 114471 | AA028074 | Hs.104613 | RP42 homolog | 1.9 | ? | |
| | 114480 | BE066778 | Hs.151678 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 13.4 | other | |
| | 114671 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 2 | other | |
| | 114698 | AA476966 | Hs.110857 | polymerase (RNA) III (DNA directed) poly | 3.6 | other | |
| 35 | 114730 | AI373544 | Hs.331328 | intermediate filament protein syncoilin | 3.9 | other | |
| | 114767 | A1859865 | Hs.154443 | minichromosome maintenance deficient (S. | 1.7 | other | |
| | 114774 | AV656017 | Hs.184325 | CGI-76 protein | 3.2 | other | |
| | 114798 | AA159181 | Hs.54900 | serologically defined colon cancer antig | 3.6 | other | |
| | 114860 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.4 | other | |
| 40 | 114895 | AA236177 | Hs.76591 | KIAA0887 protein | 7.2 | other | |
| | 114896 | BE539101 | Hs.5324 | hypothetical protein | 1.3 | other | |
| | 114911 | AA236672 | | gb:zt29f02.s1 Soares ovary tumor NbHOT H | 1.5 | other | |
| | 114930 | AA237022 | Hs.188717 | ESTs | 2 | SS, | |
| | 114938 | AA242834 | Hs.58384 | ESTs | 2.9 | other | |
| 45 | 114965 | AI733881 | Hs.72472 | BMP-R1B | 2.3 | ? | |
| | 115023 | AF102546 | Hs.63931 | dachshund (Drosophila) homolog | 1.3 | other | |
| | 115038 | AA252360 | Hs.87968 | toll-like receptor 9 | 1.6 | other | |
| | 115061 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 11.8 | other | |
| | 115117 | AI670847 | Hs.5324 | hypothetical protein | 1.5 | other | |
| 50 | 115206 | AW183695 | Hs.186572 | ESTs | 2.5 | other | |
| | 115221 | AW365434 | Hs.79741 | hypothetical protein FLJ10116 | 1.5 | other | |
| | 115239 | BE251328 | Hs.73291 | hypothetical protein FLJ10881 | 1.3 | TM | |
| | 115242 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 1.4 | other | |
| | 115278 | AK002163 | Hs.301724 | hypothetical protein FLJ11301 | 1.5 | other | |
| 55 | 115285 | AW972872 | Hs.293736 | ESTs | 2.4 | other | |
| | 115291 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 6.3 | SS, | |
| | 115400 | AI215069 | Hs.89113 | ESTs | 6.7 | ? | |
| | 115468 | AA314349 | Hs.48499 | tumor antigen SLP-8p | 7.5 | ? | |
| | 115471 | AK001376 | Hs.59346 | hypothetical protein FLJ10514 | 1.4 | TM | |
| 60 | 115479 | AW301608 | Hs.278188 | ESTs, Moderately similar to I54374 gene | 4.1 | TM | |
| | 115496 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 16.3 | other | |
| | 115500 | Y14443 | Hs.88219 | zinc finger protein 200 | 5 | other | |
| | 115553 | AJ275986 | Hs.71414 | transcription factor (SMIF gene) | 2.5 | other | |
| | 115581 | AI540842 | Hs.61082 | ESTs | 6.2 | other | |
| 65 | 115587 | BE081342 | Hs.283037 | HSPC039 protein | 2.9 | other | |
| | 115590 | AA399477 | Hs.67896 | 7-60 protein | 5.3 | TM | |
| | 115646 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glu | 4.8 | ? | |
| | 115652 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 10.6 | other | |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 115655 | AL048269 | Hs.288544 | Homo sapiens, clone MGC:16063, mRNA, com | 12.7 | TM |
| | 115663 | AI138785 | Hs.40507 | ESTs | 2 | other |
| | 115676 | AA953006 | Hs.88143 | ESTs | 3.1 | other |
| | 115690 | AA625132 | Hs.44159 | hypothetical protein FLJ21615 | 1.7 | TM |
| | 115693 | AF231023 | Hs.55173 | cadherin, EGF LAG seven-pass G-type rece | 6.9 | other |
| 10 | 115715 | BE395161 | Hs.1390 | proteasome (prosome, macropain) subunit, | 1.7 | other |
| | 115734 | AI950339 | Hs.40782 | ESTs | 2.7 | TM |
| | 115811 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.1 | other |
| | 115823 | AI732742 | Hs.87440 | ESTs | 2.1 | other |
| | 115837 | AI675217 | Hs.42761 | ESTs | 1.3 | other |
| 15 | 115844 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 4.4 | other |
| | 115866 | AW062629 | Hs.52081 | KIAA0867 protein | 7.3 | other |
| | 115875 | N55669 | Hs.333823 | mitochondrial ribosomal protein L13 | 1.2 | other |
| | 115941 | AI867451 | Hs.46679 | hypothetical protein FLJ20739 | 5.5 | other |
| | 115968 | AB037753 | Hs.62767 | KIAA1332 protein | 9.8 | other |
| 20 | 116003 | BE275469 | Hs.66493 | Down syndrome critical region gene 5 | 1.4 | other |
| | 116011 | AL359053 | Hs.57664 | Homo sapiens mRNA full length insert cDN | 2.4 | other |
| | 116108 | AA770688 | Hs.28777 | H2A histone family, member L | 1.8 | other |
| | 116134 | BE243834 | Hs.50441 | CGI-04 protein | 1.4 | other |
| | 116189 | N35719 | Hs.44749 | ESTs, Moderately similar to T00358 hypot | 1.2 | other |
| 25 | 116195 | AW821113 | Hs.72402 | ESTs | 2.1 | other |
| | 116238 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 1.7 | other |
| | 116246 | AF265555 | Hs.250646 | baculoviral IAP repeat-containing 6 | 1.7 | other |
| | 116262 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 1.8 | ? |
| | 116298 | AI955411 | Hs.94109 | Homo sapiens cDNA FLJ13634 fis, clone PL | 1.9 | other |
| 30 | 116318 | AF097645 | Hs.58570 | deleted in cancer 1; RNA helicase HDB/DI | 5 | SS, |
| | 116325 | AI472106 | Hs.49303 | Homo sapiens cDNA FLJ11663 fis, clone HE | 1.4 | SS, |
| | 116336 | AL133033 | Hs.4084 | KIAA1025 protein | 1.9 | ? |
| | 116339 | AK000290 | Hs.44033 | dipeptidyl peptidase 8 | 1.5 | other |
| | 116350 | AA497129 | Hs.184771 | nuclear factor Y/C (CCAAT-binding transc | 1.9 | ? |
| 35 | 116358 | AI149586 | Hs.38125 | interferon-induced protein 75, 52kD | 1.9 | ? |
| | 116365 | N50174 | Hs.46765 | ESTs | 6.1 | other |
| | 116368 | N90466 | Hs.71109 | KIAA1229 protein | 1.6 | ? |
| | 116417 | AW499664 | Hs.12484 | Human clone Z3826 mRNA sequence | 7.4 | other |
| | 116436 | AA161411 | Hs.58668 | chromosome 21 open reading frame 57 | 2.1 | other |
| 40 | 116462 | AF218313 | Hs.236828 | putative helicase RUVBL | 1.5 | TM |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.1 | TM |
| | 116575 | AA312572 | Hs.6241 | phosphoinositide-3-kinase, regulatory su | 1.5 | other |
| | 116637 | AK001043 | Hs.92033 | Integrin-linked kinase-associated serine | 2.7 | other |
| | 116640 | X89984 | Hs.211563 | B-cell CLL/lymphoma 7A | 2.3 | other |
| 45 | 116700 | AI800202 | Hs.317589 | hypothetical protein MGC10765 | 1.4 | other |
| | 116705 | AW074819 | Hs.12313 | hypothetical protein FLJ14566 | 3.4 | other |
| | 116732 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 2.9 | other |
| | 116926 | H73608 | Hs.290830 | ESTs | 1.7 | TM |
| | 117034 | U72209 | Hs.180324 | YY1-associated factor 2 | 3.4 | TM |
| 50 | 117132 | AI393666 | Hs.42315 | p10-binding protein | 5.2 | ? |
| | 117247 | N21032 | | gb:yx46f06.s1 Soares melanocyte 2NbHM Ho | 5.5 | TM |
| | 117276 | N71183 | Hs.121806 | Homo sapiens cDNA FLJ11971 fis, clone HE | 1.5 | TM |
| | 117284 | AK001701 | Hs.183779 | Homo sapiens cDNA FLJ10590 fis, clone NT | 2 | other |
| | 117367 | AI041793 | Hs.42502 | ESTs | 2 | other |
| 55 | 117368 | AI878942 | Hs.90336 | ATPase, H+ transporting, lysosomal (vacu | 2.1 | ? |
| | 117382 | AF150275 | Hs.40173 | ESTs | 2.7 | TM |
| | 117412 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 1.4 | other |
| | 117557 | AF123050 | Hs.44532 | diubiquitin | 3.4 | TM |
| | 117588 | N34895 | Hs.44648 | ESTs | 3.4 | ? |
| 60 | 117745 | BE294925 | Hs.46680 | CGI-12 protein | 3 | SS, |
| | 117754 | AA121673 | Hs.59757 | zinc finger protein 281 | 1.9 | other |
| | 117879 | N54706 | Hs.303025 | chromosome 11 open reading frame 24 | 1.8 | other |
| | 117904 | BE540675 | Hs.332938 | hypothetical protein MGC5370 | 6 | ? |
| | 117911 | AL137379 | Hs.47125 | hypothetical protein FLJ13912 | 1.7 | other |
| 65 | 117933 | Y10518 | Hs.116470 | hypothetical protein FLJ20048 | 1.7 | other |
| | 117983 | AL110246 | Hs.47367 | KIAA1785 protein | 5.4 | other |
| | 118078 | N54321 | Hs.47790 | EST | 5.2 | other |
| | 118301 | AA453902 | Hs.293264 | ESTs | 2.6 | other |
| | 118429 | AA243332 | Hs.74649 | cytochrome c oxidase subunit VIc | 2.5 | TM |
| | 118472 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.1 | other |
| | 118488 | AJ277275 | Hs.50102 | rapa-2 (rapa gene) | 1.2 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 118509 | N22617 | Hs.43228 | Homo sapiens cDNA FLJ11835 fis, clone HE | 1.5 | other |
| | 118528 | AI949952 | Hs.49397 | ESTs | 7.4 | ? |
| | 118656 | AI458020 | Hs.293287 | ESTs | 2.5 | other |
| 5 | 118670 | AA332845 | Hs.152618 | ESTs, Moderately similar to ZN91_HUMAN Z | 1.2 | TM |
| | 118698 | AB033113 | Hs.50187 | KIAA1287 protein | 2.1 | TM |
| | 118737 | AA199686 | | gb:zq75g09.r1 Stratagene hNT neuron (937 | 5.2 | other |
| | 118925 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN A | 1.4 | other |
| | 118984 | AI668709 | Hs.240722 | ESTs, Moderately similar to ALU8_HUMAN A | 3.6 | other |
| | 118986 | AF148713 | Hs.125830 | bladder cancer overexpressed protein | 4.9 | ? |
| 10 | 119206 | W24781 | Hs.293798 | KIAA1710 protein | 1.7 | TM |
| | 119235 | AW453069 | Hs.3657 | activity-dependent neuroprotective prote | 2.2 | other |
| | 119265 | BE539706 | Hs.285363 | ESTs | 1.4 | ? |
| | 119279 | N57568 | Hs.48028 | EST | 25.1 | other |
| | 119298 | NM_001241 | Hs.155478 | cyclin T2 | 1.6 | ? |
| 15 | 119338 | AI417240 | Hs.320836 | ESTs, Weakly similar to A47582 B-cell gr | 1.3 | other |
| | 119403 | AL117554 | Hs.119908 | nucleolar protein NOP5/NOP58 | 6.7 | TM |
| | 119478 | AI624342 | Hs.170042 | ESTs | 2.4 | other |
| | 119486 | AI796730 | Hs.55513 | ESTs | 2.1 | other |
| | 119513 | W37933 | | Empirically selected from AFFX single pr | 1.9 | other |
| 20 | 119601 | AK000155 | Hs.91684 | Homo sapiens mRNA; cDNA DKFZp6671103 (fr | 3.7 | TM |
| | 119602 | AW675298 | Hs.233694 | hypothetical protein FLJ11350 | 3 | other |
| | 119676 | AA243837 | Hs.57787 | ESTs | 1.4 | other |
| | 119682 | W61019 | Hs.57811 | ESTs | 1.2 | ? |
| | 119774 | AB032977 | Hs.6298 | KIAA1151 protein | 1.8 | TM |
| 25 | 119780 | NM_016625 | Hs.191381 | hypothetical protein | 3.1 | other |
| | 119789 | BE393948 | Hs.50915 | kallikrein 5 (KLK5; KLK-L2; stratum com | 9.2 | other |
| | 119805 | AI223810 | Hs.43213 | ESTs, Weakly similar to IEFS_HUMAN TRANS | 3.6 | TM |
| | 119818 | AA130970 | Hs.58382 | hypothetical protein FLJ11101 | 2.5 | ? |
| | 119863 | AA081218 | Hs.58608 | Homo sapiens cDNA FLJ14206 fis, clone NT | 2.7 | TM |
| 30 | 119905 | AW449064 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 2.6 | other |
| | 119966 | AA703129 | Hs.58963 | ESTs | 2.7 | other |
| | 120132 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 1.2 | other |
| | 120206 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 45.7 | other |
| | 120248 | AI924294 | Hs.173259 | uncharacterized bone marrow protein BM03 | 1.2 | other |
| 35 | 120269 | AW131940 | Hs.104030 | ESTs | 9.6 | other |
| | 120274 | AA177051 | | gb:nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens | 4.7 | other |
| | 120280 | AA190577 | | gb:zp52g02.s1 Stratagene HeLa cell s3 93 | 2.1 | other |
| | 120296 | AW995911 | Hs.299883 | hypothetical protein FLJ23399 | 1.9 | TM |
| | 120297 | AA191384 | Hs.104072 | ESTs, Weakly similar to Z195_HUMAN ZINC | 15.2 | other |
| 40 | 120324 | AA195517 | Hs.191643 | ESTs | 5.6 | ? |
| | 120325 | AA195651 | Hs.104106 | ESTs | 6.5 | other |
| | 120327 | AK000292 | Hs.278732 | hypothetical protein FLJ20285 | 16.1 | other |
| | 120336 | N85785 | Hs.181165 | eukaryotic translation elongation factor | 3 | other |
| | 120342 | AW450669 | Hs.45068 | hypothetical protein DKFZp4341143 | 5.8 | other |
| 45 | 120345 | AA210722 | Hs.104158 | ESTs | 4.6 | SS, TM |
| | 120349 | AW969481 | Hs.55189 | hypothetical protein | 16.8 | other |
| | 120352 | R06859 | Hs.193172 | ESTs, Weakly similar to I38022 hypotheti | 5.1 | other |
| | 120356 | AF000545 | Hs.296433 | putative purinergic receptor | 28.1 | TM |
| | 120371 | AA219305 | Hs.104196 | EST | 12.4 | ? |
| 50 | 120382 | AA228026 | Hs.38774 | ESTs | 4.1 | TM |
| | 120383 | AL109963 | Hs.123122 | FSH primary response (LRPR1, rat) homolo | 9.7 | TM |
| | 120386 | AW969665 | Hs.154848 | hypothetical protein DKFZp434D0127 | 32.6 | other |
| | 120388 | AA232874 | Hs.104245 | ESTs | 3.2 | other |
| | 120389 | AW967985 | Hs.325572 | ESTs, Moderately similar to ALU7_HUMAN A | 21.7 | other |
| 55 | 120396 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 12.5 | other |
| | 120404 | AB023230 | Hs.96427 | KIAA1013 protein | 7.3 | other |
| | 120418 | AW966893 | Hs.26613 | Homo sapiens mRNA; cDNA DKFZp586F1323 (f | 11.4 | other |
| | 120423 | AA236453 | Hs.18978 | Homo sapiens cDNA: FLJ22822 fis, clone K | 1.9 | other |
| | 120472 | AI950087 | | gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien | 19.4 | other |
| 60 | 120473 | AA251973 | Hs.269988 | ESTs | 5.5 | ? |
| | 120484 | AA253170 | Hs.96473 | EST | 10.4 | ? |
| | 120504 | AA256837 | | gb:zr84d10.s1 Soares_NhHMPu_S1 Homo sapi | 4 | ? |
| | 120509 | BE047718 | Hs.96545 | ESTs | 9.4 | other |
| | 120520 | AA258601 | Hs.161731 | EST | 2.4 | other |
| 65 | 120535 | BE350244 | Hs.96547 | ESTs | 2.5 | ? |
| | 120551 | AA279160 | Hs.111407 | Homo sapiens, clone IMAGE:3613029, mRNA, | 5.3 | other |
| | 120570 | AA280679 | Hs.271445 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 14.4 | ? |

| | | | | | | |
|----|--------|----------|-----------|--|------|-------|
| | 120582 | BE244830 | Hs.284228 | ZNF135-like protein | 10.2 | ? |
| | 120590 | AW372799 | Hs.125790 | leucine-rich repeat-containing 2 | 2.2 | ? |
| | 120596 | AA282074 | Hs.237323 | N-acetylglucosamine-phosphate mutase | 7.6 | other |
| | 120619 | AW965339 | Hs.111471 | ESTs | 2.5 | other |
| 5 | 120624 | AW407987 | Hs.173518 | M-phase phosphoprotein homolog | 52 | other |
| | 120639 | AA286942 | | gb:zs56f05.s1 NCL CGAP_GCB1 Homo sapiens | 2.4 | other |
| | 120648 | AA287095 | Hs.140309 | Homo sapiens, clone IMAGE:3677194, mRNA, | 5 | other |
| | 120653 | AW063659 | Hs.191649 | ESTs | 2.2 | other |
| | 120668 | AW969638 | Hs.112318 | 6.2 kd protein | 2.2 | TM |
| 10 | 120669 | BE536739 | Hs.109909 | ESTs | 1.9 | TM |
| | 120695 | AA976503 | | gb:qq30a04.s1 NCL CGAP_GC4 Homo sapiens | 46.8 | TM |
| | 120696 | AI821539 | Hs.97249 | ESTs | 2.5 | other |
| | 120713 | AW449855 | Hs.96557 | Homo sapiens cDNA FLJ12727 fis, clone NT | 6 | other |
| | 120718 | AA292747 | Hs.97296 | ESTs | 2.9 | other |
| 15 | 120750 | AI191410 | Hs.96693 | ESTs, Moderately similar to 2109260A B c | 7.1 | SS, |
| | 120774 | AI608909 | Hs.193985 | ESTs | 7.9 | other |
| | 120807 | AA346385 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 7 | TM |
| | 120809 | AA346495 | | gb:EST52657 Fetal heart II Homo sapiens | 4.5 | other |
| | 120938 | AA386260 | Hs.104632 | EST | 4.5 | ? |
| 20 | 120977 | AA398155 | Hs.97600 | ESTs | 4.5 | other |
| | 120984 | BE262951 | Hs.99052 | ESTs | 5.6 | other |
| | 120985 | AI219896 | Hs.97592 | ESTs | 1.3 | other |
| | 121011 | AA398360 | Hs.97608 | EST | 3.2 | other |
| | 121026 | AI439713 | Hs.165295 | ESTs | 3.6 | other |
| 25 | 121081 | AA398721 | Hs.186749 | ESTs, Highly similar to I37550 mismatch | 5.5 | other |
| | 121133 | AA363307 | Hs.97032 | ESTs | 3.8 | other |
| | 121176 | AL121523 | Hs.97774 | ESTs | 1.7 | TM |
| | 121223 | AI002110 | Hs.97169 | ESTs, Weakly similar to dJ667H12.2.1 [H. | 2.9 | other |
| | 121320 | AA403008 | Hs.301927 | c6.1A | 1.9 | other |
| 30 | 121340 | AW956981 | Hs.97910 | Homo sapiens cDNA FLJ13383 fis, clone PL | 3.5 | other |
| | 121408 | AA406137 | Hs.98019 | EST | 6.1 | ? |
| | 121439 | AA410190 | Hs.98076 | ESTs, Weakly similar to A47582 B-cell gr | 7.5 | other |
| | 121450 | AA406430 | Hs.105362 | Homo sapiens, clone MGC:18257, mRNA, com | 7.1 | other |
| | 121452 | AW971063 | Hs.292882 | ESTs | 1.8 | other |
| 35 | 121455 | H58306 | Hs.15165 | retinoic acid induced 14 | 10.5 | other |
| | 121457 | W07404 | Hs.144502 | hypothetical protein FLJ22055 | 3.5 | TM |
| | 121496 | AA442224 | Hs.97900 | ESTs | 14.4 | other |
| | 121505 | AA494172 | Hs.194417 | ESTs | 13.1 | other |
| | 121508 | AA402515 | Hs.97887 | ESTs | 28 | other |
| 40 | 121513 | AA416653 | Hs.181510 | ESTs | 6.3 | other |
| | 121514 | AA412112 | | gb:zt69b02.s1 Soares_testis_NHT Homo sap | 2.7 | SS, |
| | 121549 | AA412477 | Hs.98142 | EST | 7.5 | ? |
| | 121558 | AA412497 | | gb:zt95g12.s1 Soares_testis_NHT Homo sap | 2.8 | other |
| | 121577 | AA411970 | Hs.98096 | EST | 3.5 | ? |
| 45 | 121581 | AA416568 | | gb:zu05c10.s1 Soares_testis_NHT Homo sap | 6.2 | TM |
| | 121589 | AD001528 | Hs.89718 | spermine synthase | 4 | other |
| | 121594 | AA626010 | Hs.98247 | ESTs | 2.2 | other |
| | 121622 | AA416931 | Hs.126065 | ESTs | 4.3 | TM |
| | 121655 | AA421537 | Hs.178072 | Homo sapiens mRNA; cDNA DKFZp434B1023 (f | 7.9 | other |
| 50 | 121682 | AA418160 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PL | 2 | other |
| | 121690 | AV660305 | Hs.110286 | ESTs | 4.7 | ? |
| | 121706 | U55184 | Hs.154145 | hypothetical protein FLJ11585 | 12.7 | other |
| | 121714 | AA419225 | Hs.98269 | Homo sapiens cDNA FLJ11953 fis, clone HE | 8.3 | ? |
| | 121729 | AI949597 | Hs.98325 | ESTs | 1.8 | TM |
| 55 | 121731 | AA421041 | Hs.180744 | ESTs | 4.1 | TM |
| | 121744 | AA398784 | Hs.97514 | ESTs | 7.1 | SS, |
| | 121748 | BE536911 | Hs.234545 | hypothetical protein NUF2R | 19.5 | other |
| | 121773 | AB033022 | Hs.158654 | KIAA1196 protein | 8 | other |
| | 121775 | AA421773 | Hs.161008 | ESTs | 1.7 | other |
| 60 | 121776 | AA292579 | Hs.125133 | hypothetical protein FLJ22501 | 6.7 | other |
| | 121786 | AI810774 | Hs.98376 | ESTs | 10.5 | other |
| | 121832 | AW340797 | Hs.98434 | ESTs | 5.9 | other |
| | 121836 | AA328348 | Hs.218289 | ESTs | 3.9 | other |
| | 121839 | AA425691 | Hs.191606 | ESTs, Highly similar to KIAA1048 protein | 5 | other |
| 65 | 121842 | AF027406 | Hs.104865 | serine/threonine kinase 23 | 2.7 | ? |
| | 121847 | AA446628 | Hs.2799 | cartilage linking protein 1 | 2.3 | other |
| | 121871 | AW972668 | Hs.293044 | ESTs | 2.9 | TM |

| | | | | | | |
|----|--------|----------|-----------|--|-------|--------|
| | 121882 | AA426376 | Hs.98459 | ESTs | 5 | other |
| | 121911 | AA427950 | | gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_ | 7.3 | TM |
| | 121915 | AA428179 | Hs.223405 | ESTs, Moderately similar to A46010 X-in | 2.5 | other |
| | 121935 | AA428647 | Hs.98611 | EST | 2.3 | other |
| 5 | 121983 | AA298760 | Hs.180191 | hypothetical protein FLJ14904 | 3.4 | other |
| | 121985 | AI862570 | Hs.299214 | Homo sapiens, clone IMAGE:2822295, mRNA, | 11.4 | other |
| | 121995 | AA210863 | Hs.3532 | nemo-like kinase | 3.8 | ? |
| | 121999 | AA430211 | Hs.98668 | EST | 6.5 | other |
| | 122009 | AW292763 | Hs.160822 | Homo sapiens cDNA: FLJ20863 fis, clone A | 2.2 | other |
| 10 | 122013 | AA431085 | Hs.98706 | ESTs | 6.6 | other |
| | 122036 | W92142 | Hs.271963 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 13.1 | other |
| | 122050 | AI453076 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 9.1 | other |
| | 122060 | AA431738 | Hs.98750 | EST | 13.1 | ? |
| | 122114 | AW161023 | Hs.104921 | ESTs | 1.5 | other |
| 15 | 122188 | AA398838 | | gb:zt80d01.r1 Soares_testis_NHT Homo sap | 3.4 | other |
| | 122204 | AA435936 | Hs.98842 | EST | 5.6 | other |
| | 122246 | AA329550 | Hs.29417 | HCF-binding transcription factor Zhangfe | 5.2 | other |
| | 122257 | AA436819 | Hs.98899 | ESTs | 5.6 | other |
| | 122302 | AA441801 | Hs.104947 | ESTs | 5.8 | other |
| 20 | 122341 | AW601969 | Hs.99010 | hypothetical protein FLJ22263 similar to | 2 | other |
| | 122356 | AA443794 | Hs.98390 | ESTs | 7.4 | SS, TM |
| | 122369 | AA443985 | Hs.303222 | ESTs | 12.2 | ? |
| | 122371 | AA868555 | Hs.178222 | ESTs | 5 | ? |
| | 122372 | AA446008 | Hs.336677 | EST | 7.8 | ? |
| 25 | 122378 | AB032948 | Hs.21356 | hypothetical protein DKFZp762K2015 | 2.5 | ? |
| | 122405 | AA446572 | Hs.303223 | EST | 2.8 | TM |
| | 122412 | AA446869 | Hs.119316 | ESTs | 7.4 | other |
| | 122415 | AA446918 | Hs.99088 | EST | 1.9 | other |
| | 122418 | AA446966 | Hs.99090 | ESTs, Moderately similar to similar to K | 6.9 | ? |
| 30 | 122440 | AW505139 | Hs.9460 | Homo sapiens mRNA; cDNA DKFZp547C244 (fr | 2.6 | other |
| | 122446 | AA447603 | Hs.99123 | EST | 1.8 | TM |
| | 122448 | AA447626 | Hs.99127 | EST | 3.5 | other |
| | 122458 | AI266159 | Hs.104980 | ESTs | 1.5 | other |
| | 122460 | AW418788 | Hs.99148 | ESTs, Weakly similar to S43569 R01H10.6 | 9.7 | other |
| 35 | 122464 | AA448158 | Hs.99152 | EST | 4.9 | other |
| | 122490 | AA448349 | Hs.238151 | EST | 6.2 | ? |
| | 122492 | AA448417 | Hs.104990 | ESTs | 5.5 | other |
| | 122502 | AA204969 | Hs.234863 | Homo sapiens cDNA FLJ12082 fis, clone HE | 1.3 | other |
| | 122510 | AA449232 | Hs.99195 | ESTs | 11.2 | ? |
| 40 | 122530 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 10.1 | other |
| | 122547 | AA779725 | Hs.164589 | ESTs | 2.5 | SS, |
| | 122555 | AA194055 | Hs.293858 | ESTs | 1.9 | other |
| | 122570 | AA452578 | Hs.262907 | ESTs | 9.5 | other |
| | 122572 | AA452601 | Hs.99287 | EST | 11 | ? |
| 45 | 122586 | AK001910 | Hs.99303 | Homo sapiens cDNA FLJ11048 fis, clone PL | 3.4 | other |
| | 122587 | AB040893 | Hs.6968 | KIAA1460 protein | 2 | other |
| | 122598 | AI028173 | Hs.99329 | ESTs | 1.7 | ? |
| | 122599 | AL355841 | Hs.99330 | hypothetical protein FLJ23588 | 4.4 | ? |
| | 122602 | AA411925 | Hs.301960 | ESTs | 4.7 | other |
| 50 | 122607 | AA453518 | Hs.98023 | ESTs | 61.5 | other |
| | 122614 | AA453630 | Hs.99339 | EST | 10.7 | ? |
| | 122616 | AA453638 | Hs.161873 | ESTs | 107.3 | ? |
| | 122617 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 121.4 | other |
| | 122618 | AA453641 | | gb:zx48e06.s1 Soares_testis_NHT Homo sap | 31.1 | SS, |
| 55 | 122622 | AA453987 | Hs.144802 | ESTs | 5.6 | other |
| | 122717 | AA456859 | Hs.178358 | ESTs | 8.5 | SS, |
| | 122762 | AI376875 | Hs.105119 | ESTs | 10.4 | other |
| | 122829 | AW204530 | Hs.99500 | ESTs | 81.8 | ? |
| | 122834 | AA461492 | Hs.99545 | Homo sapiens cDNA FLJ10658 fis, clone NT | 3.7 | ? |
| 60 | 122836 | AA460581 | Hs.290996 | ESTs | 4.6 | other |
| | 122837 | AA461509 | Hs.293565 | ESTs, Weakly similar to putative p150 [H | 2.7 | TM |
| | 122838 | AA460584 | Hs.334386 | ESTs | 75.3 | other |
| | 122854 | AA600235 | Hs.9625 | NIMA (never in mitosis gene a)-related k | 7.8 | other |
| | 122856 | AI929374 | Hs.75367 | Src-like-adaptor | 5.8 | other |
| 65 | 122861 | AA335721 | Hs.119394 | ESTs | 1.3 | other |
| | 122866 | BE539656 | Hs.283705 | ESTs | 4.2 | other |
| | 122868 | AF005216 | Hs.115541 | Janus kinase 2 (a protein tyrosine kinas | 5.3 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 122870 | AW576312 | Hs.318722 | Homo sapiens cDNA: FLJ21766 fis, clone C | 9.9 | ? |
| | 122872 | AW081394 | Hs.97103 | ESTs | 5.3 | other |
| | 122879 | AA769410 | Hs.128654 | ESTs | 13.9 | other |
| | 122907 | AA470074 | Hs.169896 | ESTs | 11.5 | other |
| 5 | 122916 | AA470140 | Hs.229170 | EST | 1.7 | TM |
| | 122981 | AA478951 | Hs.105629 | ESTs | 5 | other |
| | 123013 | AW968324 | Hs.17384 | ESTs | 15.4 | other |
| | 123016 | AW338067 | Hs.323231 | Homo sapiens cDNA FLJ11946 fis, clone HE | 2.8 | other |
| | 123034 | AL359571 | Hs.44054 | ninein (GSK3B interacting protein) | 8.7 | other |
| 10 | 123072 | AI382600 | Hs.104308 | ESTs, Weakly similar to KIAA1395 protein | 8.8 | other |
| | 123082 | AA485360 | Hs.105661 | ESTs | 4 | ? |
| | 123088 | AI343652 | Hs.105667 | ESTs | 3.8 | other |
| | 123110 | AA486256 | Hs.193510 | EST | 7.4 | other |
| | 123114 | BE304942 | Hs.265848 | myomegalin | 2.8 | ? |
| 15 | 123131 | T52027 | Hs.271795 | ESTs, Weakly similar to I38022 hypotheti | 2.4 | other |
| | 123132 | AI061582 | Hs.324179 | Homo sapiens cDNA FLJ12371 fis, clone MA | 15.6 | TM |
| | 123136 | AW451999 | Hs.194024 | ESTs | 5.2 | other |
| | 123149 | AI734179 | Hs.105676 | ESTs | 23.8 | TM |
| | 123152 | AW601773 | Hs.270259 | ESTs | 5.2 | other |
| 20 | 123258 | AA490929 | Hs.105274 | ESTs, Weakly similar to RMS1_HUMAN REGUL | 9.3 | ? |
| | 123315 | AA496369 | | gb:zv37d10.s1 Soares ovary tumor NbHOT H | 4.2 | TM |
| | 123369 | AA504757 | Hs.105738 | ESTs | 7 | other |
| | 123394 | AA731404 | Hs.105510 | ESTs | 3.7 | other |
| | 123433 | AW450922 | Hs.112478 | ESTs | 3.8 | other |
| 25 | 123466 | AA599042 | Hs.112503 | EST | 7.4 | other |
| | 123470 | AW303285 | Hs.303632 | Human DNA sequence from clone RP11-110H4 | 3.5 | other |
| | 123471 | AB021644 | Hs.197219 | zinc finger protein 14 (KOX 6) | 5.2 | ? |
| | 123475 | BE439553 | Hs.250528 | Homo sapiens, clone IMAGE:4098694, mRNA, | 1.7 | other |
| | 123482 | N95059 | Hs.55098 | ESTs | 1.6 | other |
| 30 | 123486 | BE019072 | Hs.334802 | Homo sapiens cDNA FLJ14680 fis, clone NT | 2.4 | other |
| | 123508 | AW380388 | Hs.155546 | KIAA1080 protein; Golgi-associated, gamm | 2.2 | TM |
| | 123615 | AA609170 | | gb:af12a12.s1 Soares_testis_NHT Homo sap | 7.9 | other |
| | 123619 | AA602964 | | gb:no97c02.s1 NCL_CGAP_Pr2 Homo sapiens | 2.8 | other |
| | 123658 | AA609364 | | gb:zu71d09.s1 Soares_testis_NHT Homo sap | 1.7 | ? |
| 35 | 123674 | AI269609 | Hs.105187 | kinesin protein 9 gene | 5.7 | ? |
| | 123735 | NM_013241 | Hs.95231 | FH1/FH2 domain-containing protein | 10 | other |
| | 123738 | AA609891 | Hs.112777 | EST | 5.2 | other |
| | 123753 | AA609955 | Hs.234961 | Huntingtin interacting protein E | 30.6 | TM |
| 40 | 123804 | AA620464 | Hs.261915 | EST, Weakly similar to S65657 alpha-1C-a | 2.1 | other |
| | 123811 | AA620586 | | gb:ae60g05.s1 Stratagene lung carcinoma | 2.7 | other |
| | 123951 | AB012922 | Hs.173043 | metastasis-associated 1-like 1 | 6.3 | ? |
| | 123983 | AJ272267 | Hs.146178 | choline dehydrogenase | 4.4 | other |
| | 124001 | L42542 | Hs.75447 | raIA binding protein 1 | 7.1 | ? |
| | 124006 | AI147155 | Hs.270016 | ESTs | 8.3 | SS, |
| 45 | 124070 | AJ950314 | Hs.154762 | HIV-1 rev binding protein 2 | 3.8 | other |
| | 124074 | H05635 | Hs.294030 | topoisomerase-related function protein 4 | 1.2 | SS, |
| | 124178 | BE463721 | Hs.971101 | putative G protein-coupled receptor | 3.2 | ? |
| | 124203 | AA372796 | Hs.269339 | ESTs, Weakly similar to AF161356 1 HSPC0 | 5.7 | other |
| | 124352 | AA640891 | Hs.102406 | ESTs | 3.1 | TM |
| 50 | 124375 | D87454 | Hs.192966 | KIAA0265 protein | 3.5 | other |
| | 124385 | AI267847 | | gb:aq49a10.x1 Stanley Frontal NB pool 2 | 57.1 | ? |
| | 124390 | AA317338 | Hs.7535 | COBW-like protein | 2.8 | other |
| | 124391 | AF155099 | Hs.279780 | NY-REN-18 antigen | 7.1 | other |
| | 124417 | N34059 | | gb:yv28h09.s1 Soares fetal liver spleen | 3.3 | other |
| 55 | 124428 | H13540 | Hs.82202 | ribosomal protein L17 | 2.9 | other |
| | 124440 | AA532519 | Hs.129043 | Human DNA sequence from clone 989H11 on | 7.9 | other |
| | 124466 | R10084 | Hs.113319 | kinesin heavy chain member 2 | 2.6 | TM |
| | 124482 | N53935 | | gb:yv59d09.s1 Soares fetal liver spleen | 7.9 | TM |
| | 124498 | H79433 | Hs.268997 | ESTs | 7.8 | other |
| 60 | 124515 | AA669097 | Hs.109370 | ESTs | 3.3 | other |
| | 124608 | N71076 | Hs.102800 | ESTs, Weakly similar to neuronal thread | 4.6 | ? |
| | 124631 | NM_014053 | Hs.270594 | FLVCR protein | 3.2 | other |
| | 124634 | AI765123 | Hs.143671 | Homo sapiens cDNA FLJ13533 fis, clone PL | 5.8 | other |
| | 124637 | AA160474 | Hs.75798 | hypothetical protein | 9.3 | other |
| 65 | 124642 | AW968856 | Hs.278569 | sorting nexin 17 | 3.5 | other |
| | 124649 | N92593 | Hs.313054 | ESTs | 6.1 | TM |
| | 124661 | R48170 | Hs.78436 | EphB1 | 5.6 | other |

| | | | | | | |
|----|--------|-----------|-----------|---|-------|--------|
| | 124683 | AA381661 | Hs.119878 | ESTs, Weakly similar to M3K9_HUMAN MITOG | 7.9 | TM |
| | 124712 | R09166 | Hs.191148 | ESTs | 5.7 | other |
| | 124735 | R22952 | Hs.268685 | ESTs | 11.3 | ? |
| 5 | 124761 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 9 | other |
| | 124768 | AW368528 | Hs.100855 | ESTs | 8.3 | other |
| | 124775 | R41772 | Hs.100878 | ESTs | 4.9 | other |
| | 124777 | R41933 | Hs.140237 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.8 | other |
| | 124788 | R43543 | Hs.100912 | Homo sapiens cDNA: FLJ22726 fis, clone H | 5.1 | other |
| 10 | 124809 | AL355722 | Hs.106875 | Homo sapiens EST from clone 35214, full | 4.2 | other |
| | 124811 | R46068 | Hs.288912 | hypothetical protein FLJ22604 | 14.2 | other |
| | 124812 | R47948 | Hs.188732 | ESTs | 7.9 | other |
| | 124822 | AA418160 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PL | 6.6 | other |
| | 124825 | AA501669 | Hs.336693 | ESTs | 2.3 | SS, TM |
| | 124833 | AW975868 | Hs.294100 | ESTs | 2.7 | SS, TM |
| 15 | 124857 | R63652 | Hs.137190 | ESTs | 2.3 | other |
| | 124860 | R65763 | Hs.101477 | EST | 23.9 | ? |
| | 124863 | AI382555 | Hs.127950 | bromodomain-containing 1 | 2 | other |
| | 124876 | AF135422 | Hs.27059 | GDP-mannose pyrophosphorylase A | 4.4 | SS, |
| | 124878 | BE397530 | Hs.288057 | hypothetical protein FLJ22242 | 2.7 | other |
| 20 | 124902 | H37941 | Hs.101883 | ESTs | 5.7 | other |
| | 124903 | AW296713 | Hs.221441 | ESTs | 32.4 | other |
| | 124930 | AI076343 | Hs.173939 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 22.8 | other |
| | 124942 | R99978 | Hs.268892 | ESTs, Moderately similar to B34087 hypot | 6.1 | other |
| | 124958 | AI078645 | Hs.431 | murine leukemia viral (bmi-1) oncogene h | 1.9 | other |
| 25 | 124980 | T40841 | Hs.98681 | ESTs | 4.5 | ? |
| | 125002 | T59338 | Hs.269463 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.9 | other |
| | 125047 | T79815 | Hs.279793 | ESTs | 5 | ? |
| | 125051 | T79956 | Hs.100588 | EST | 135.3 | ? |
| | 125056 | T81310 | Hs.100592 | ESTs | 5.4 | other |
| 30 | 125101 | AI472068 | Hs.286236 | KIAA1856 protein | 5.6 | other |
| | 125113 | T96595 | Hs.302270 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 1.8 | other |
| | 125115 | T97341 | | gb:ye57e05.s1 Soares fetal liver spleen | 9.6 | ? |
| | 125125 | AI222382 | Hs.240767 | Human DNA sequence from clone RP1-12G14 | 1.5 | TM |
| | 125147 | W38150 | | Empirically selected from AFFX single pr | 1.7 | ? |
| 35 | 125161 | W44657 | Hs.144232 | EST | 10.7 | ? |
| | 125249 | AA630863 | Hs.131375 | ESTs, Moderately similar to ALUB_HUMAN ! | 1.3 | other |
| | 125255 | AF098162 | Hs.118631 | timeless (Drosophila) homolog | 9.4 | other |
| | 125279 | AW401809 | Hs.4779 | KIAA1150 protein | 1.5 | ? |
| | 125280 | AI123705 | Hs.106932 | ESTs | 8.1 | ? |
| 40 | 125298 | AW972542 | Hs.289008 | Homo sapiens cDNA: FLJ21814 fis, clone H | 1.5 | other |
| | 125660 | AW292171 | Hs.23978 | scaffold attachment factor B | 5.9 | other |
| | 125827 | NM_003403 | Hs.97496 | YY1 transcription factor | 1.2 | ? |
| | 125891 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 6.5 | ? |
| 45 | 126005 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 14.3 | ? |
| | 126202 | AA157632 | Hs.272630 | vacuolar proton pump delta polypeptide | 2.5 | SS, |
| | 126695 | AA643322 | Hs.172028 | a disintegrin and metalloproteinase doma | 9.1 | SS, TM |
| | 127050 | AW411066 | Hs.274351 | CGI-89 protein | 17 | other |
| | 127274 | AW966158 | Hs.58582 | Homo sapiens cDNA FLJ12789 fis, clone NT | 12.8 | other |
| 50 | 128355 | AW293012 | Hs.161623 | ESTs | 7.4 | SS, |
| | 128493 | D87466 | Hs.240112 | KIAA0276 protein | 3.1 | TM |
| | 128522 | BE173977 | Hs.10098 | putative nucleolar RNA helicase | 9.4 | other |
| | 128527 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 1.5 | other |
| | 128528 | R39234 | Hs.251699 | ESTs, Weakly similar to IDN4-GGTR14 [H.s | 2.8 | other |
| 55 | 128595 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | 12.1 | TM |
| | 128599 | NM_015366 | Hs.102336 | Rho GTPase activating protein 8 | 2.4 | ? |
| | 128604 | AI879099 | Hs.102397 | GIOT-3 for gonadotropin inducible transc | 1.3 | other |
| | 128608 | BE267994 | Hs.102419 | zinc finger protein | 7.2 | other |
| | 128625 | AB037841 | Hs.102652 | hypothetical protein ASH1 | 1.3 | other |
| 60 | 128629 | AL096748 | Hs.102708 | DKFZP434A043 protein | 3.2 | other |
| | 128639 | AW582962 | Hs.102897 | CGI-47 protein | 2 | TM |
| | 128656 | AA458542 | Hs.10326 | coatamer protein complex, subunit epsilo | 1.4 | other |
| | 128658 | BE397354 | Hs.324830 | diphtheria toxin resistance protein requi | 2.5 | other |
| | 128670 | AA975486 | Hs.103441 | Homo sapiens, Similar to RIKEN cDNA 1700 | 7.1 | ? |
| | 128691 | W27939 | Hs.103834 | hypothetical protein MGC5576 | 7.8 | ? |
| 65 | 128696 | BE081143 | Hs.225977 | nuclear receptor coactivator 3 | 3.8 | other |
| | 128700 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 1.6 | other |
| | 128714 | T85231 | Hs.179661 | tubulin, beta 5 | 7.8 | other |

| | | | | | | |
|----|--------|-----------|-----------|---|------|--------|
| | 128717 | AK001564 | Hs.104222 | hypothetical protein FLJ10702 | 5.5 | other |
| | 128733 | BE147740 | Hs.104558 | ESTs, Moderately similar to I38022 hypot | 2.7 | TM |
| | 128737 | AF292100 | Hs.104613 | RP42 homolog | 2.8 | TM |
| 5 | 128742 | AA307211 | Hs.251531 | proteasome (prosome, macropain) subunit, | 4.5 | ? |
| | 128746 | AI470163 | Hs.323342 | actin related protein 2/3 complex, subun | 2.2 | other |
| | 128747 | AB027249 | Hs.104741 | PDZ-binding kinase; T-cell originated pr | 2.8 | other |
| | 128772 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 5.4 | other |
| | 128781 | N71826 | Hs.105465 | small nuclear ribonucleoprotein polypept | 53.9 | TM |
| | 128797 | NM_002975 | Hs.105927 | stem cell growth factor; lymphocyte secr | 13.3 | other |
| 10 | 128806 | AW630942 | Hs.106061 | RD RNA-binding protein | 2.6 | other |
| | 128814 | AW248431 | Hs.256526 | nuclear prelamin A recognition factor | 2.2 | other |
| | 128830 | BE281170 | Hs.106357 | valosin-containing protein | 6 | other |
| | 128835 | AK001731 | Hs.106390 | Homo sapiens mRNA; cDNA DKFZp586H0924 (f | 1.6 | SS, |
| | 128854 | BE159181 | Hs.168232 | hypothetical protein FLJ13855 | 2.3 | other |
| 15 | 128871 | AF189723 | Hs.106778 | ATPase, Ca++ transporting, type 2C, memb | 1.5 | ? |
| | 128906 | R57988 | Hs.10706 | epithelial protein lost in neoplasm beta | 4.8 | other |
| | 128920 | AA622037 | Hs.166468 | programmed cell death 5 | 1.4 | other |
| | 128925 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 1.9 | other |
| 20 | 128946 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | 7.3 | ? |
| | 128949 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 2.5 | other |
| | 128959 | AI580127 | Hs.107381 | hypothetical protein FLJ11200 | 1.3 | other |
| | 128965 | AW150697 | Hs.107418 | ESTs | 1.4 | ? |
| | 128970 | AI375672 | Hs.165028 | ESTs | 1.3 | other |
| | 128975 | BE560779 | Hs.284233 | NICE-5 protein | 14 | other |
| 25 | 128979 | AW271217 | Hs.281434 | Homo sapiens cDNA FLJ14028 fis, clone HE | 1.6 | TM |
| | 128995 | AI816224 | Hs.107747 | DKFZP566C243 protein | 1.9 | other |
| | 129019 | AI950087 | | gb:wc05cd02.x1 NCI_CGAP_Kid12 Homo sapien | 2.9 | other |
| | 129021 | AL044675 | Hs.173081 | KIAA0530 protein | 3.8 | other |
| 30 | 129032 | R80088 | Hs.108104 | ubiquitin-conjugating enzyme E2L 3 | 3.4 | other |
| | 129076 | AW296806 | Hs.326234 | ESTs, Highly similar to T46422 hypotheti | 5 | other |
| | 129078 | AI351010 | Hs.102267 | lysosomal | 2.1 | other |
| | 129088 | AA744610 | Hs.194431 | palladin | 17.1 | other |
| | 129095 | L12350 | Hs.108623 | thrombospondin 2 | 2.7 | other |
| | 129096 | AA463189 | Hs.288906 | WW Domain-Containing Gene | 20.9 | TM |
| 35 | 129097 | BE243933 | Hs.108642 | zinc finger, protein 22 (KOX 15) | 3 | other |
| | 129099 | AF146074 | Hs.108660 | ATP-binding cassette, sub-family C (CFTR | 5.8 | TM |
| | 129136 | W93048 | Hs.250723 | hypothetical protein MGC2747 | 6 | other |
| | 129149 | AA356620 | Hs.108947 | KIAA0050 gene product | 6.4 | TM |
| | 129172 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 1.8 | TM |
| 40 | 129192 | AA286914 | Hs.183299 | ESTs | 2.1 | ? |
| | 129194 | AA150797 | Hs.109276 | latexin protein | 3.3 | SS, TM |
| | 129198 | N57532 | Hs.109315 | KIAA1415 protein | 5.9 | other |
| | 129207 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mime | 8.1 | other |
| | 129228 | U40714 | Hs.239307 | tyrosyl-tRNA synthetase | 2.9 | other |
| 45 | 129229 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 3.3 | ? |
| | 129254 | AA252468 | Hs.1098 | DKFZp434J1813 protein | 2.6 | SS, TM |
| | 129255 | AI961727 | Hs.109804 | H1 histone family, member X | 7.4 | other |
| | 129288 | W26392 | Hs.110080 | ESTs, Weakly similar to S13495 pregnancy | 9.6 | other |
| | 129296 | AI051967 | Hs.110122 | ESTs | 1.2 | other |
| 50 | 129323 | AA287239 | Hs.5518 | Homo sapiens cDNA FLJ11311 fis, clone PL | 5.2 | other |
| | 129340 | H75334 | Hs.11050 | F-box only protein 9 | 4.7 | SS, |
| | 129347 | BE614192 | Hs.279869 | melanoma-associated antigen recognised b | 7.7 | TM |
| | 129362 | U30246 | Hs.110736 | solute carrier family 12 (sodium/potassi | 6.7 | TM |
| | 129366 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 8.6 | SS, |
| 55 | 129370 | AI686379 | Hs.110796 | SAR1 protein | 1.4 | TM |
| | 129372 | NM_016039 | Hs.110803 | CGI-99 protein | 2 | other |
| | 129403 | AF149785 | Hs.111126 | pituitary tumor-transforming 1 interacti | 7.5 | other |
| | 129404 | AI267700 | Hs.317584 | ESTs | 5.1 | other |
| | 129423 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 10.2 | other |
| 60 | 129482 | AA188185 | Hs.289043 | spindlin | 6.8 | other |
| | 129513 | AW843633 | Hs.306163 | hypothetical protein AL110115 | 7.1 | SS, |
| | 129515 | AF255303 | Hs.112227 | membrane-associated nucleic acid binding | 2.5 | other |
| | 129527 | AA769221 | Hs.270847 | delta-tubulin | 3.2 | other |
| | 129559 | W01296 | Hs.11360 | hypothetical protein FLJ14784 | 7.5 | other |
| 65 | 129560 | AA317841 | Hs.7845 | hypothetical protein MGC2752 | 6.8 | other |
| | 129570 | AI923097 | Hs.11441 | chromosome 1 open reading frame 8 | 2.1 | other |
| | 129575 | F08282 | Hs.278428 | progesterone induced protein | 1.6 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 129587 | H14718 | Hs.11506 | Human clone 23589 mRNA sequence | 6.8 | other |
| | 129588 | BE408300 | Hs.301862 | postmeiotic segregation increased 2-like | 1.4 | TM |
| | 129591 | N57423 | Hs.179898 | HSPC055 protein | 7.4 | other |
| 5 | 129594 | AW403724 | Hs.36989 | coagulation factor VII (serum prothrombi | 9 | ? |
| | 129596 | AF035537 | Hs.115521 | REV3 (yeast homolog)-like, catalytic sub | 1.6 | other |
| | 129628 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 2.2 | other |
| | 129649 | AD000092 | Hs.16488 | calreticulin | 3.3 | other |
| | 129675 | NM_015556 | Hs.172180 | KIAA0440 protein | 13.4 | other |
| 10 | 129680 | U03749 | | gb:Human chromogranin A (CHGA) gene, pro | 14.1 | ? |
| | 129689 | AW748482 | Hs.77873 | B7 homolog 3 | 2.6 | other |
| | 129702 | AI304966 | Hs.12035 | ESTs, Weakly similar to I38022 hypotheti | 7.5 | TM |
| | 129720 | AA156214 | Hs.12152 | APMCF1 protein | 2 | other |
| | 129721 | NM_001415 | Hs.211539 | eukaryotic translation initiation factor | 1.7 | TM |
| 15 | 129778 | AK001676 | Hs.12457 | hypothetical protein FLJ10814 | 1.8 | other |
| | 129779 | AA394090 | Hs.12460 | Homo sapiens clone 23870 mRNA sequence | 5.5 | TM |
| | 129800 | AF052112 | Hs.12540 | lysosomal | 1.7 | ? |
| | 129806 | AB023148 | Hs.173373 | KIAA0931 protein | 1.2 | other |
| | 129815 | BE565817 | Hs.26498 | hypothetical protein FLJ21657 | 3.1 | other |
| 20 | 129840 | NM_006590 | Hs.12820 | SnRNP assembly defective 1 homolog | 1.8 | other |
| | 129861 | AL049999 | Hs.85963 | DKFZP564M182 protein | 2.3 | other |
| | 129864 | AI393237 | Hs.129914 | runt-related transcription factor 1 (acu | 1.7 | SS, |
| | 129869 | AI222069 | Hs.13015 | hypothetical protein similar to mouse Dn | 2.8 | TM |
| | 129945 | BE514376 | Hs.165998 | PAI-1 mRNA-binding protein | 1.8 | other |
| 25 | 129953 | AA412195 | Hs.13740 | ESTs | 2.5 | other |
| | 129972 | AW753185 | Hs.180628 | dynamlin 1-like | 1.8 | ? |
| | 129983 | U09848 | Hs.132390 | zinc finger protein 36 (KOX 18) | 1.3 | other |
| | 130010 | AA301116 | Hs.142838 | nucleolar phosphoprotein Nopp34 | 1.6 | other |
| | 130081 | AA287325 | Hs.14713 | ESTs | 4.1 | other |
| 30 | 130082 | S73265 | Hs.1473 | gastrin-releasing peptide | 1.9 | other |
| | 130097 | AL046962 | Hs.14845 | forkhead box O3A | 2.8 | other |
| | 130100 | AL135561 | Hs.14891 | hypothetical protein FLJ21047 | 2.3 | other |
| | 130111 | X53002 | Hs.149846 | integrin, beta 5 | 2.3 | other |
| | 130112 | AA916785 | Hs.180610 | splicing factor proline/glutamine rich (| 3 | other |
| 35 | 130128 | L76937 | Hs.150477 | Werner syndrome | 1.8 | other |
| | 130135 | AA311426 | Hs.21635 | tubulin, gamma 1 | 6.1 | other |
| | 130211 | NM_003358 | Hs.23703 | ESTs, Moderately similar to CEGT_HUMAN C | 1.6 | other |
| | 130212 | D80001 | Hs.152629 | KIAA0179 protein | 1.3 | other |
| | 130236 | R85367 | Hs.51957 | splicing factor, arginine/serine-rich 2, | 2 | other |
| 40 | 130241 | AL035588 | Hs.153203 | MyoD family inhibitor | 3.2 | other |
| | 130242 | X79201 | Hs.153221 | synovial sarcoma, translocated to X chro | 5.4 | ? |
| | 130249 | D81983 | Hs.322852 | GAS2-related on chromosome 22 | 4.9 | other |
| | 130263 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 1.4 | other |
| | 130287 | AA479005 | Hs.154036 | tumor suppressing subtransferable candi | 2.6 | other |
| 45 | 130310 | AB011121 | Hs.154248 | amyotrophic lateral sclerosis 2 (juvenil | 6.3 | other |
| | 130353 | Z19084 | Hs.172210 | MUF1 protein | 6.2 | other |
| | 130356 | AF127577 | Hs.155017 | nuclear receptor interacting protein 1 | 2.4 | other |
| | 130357 | AJ224442 | Hs.155020 | putative methyltransferase | 3.5 | TM |
| | 130359 | NM_013449 | Hs.277401 | bromodomain adjacent to zinc finger doma | 8.5 | other |
| 50 | 130367 | AL135301 | Hs.8768 | hypothetical protein FLJ10849 | 1.4 | other |
| | 130372 | AI077464 | Hs.5011 | RNA binding motif protein 9 | 3.3 | ? |
| | 130393 | N89487 | Hs.155291 | KIAA0005 gene product | 1.8 | other |
| | 130399 | AW374106 | Hs.155356 | hypothetical protein MGC2840 similar to | 3.4 | other |
| | 130407 | BE385099 | Hs.334727 | hypothetical protein MGC3017 | 2.3 | other |
| 55 | 130409 | NM_001197 | Hs.155419 | BCL2-interacting killer (apoptosis-induc | 2.7 | TM |
| | 130419 | AF037448 | Hs.155489 | NS1-associated protein 1 | 1.8 | other |
| | 130441 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 2.3 | other |
| | 130448 | BE513202 | Hs.15569 | PPAR binding protein | 4 | TM |
| | 130455 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 33.6 | ? |
| 60 | 130485 | BE245851 | Hs.180779 | H2B histone family, member B | 5 | other |
| | 130487 | U49844 | Hs.77613 | ataxia telangiectasia and Rad3 related | 4.4 | other |
| | 130498 | L38951 | Hs.180446 | karyopherin (importin) beta 1 | 1.6 | SS, TM |
| | 130503 | BE208491 | Hs.295112 | KIAA0618 gene product | 16.1 | other |
| | 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 6.1 | other |
| | 130526 | AW876523 | Hs.15929 | hypothetical protein FLJ12910 | 2.1 | other |
| 65 | 130544 | AA321238 | Hs.4310 | eukaryotic translation initiation factor | 1.5 | other |
| | 130553 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 14.4 | ? |
| | 130556 | AI907018 | Hs.15977 | Empirically selected from AFFX single pr | 4.8 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 130567 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 8 | other |
| | 130568 | AA232119 | Hs.16085 | putative G-protein coupled receptor | 3.4 | other |
| | 130574 | AF083208 | Hs.16178 | apoptosis antagonizing transcription fac | 1.2 | other |
| | 130598 | AL042210 | Hs.16493 | hypothetical protein DKFZp762N2316; KIAA | 1.4 | other |
| 5 | 130601 | AA609738 | Hs.16525 | ESTs | 1.5 | TM |
| | 130614 | AI354355 | Hs.16697 | down-regulator of transcription 1, TBP-b | 1.3 | other |
| | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 12.1 | TM |
| | 130618 | AA383439 | Hs.16758 | Spir-1 protein | 15.9 | other |
| | 130667 | BE246961 | Hs.17639 | Homo sapiens ubiquitin protein ligase (U | 13.9 | other |
| 10 | 130674 | AL048842 | Hs.194019 | atractin | 1.5 | other |
| | 130675 | AA442233 | Hs.17731 | hypothetical protein FLJ12892 | 5.4 | other |
| | 130692 | AA652501 | Hs.13561 | hypothetical protein MGC4692 | 5 | other |
| | 130693 | R68537 | Hs.17962 | ESTs | 2 | other |
| | 130712 | AJ271881 | Hs.279762 | bromodomain-containing 7 | 1.8 | TM |
| 15 | 130714 | AI348274 | Hs.18212 | DNA segment on chromosome X (unique) 987 | 2 | TM |
| | 130730 | AB007920 | Hs.18586 | KIAA0451 gene product | 3.8 | ? |
| | 130744 | H59696 | Hs.18747 | POP7 (processing of precursor, S. cerevi | 3.2 | ? |
| | 130751 | AF052105 | Hs.18879 | chromosome 12 open reading frame | 1.4 | other |
| | 130757 | AL036067 | Hs.18925 | protein x 0001 | 5.7 | other |
| 20 | 130768 | AF258627 | Hs.211562 | ATP-binding cassette, sub-family A (ABC1 | 5.2 | ? |
| | 130789 | AK000355 | Hs.8899 | sirtuin (silent mating type information | 1.6 | other |
| | 130836 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 15.7 | SS, |
| | 130841 | AL157468 | Hs.325825 | Homo sapiens cDNA FLJ20848 fis, clone AD | 2.8 | other |
| | 130843 | AA447492 | Hs.20183 | ESTs, Weakly similar to AF164793 1 prote | 1.5 | other |
| 25 | 130844 | U76248 | Hs.20191 | seven in absentia (Drosophila) homolog 2 | 3.5 | other |
| | 130855 | AJ243706 | Hs.143323 | putative DNA/chromatin binding motif | 1.7 | other |
| | 130861 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 1.9 | other |
| | 130879 | NM_003416 | Hs.2076 | zinc finger protein 7 (KOX 4, clone HF.1 | 1.4 | other |
| | 130880 | BE514434 | Hs.20830 | kinesin-like 2 | 2.1 | TM |
| 30 | 130892 | AL120837 | Hs.20993 | high-glucose-regulated protein 8 | 2.5 | other |
| | 130898 | AB033078 | Hs.186613 | sphingosine-1-phosphate lyase 1 | 1.7 | other |
| | 130911 | BE409769 | Hs.21189 | DnaJ (Hsp40) homolog, subfamily A, membe | 1.8 | other |
| | 130919 | N79110 | Hs.21276 | collagen, type IV, alpha 3 (Goodpasture | 2.3 | TM |
| | 130944 | BE382657 | Hs.21486 | signal transducer and activator of trans | 5.4 | other |
| 35 | 130971 | N39842 | Hs.301444 | KIAA1673 | 2.2 | SS, |
| | 130993 | T97401 | Hs.21929 | ESTs | 1.6 | other |
| | 131005 | AV658308 | Hs.2210 | thyroid hormone receptor interactor 3 | 1.6 | ? |
| | 131028 | AI879165 | Hs.2227 | CCAAT/enhancer binding protein (C/EBP), | 1.2 | other |
| | 131042 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 1.6 | other |
| 40 | 131046 | AA321649 | Hs.22248 | small inducible cytokine subfamily B (Cy | 7.4 | ? |
| | 131060 | AA194422 | Hs.22564 | myosin VI | 5.1 | other |
| | 131070 | N53344 | Hs.22607 | ESTs | 7.1 | other |
| | 131076 | AA749230 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosam | 2.1 | TM |
| | 131099 | AL133353 | Hs.226581 | COX15 (yeast) homolog, cytochrome c oxid | 7.1 | other |
| 45 | 131174 | NM_006540 | Hs.29131 | nuclear receptor coactivator 2 | 1.9 | ? |
| | 131185 | BE280074 | Hs.23960 | cyclin B1 | 5.8 | ? |
| | 131206 | AW138839 | Hs.24210 | ESTs | 2 | other |
| | 131213 | AA885699 | Hs.24332 | CGI-26 protein | 7.1 | TM |
| | 131225 | H62087 | Hs.31659 | thyroid hormone receptor-associated prot | 7.6 | ? |
| 50 | 131231 | N47468 | Hs.59757 | zinc finger protein 281 | 2.9 | other |
| | 131233 | D89053 | Hs.268012 | fatty acid-Coenzyme A ligase, long-chain | 3.5 | other |
| | 131243 | AW383256 | Hs.24752 | spectrin SH3 domain binding protein 1 | 2.8 | ? |
| | 131245 | AL080080 | Hs.24766 | thioredoxin domain-containing | 2.8 | SS, TM |
| | 131247 | AL043100 | Hs.326190 | fatty acid amide hydrolase | 5.6 | other |
| 55 | 131281 | AA251716 | Hs.25227 | ESTs | 5.8 | other |
| | 131283 | X80038 | Hs.339713 | Homo sapiens clone F19374 APO E-C2 gene | 1.3 | other |
| | 131305 | AV656017 | Hs.184325 | CGI-76 protein | 5 | ? |
| | 131320 | AA505691 | Hs.145696 | splicing factor (CC1.3) | 1.8 | TM |
| | 131339 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nibrin) | 2.6 | other |
| 60 | 131375 | AW293165 | Hs.143134 | ESTs | 5.4 | other |
| | 131390 | BE269388 | Hs.182698 | mitochondrial ribosomal protein L20 | 5.3 | other |
| | 131410 | BE259110 | Hs.279836 | HSPC166 protein | 2.2 | other |
| | 131412 | NM_012247 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selen | 2 | ? |
| | 131429 | AL046302 | Hs.26750 | hypothetical protein FLJ21908 | 1.4 | other |
| 65 | 131458 | BE297567 | Hs.27047 | hypothetical protein FLJ20392 | 1.7 | other |
| | 131475 | AA992841 | Hs.27263 | KIAA1458 protein | 2 | other |
| | 131501 | AV661958 | Hs.8207 | GK001 protein | 2.6 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|--------|
| | 131511 | AA732153 | Hs.27865 | Homo sapiens cDNA: FLJ21333 fis, clone C | 2 | other |
| | 131528 | AU076408 | Hs.28309 | UDP-glucose dehydrogenase | 1.6 | TM |
| | 131532 | BE268278 | Hs.28393 | hypothetical protein MGC2592 | 7.4 | other |
| | 131543 | AW966881 | Hs.41639 | programmed cell death 2 | 2.2 | other |
| 5 | 131544 | AL355715 | Hs.28555 | programmed cell death 9 (PDCD9) | 2.1 | other |
| | 131562 | NM_003512 | Hs.28777 | H2A histone family, member L | 1.7 | other |
| | 131564 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 5.2 | other |
| | 131569 | AL389951 | Hs.271623 | nucleoporin 50kD | 5 | other |
| | 131618 | BE393822 | Hs.29645 | Homo sapiens mRNA; cDNA DKFZp761C029 (fr | 1.8 | other |
| 10 | 131622 | R78195 | Hs.29692 | Homo sapiens cDNA FLJ11436 fis, clone HE | 1.3 | other |
| | 131623 | AB037791 | Hs.29716 | hypothetical protein FLJ10980 | 2.2 | TM |
| | 131643 | AW410601 | Hs.30026 | HSPC182 protein | 3 | other |
| | 131653 | AW960597 | Hs.30164 | ESTs | 1.3 | other |
| | 131656 | AI218918 | Hs.30209 | KIAA0854 protein | 2.8 | other |
| 15 | 131669 | X52486 | Hs.3041 | uracil-DNA glycosylase 2 | 2.8 | other |
| | 131692 | BE559681 | Hs.30736 | KIAA0124 protein | 5.6 | ? |
| | 131714 | AA642831 | Hs.31016 | putative DNA binding protein | 2.9 | ? |
| | 131722 | D13757 | Hs.311 | phosphoribosyl pyrophosphate amidotransf | 3.4 | other |
| | 131737 | AK001641 | Hs.31323 | inhibitor of kappa light polypeptide gen | 3.9 | ? |
| 20 | 131763 | AI878932 | Hs.317 | topoisomerase (DNA) I | 3.4 | other |
| | 131772 | AA382590 | Hs.170980 | KIAA0948 protein | 25.5 | other |
| | 131787 | D87077 | Hs.196275 | KIAA0240 protein | 2.4 | SS, |
| | 131793 | AW966127 | Hs.32246 | Homo sapiens cDNA FLJ14656 fis, clone NT | 8 | TM |
| | 131795 | BE501849 | Hs.32317 | high-mobility group 20B | 1.5 | other |
| 25 | 131798 | X86098 | Hs.301449 | adenovirus 5 E1A binding protein | 4.2 | other |
| | 131817 | U20536 | Hs.3280 | caspase 6, apoptosis-related cysteine pr | 4.3 | other |
| | 131824 | U28838 | Hs.32935 | TATA box binding protein (TBP)-associate | 3.5 | other |
| | 131850 | AI251317 | Hs.33184 | ESTs | 5.2 | TM |
| | 131878 | AA083764 | Hs.6101 | hypothetical protein MGC3178 | 5.9 | other |
| 30 | 131885 | BE502341 | Hs.3402 | ESTs | 13.7 | other |
| | 131900 | AA099014 | Hs.231029 | Homo sapiens, clone MGC:15961, mRNA, com | 8.7 | other |
| | 131904 | AF078866 | Hs.284296 | Homo sapiens cDNA: FLJ22993 fis, clone K | 5.5 | other |
| | 131905 | AA179298 | Hs.3439 | stomatin-like 2 | 11.3 | other |
| | 131913 | AW207440 | Hs.185973 | degenerative spermatocyte (homolog Droso | 1.7 | SS, |
| 35 | 131916 | AA025976 | Hs.34569 | ESTs | 5.2 | TM |
| | 131925 | AF151048 | Hs.183180 | anaphase promoting complex subunit 11 (y | 2.8 | other |
| | 131929 | BE541211 | Hs.34804 | Homo sapiens cDNA FLJ11472 fis, clone HE | 5.4 | TM |
| | 131941 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 2.4 | other |
| | 131950 | AA355113 | Hs.35380 | x 001 protein | 1.5 | ? |
| 40 | 131962 | AK000046 | Hs.267448 | hypothetical protein FLJ20039 | 2.3 | other |
| | 131965 | W79283 | Hs.35962 | ESTs | 1.4 | other |
| | 131971 | BE567100 | Hs.154938 | hypothetical protein MDS025 | 3.5 | other |
| | 131977 | U90441 | Hs.3622 | procollagen-proline, 2-oxoglutarate 4-dl | 6.6 | TM |
| | 131985 | AA503020 | Hs.36563 | hypothetical protein FLJ22418 | 2.4 | ? |
| 45 | 131991 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 2.2 | SS, TM |
| | 132019 | H56995 | Hs.37372 | Homo sapiens DNA binding peptide mRNA, p | 3.3 | TM |
| | 132062 | BE266155 | Hs.3832 | clathrin-associated protein AP47 | 1.5 | other |
| | 132084 | NM_002267 | Hs.3886 | karyopherin alpha 3 (importin alpha 4) | 3.7 | other |
| | 132103 | BE171921 | Hs.3991 | ESTs | 1.5 | other |
| 50 | 132105 | AV646076 | Hs.39959 | ESTs | 5.8 | TM |
| | 132116 | AW960474 | Hs.40289 | ESTs | 1.7 | other |
| | 132176 | AA857025 | Hs.8878 | kinesin-like 1 | 3.4 | other |
| | 132180 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 14.7 | SS, |
| | 132194 | R42432 | Hs.4212 | ESTs | 2.2 | other |
| 55 | 132207 | BE206939 | Hs.42287 | E2F transcription factor 6 | 1.5 | other |
| | 132235 | AV658411 | Hs.42656 | KIAA1681 protein | 5.7 | other |
| | 132252 | AI566004 | Hs.141269 | Homo sapiens cDNA: FLJ21550 fis, clone C | 2.1 | other |
| | 132266 | AA301228 | Hs.43299 | hypothetical protein FLJ12890 | 1.5 | other |
| | 132273 | AA227710 | Hs.43658 | DKFZP586L151 protein | 10 | other |
| 60 | 132276 | AA653507 | Hs.285711 | hypothetical protein FLJ13089 | 2 | other |
| | 132288 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glu | 9.2 | other |
| | 132294 | AB023191 | Hs.44131 | KIAA0974 protein | 2 | other |
| | 132298 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 6.6 | SS, |
| | 132299 | AW405882 | Hs.44205 | cortistatin | 3.8 | other |
| 65 | 132325 | N37065 | Hs.44856 | hypothetical protein FLJ12116 | 1.5 | other |
| | 132370 | AW572805 | Hs.46645 | ESTs | 28.3 | ? |
| | 132374 | AF155582 | Hs.46744 | core1 UDP-galactose:N-acetylgalactosamin | 1.9 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 132376 | AI279892 | Hs.46801 | sorting nexin 14 | 2 | ? |
| | 132384 | AA312135 | Hs.46967 | HSPCO34 protein | 6.1 | ? |
| | 132393 | AL135094 | Hs.47334 | hypothetical protein FLJ14495 | 1.7 | other |
| | 132450 | AA100012 | Hs.48827 | hypothetical protein FLJ12085 | 8.6 | other |
| 5 | 132452 | AW973521 | Hs.247324 | mitochondrial ribosomal protein S14 | 5.3 | other |
| | 132456 | AB011084 | Hs.48924 | KIAA0512 gene product; ALEX2 | 1.5 | other |
| | 132470 | AI224456 | Hs.4934 | H.sapiens polyA site DNA | 2 | other |
| | 132484 | X16660 | Hs.119007 | RAB4, member RAS oncogene family | 2.9 | SS, |
| | 132518 | AW885606 | Hs.5064 | ESTs | 2.2 | other |
| 10 | 132530 | AA306105 | Hs.50785 | SEC22, vesicle trafficking protein (S. c | 1.7 | other |
| | 132532 | AA454132 | Hs.5080 | mitochondrial ribosomal protein L16 | 7.2 | TM |
| | 132534 | BE388673 | Hs.5086 | hypothetical protein MGC10433 | 2.2 | SS, |
| | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 2.2 | other |
| | 132574 | AW631437 | Hs.5184 | TH1 drosophila homolog | 14 | ? |
| 15 | 132596 | AK001484 | Hs.5298 | CGI-45 protein | 1.9 | other |
| | 132611 | AA345547 | Hs.53263 | hypothetical protein FLJ13287 | 2.6 | TM |
| | 132612 | H12751 | Hs.5327 | PRO1914 protein | 2 | other |
| | 132616 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 3.1 | other |
| | 132638 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 12.4 | TM |
| 20 | 132668 | AB018319 | Hs.5460 | KIAA0776 protein | 2.8 | SS, |
| | 132692 | AW191962 | Hs.249239 | collagen, type VIII, alpha 2 | 3 | other |
| | 132715 | F11875 | Hs.5534 | Homo sapiens cDNA FLJ12961 fis, clone NT | 1.8 | other |
| | 132718 | NM_004600 | Hs.554 | Sjogren syndrome antigen A2 (60kD, ribon | 3.7 | other |
| | 132724 | AI142265 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 1.8 | TM |
| 25 | 132731 | AI189075 | Hs.301872 | hypothetical protein MGC4840 | 5.9 | other |
| | 132744 | AA010233 | Hs.55921 | glutamyl-prolyl-tRNA synthetase | 8.7 | other |
| | 132760 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 3.6 | other |
| | 132771 | Y10275 | Hs.56407 | phosphoserine phosphatase | 2.8 | TM |
| | 132773 | AA459713 | Hs.295901 | KIAA0493 protein | 14.6 | other |
| 30 | 132784 | AI142133 | Hs.56845 | GDP dissociation inhibitor 2 | 1.7 | other |
| | 132798 | AI026701 | Hs.5716 | KIAA0310 gene product | 2.5 | other |
| | 132807 | U07418 | Hs.57301 | mutL (E. coli) homolog 1 (colon cancer, | 1.4 | other |
| | 132810 | AB007944 | Hs.5737 | KIAA0475 gene product | 4.3 | SS, |
| | 132813 | BE313625 | Hs.57435 | solute carrier family 11 (proton-coupled | 2.8 | other |
| 35 | 132815 | AI815189 | Hs.57475 | sex comb on midleg homolog 1 | 1.6 | other |
| | 132817 | N27852 | Hs.57553 | tousled-like kinase 2 | 1.4 | other |
| | 132821 | AJ251595 | Hs.169610 | CD44 antigen (homing function and Indian | 5.4 | other |
| | 132833 | U78525 | Hs.57783 | eukaryotic translation initiation factor | 6.1 | ? |
| | 132842 | NM_016154 | Hs.279771 | Homo sapiens clone PP1596 unknown mRNA | 7.2 | other |
| 40 | 132844 | F12200 | Hs.5811 | chromosome 21 open reading frame 59 | 2.9 | other |
| | 132851 | U09716 | Hs.287912 | lectin, mannose-binding, 1 | 6.1 | other |
| | 132869 | AW963217 | Hs.203961 | ESTs, Moderately similar to AF116721 89 | 1.8 | other |
| | 132873 | AW007683 | Hs.58598 | KIAA1266 protein | 2.2 | other |
| | 132875 | NM_004850 | Hs.58617 | Rho-associated, coiled-coil containing p | 5 | TM |
| 45 | 132891 | BE267143 | Hs.59271 | U2(RNU2) small nuclear RNA auxiliary fac | 2.7 | ? |
| | 132897 | AW503667 | Hs.59545 | ring finger protein 15 | 5.4 | ? |
| | 132902 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 3.2 | other |
| | 132912 | AW732760 | Hs.167578 | Homo sapiens cDNA FLJ11095 fis, clone PL | 1.4 | other |
| | 132913 | W78714 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 3 | other |
| 50 | 132940 | T79136 | Hs.127243 | Homo sapiens mRNA for KIAA1724 protein, | 10.3 | other |
| | 132942 | AA554458 | Hs.197751 | KIAA0666 protein | 2.1 | SS, |
| | 132952 | AI658580 | Hs.61426 | Homo sapiens mesenchymal stem cell prote | 1.3 | other |
| | 132962 | AA576635 | Hs.6153 | CGI-48 protein | 4.9 | other |
| | 132972 | AA034365 | Hs.288924 | Homo sapiens cDNA FLJ11392 fis, clone HE | 3.6 | TM |
| 55 | 132973 | AA035446 | Hs.323277 | ESTs | 13.1 | other |
| | 132977 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 1.3 | other |
| | 132980 | AA040696 | Hs.62016 | ESTs | 2.3 | ? |
| | 132994 | AA112748 | Hs.279905 | clone HQ0310 PRO0310p1 | 17.1 | other |
| | 133012 | AA847843 | Hs.62711 | Homo sapiens, clone IMAGE:3351295, mRNA | 1.9 | other |
| 60 | 133015 | AJ002744 | Hs.246315 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 5 | TM |
| | 133062 | AW500374 | Hs.64056 | PRO0149 protein | 6.1 | other |
| | 133069 | BE247441 | Hs.6430 | protein with polyglutamine repeat; calci | 1.5 | TM |
| | 133091 | AK001628 | Hs.64691 | KIAA0483 protein | 1.4 | other |
| | 133110 | AA808177 | Hs.65228 | ESTs | 5.6 | other |
| 65 | 133134 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 1.9 | other |
| | 133145 | H94227 | Hs.6592 | Homo sapiens, clone IMAGE:2961368, mRNA, | 4.8 | ? |
| | 133152 | Z11695 | Hs.324473 | mitogen-activated protein kinase 1 | 5 | other |

| | | | | | | | | |
|----|--------|---------------|-----------|--|------|-------|--|--|
| | 133174 | AA431620 | Hs.324178 | hypothetical protein MGC2745 | 2.7 | other | | |
| | 133175 | AW955632 | Hs.66666 | ESTs, Weakly similar to S19560 proline-r | 9.3 | other | | |
| | 133177 | X97795 | Hs.66718 | RAD54 (S.cerevisiae)-like | 4.5 | TM | | |
| | 133208 | AI801777 | Hs.6774 | ESTs | 5.5 | TM | | |
| 5 | 133226 | AW954569 | Hs.296287 | Homo sapiens, Similar to bromodomain-con | 2.7 | other | | |
| | 133228 | AI492924 | Hs.6831 | golgi phosphoprotein 1 | 1.7 | ? | | |
| | 133254 | AI567421 | Hs.273330 | Homo sapiens, clone IMAGE:3544662, mRNA, | 1.3 | other | | |
| | 133268 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKH | 12.2 | other | | |
| | 133291 | BE297855 | Hs.69855 | NRAS-related gene | 1.2 | other | | |
| 10 | 133314 | AA102670 | Hs.70725 | gamma-aminobutyric acid (GABA) A recepto | 1.7 | TM | | |
| | 133321 | T79526 | Hs.179516 | integral type I protein | 11.1 | ? | | |
| | 133327 | AL390127 | Hs.7104 | Kruppel-like factor 13 | 2.9 | other | | |
| | 133347 | BE257758 | Hs.71475 | acid cluster protein 33 | 2.5 | ? | | |
| | 133360 | AI016521 | Hs.71816 | v-akt murine thymoma viral oncogene homo | 1.5 | other | | |
| 15 | 133366 | AA292811 | Hs.72050 | non-metastatic cells 5, protein expresse | 2.1 | other | | |
| | 133367 | AF231919 | Hs.18759 | KIAA0539 gene product | 1.3 | other | | |
| | 133370 | AF245505 | Hs.72157 | DKFZP564I1922 protein | 2.2 | other | | |
| | 133390 | AI950382 | Hs.72660 | phosphatidylserine receptor | 5.7 | TM | | |
| | 133391 | AW103364 | Hs.727 | inhibin, beta A (activin A, activin AB a | 25.5 | other | | |
| 20 | 133394 | AA305127 | Hs.237225 | hypothetical protein HT023 | 3.3 | other | | |
| | 133437 | AL031591 | Hs.7370 | phosphatidylinositol transfer protein, b | 1.6 | other | | |
| | 133452 | NM_002759 | Hs.274382 | protein kinase, interferon-inducible dou | 4.1 | other | | |
| | 133453 | AI659306 | Hs.73826 | protein tyrosine phosphatase, non-recept | 1.5 | other | | |
| | 133500 | AW964804 | Hs.74280 | hypothetical protein FLJ22237 | 6.3 | TM | | |
| 25 | 133529 | W45623 | Hs.74571 | ADP-ribosylation factor 1 | 4 | ? | | |
| | 133543 | AU077073 | Hs.108327 | damage-specific DNA binding protein 1 (1 | 1.8 | ? | | |
| | 133578 | AU077050 | Hs.75066 | translin | 1.5 | other | | |
| | 133579 | X75346 | Hs.75074 | mitogen-activated protein kinase-activat | 3.5 | TM | | |
| | 133582 | BE391579 | Hs.75087 | Fas-activated serine/threonine kinase | 6.8 | TM | | |
| 30 | 133594 | AW160781 | Hs.172589 | nuclear phosphoprotein similar to S. cer | 2.6 | TM | | |
| | 133595 | AA393273 | Hs.75133 | transcription factor 6-like 1 (mitochond | 1.4 | other | | |
| | 133599 | NM_002885 | Hs.75151 | RAP1, GTPase activating protein 1 | 8.1 | other | | |
| | 133621 | NM_004893 | Hs.75258 | H2A histone family, member Y | 13.5 | other | | |
| | 133627 | NM_002047 | Hs.75280 | glycyl-tRNA synthetase | 2.2 | other | | |
| 35 | 133631 | NM_000401 | Hs.75334 | exostoses (multiple) 2 | 1.8 | other | | |
| | 133649 | U25849 | Hs.75393 | acid phosphatase 1, soluble | 2 | other | | |
| | 133690 | AV661185 | Hs.75574 | mitochondrial ribosomal protein L19 | 2.8 | other | | |
| | 133720 | L27841 | Hs.75737 | pericentriolar material 1 | 6.8 | other | | |
| | 133722 | AW969976 | Hs.279009 | matrix Gla protein | 2.5 | other | | |
| 40 | 133751 | AW402048.comp | Hs.334787 | Homo sapiens, Similar to likely ortholog | 3.1 | TM | | |
| | 133757 | T52946 | Hs.196209 | RAE1 (RNA export 1, S.pombe) homolog | 1.4 | ? | | |
| | 133760 | BE271766 | Hs.181357 | laminin receptor 1 (67kD, ribosomal prot | 5.4 | other | | |
| | 133765 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 5 | other | | |
| | 133780 | AA557660 | Hs.76152 | decorin | 3.8 | other | | |
| 45 | 133797 | AL133921 | Hs.76272 | retinoblastoma-binding protein 2 | 3.1 | ? | | |
| | 133822 | D50525 | Hs.699 | peptidylprolyl isomerase B (cyclophilin | 9.7 | ? | | |
| | 133842 | AW797468 | Hs.285013 | putative human HLA class II associated p | 2.4 | other | | |
| | 133845 | AA147026 | Hs.76704 | ESTs | 2.5 | other | | |
| | 133865 | AB011155 | Hs.170290 | discs, large (Drosophila) homolog 5 | 5 | other | | |
| 50 | 133867 | AW340125 | Hs.76989 | KIAA0097 gene product | 2.5 | ? | | |
| | 133868 | AB012193 | Hs.183874 | cullin 4A | 2.1 | other | | |
| | 133922 | U30825 | Hs.77608 | splicing factor, arginine/serine-rich 9 | 2.8 | TM | | |
| | 133924 | D86326 | Hs.325948 | vesicle docking protein p115 | 1.8 | SS, | | |
| 55 | 133929 | NM_006306 | Hs.211602 | SMC1 (structural maintenance of chromoso | 2 | ? | | |
| | 133936 | L17128 | Hs.77719 | gamma-glutamyl carboxylase | 2.6 | other | | |
| | 133941 | BE244332 | Hs.77770 | adaptor-related protein complex 3, mu 2 | 2.9 | other | | |
| | 133959 | X81789 | Hs.77897 | splicing factor 3a, subunit 3, 60kD | 10.4 | other | | |
| | 133976 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 1.9 | other | | |
| | 133989 | AL040328 | Hs.78202 | SWI/SNF related, matrix associated, acti | 2.6 | SS, | | |
| 60 | 133997 | AI824113 | Hs.78281 | regulator of G-protein signalling 12 | 13 | other | | |
| | 134010 | AB016092 | Hs.197114 | RNA binding protein; AT-rich element bin | 8.8 | other | | |
| | 134015 | D31764 | Hs.278569 | sorting nexin 17 | 1.5 | SS, | | |
| | 134070 | NM_003590 | Hs.78946 | cullin 3 | 8.3 | other | | |
| | 134110 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | 2.7 | other | | |
| 65 | 134129 | NM_014742 | Hs.79305 | KIAA0255 gene product | 4.2 | other | | |
| | 134134 | H86504 | Hs.173328 | protein phosphatase 2, regulatory subuni | 1.7 | other | | |
| | 134200 | BE559598 | Hs.197803 | KIAA0160 protein | 2.6 | other | | |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 134206 | AF107463 | Hs.79968 | splicing factor 30, survival of motor ne | 1.3 | other |
| | 134219 | NM_000402 | Hs.80206 | glucose-6-phosphate dehydrogenase | 1.9 | other |
| | 134234 | BE300078 | Hs.80449 | Homo sapiens, clone IMAGE:3535294, mRNA, | 10.3 | SS, |
| | 134275 | AI878910 | Hs.3688 | displatin resistance-associated overexpr | 2.5 | other |
| 5 | 134292 | AI906291 | Hs.81234 | immunoglobulin superfamily, member 3 | 1.3 | TM |
| | 134301 | AW502505 | Hs.81360 | Homo sapiens cDNA: FLJ21927 fis, clone H | 1.6 | TM |
| | 134305 | U61397 | Hs.81424 | ubiquitin-like 1 (sentrin) | 2.1 | TM |
| | 134324 | AB029023 | Hs.179946 | KIAA1100 protein | 5.3 | ? |
| | 134326 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 2.5 | TM |
| 10 | 134329 | N92036 | Hs.81848 | RAD21 (S. pombe) homolog | 3.9 | ? |
| | 134337 | NM_004922 | Hs.81964 | SEC24 (S. cerevisiae) related gene famil | 2.4 | TM |
| | 134348 | AW291946 | Hs.82065 | interleukin 6 signal transducer (gp130, | 6.8 | TM |
| | 134367 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 2.3 | TM |
| | 134376 | X06560 | Hs.82396 | 2',5'-oligoadenylate synthetase 1 (40-46 | 5.5 | other |
| 15 | 134379 | AW362124 | Hs.323193 | hypothetical protein MGC3222 | 5.9 | TM |
| | 134384 | AI589941 | Hs.8254 | Homo sapiens, Similar to tumor different | 2.2 | other |
| | 134391 | AA417383 | Hs.82582 | integrin, beta-like 1 (with EGF-like rep | 2.1 | other |
| | 134395 | AA456539 | Hs.8262 | lysosomal | 2.3 | other |
| | 134405 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 72.9 | other |
| 20 | 134411 | BE272095 | Hs.167791 | reticulocalbin 1, EF-hand calcium bindin | 4.4 | other |
| | 134415 | AI750762 | Hs.82911 | protein tyrosine phosphatase type IVA, m | 2.3 | other |
| | 134421 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 6.8 | ? |
| | 134424 | Z44190 | Hs.83023 | peroxisomal biogenesis factor 11B | 2.4 | other |
| | 134446 | AA112036 | Hs.83419 | KIAA0252 protein | 2.9 | other |
| 25 | 134447 | M58603 | Hs.83428 | nuclear factor of kappa light polypeptid | 6.7 | other |
| | 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 2.4 | other |
| | 134480 | NM_005000 | Hs.83916 | Empirically selected from AFFX single pr | 6.3 | ? |
| | 134485 | X82153 | Hs.83942 | cathepsin K (pseudosostosis) | 1.9 | other |
| | 134498 | AW246273 | Hs.84131 | threonyl-tRNA synthetase | 1.8 | other |
| 30 | 134513 | AA425473 | Hs.84429 | KIAA0971 protein | 1.4 | other |
| | 134516 | AK001571 | Hs.273357 | hypothetical protein FLJ10709 | 1.4 | other |
| | 134520 | BE091005 | Hs.74861 | activated RNA polymerase II transcriptio | 5.6 | other |
| | 134529 | AW411479 | Hs.848 | FK506-binding protein 4 (59kD) | 2.8 | ? |
| | 134577 | BE244323 | Hs.85951 | exportin, tRNA (nuclear export receptor | 1.7 | other |
| 35 | 134582 | AA927177 | Hs.86041 | CGG triplet repeat binding protein 1 | 1.7 | TM |
| | 134612 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 2.1 | other |
| | 134624 | AF035119 | Hs.8700 | deleted in liver cancer 1 | 1.3 | other |
| | 134632 | X78520 | Hs.174139 | chloride channel 3 | 2.1 | ? |
| | 134654 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 2.3 | other |
| 40 | 134666 | BE391929 | Hs.8752 | transmembrane protein 4 | 4 | other |
| | 134687 | U62317 | Hs.88251 | arylsulfatase A | 6.2 | other |
| | 134692 | NM_003474 | Hs.8850 | a disintegrin and metalloproteinase doma | 2 | other |
| | 134705 | BE161887 | Hs.88799 | anaphase-promoting complex subunit 10 | 1.3 | SS, |
| | 134714 | Y14768 | Hs.890 | lysosomal | 7.2 | ? |
| 45 | 134719 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 3.2 | other |
| | 134722 | AF129536 | Hs.284226 | F-box only protein 6 | 2.5 | other |
| | 134746 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell | 5 | other |
| | 134751 | AW630803 | Hs.89497 | lamin B1 | 6.1 | other |
| | 134790 | BE002798 | Hs.287850 | Integral membrane protein 1 | 5.6 | TM |
| 50 | 134834 | AW451370 | Hs.8991 | adaptor-related protein complex 1, gamma | 5.3 | other |
| | 134850 | AI701162 | Hs.90207 | hypothetical protein MGC11138 | 9.1 | other |
| | 134853 | BE268326 | Hs.90280 | 5-aminimidazole-4-carboxamide ribonucle | 2.4 | other |
| | 134880 | AI879195 | Hs.90606 | 15 kDa selenoprotein | 2.7 | other |
| | 134925 | AW885909 | Hs.6975 | PRO1073 protein | 1.5 | other |
| 55 | 134955 | AW401361 | Hs.91773 | protein phosphatase 2 (formerly 2A), cat | 4.9 | other |
| | 134971 | AI097346 | Hs.286049 | phosphoserine aminotransferase | 2 | other |
| | 134975 | R50333 | Hs.92186 | Leman coiled-coil protein | 2.6 | TM |
| | 135011 | AB037835 | Hs.92991 | KIAA1414 protein | 1.4 | ? |
| | 135022 | NM_000408 | Hs.93201 | glycerol-3-phosphate dehydrogenase 2 (ml | 1.6 | ? |
| 60 | 135032 | AW301984 | Hs.173685 | hypothetical protein FLJ12619 | 1.4 | other |
| | 135077 | AW503733 | Hs.9414 | KIAA1488 protein | 1.8 | other |
| | 135083 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase s | 2.5 | other |
| | 135095 | AF027219 | Hs.9443 | zinc finger protein 202 | 1.5 | TM |
| | 135096 | AA081258 | Hs.132390 | zinc finger protein 36 (KOX 18) | 2.1 | other |
| 65 | 135153 | AI093155 | Hs.95420 | JM27 protein | 4.4 | ? |
| | 135181 | BE250865 | Hs.279529 | px19-like protein | 14.9 | ? |
| | 135199 | AA477514 | Hs.96247 | translin-associated factor X | 1.3 | other |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 135207 | N26427 | Hs.9634 | ESTs, Highly similar to C10_HUMAN PUTAT | 1.7 | other |
| | 135214 | T78802 | Hs.96560 | hypothetical protein FLJ11656 | 6.2 | other |
| | 135243 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 2.8 | TM |
| | 135245 | AI028767 | Hs.262603 | ESTs | 12.2 | TM |
| 5 | 135257 | AW291023 | Hs.97255 | ESTs, Weakly similar to A46010 X-linked | 7.7 | TM |
| | 135263 | AI088775 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 1.8 | other |
| | 135274 | AA448460 | Hs.112017 | GE36 gene | 4.2 | SS, |
| | 135294 | AA150320 | Hs.9800 | protein kinase Njmu-R1 | 1.2 | other |
| | 135295 | AI090838 | Hs.98006 | ESTs | 4.9 | other |
| 10 | 135307 | AI743770 | Hs.98368 | ESTs, Weakly similar to KIAA0822 protein | 5.9 | ? |
| | 135321 | AI652069 | Hs.98614 | ribosome binding protein 1 (dog 180kD ho | 12.3 | TM |
| | 135354 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 5.8 | ? |
| | 135361 | AA373452 | Hs.167700 | Homo sapiens cDNA FLJ10174 fis, clone HE | 8.1 | other |
| | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 1.9 | other |
| 15 | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 13.9 | TM |
| | 302256 | AA857131 | Hs.171595 | HIV TAT specific factor 1 | 1.6 | other |
| | 302276 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 5.3 | other |
| | 303135 | AW592789 | Hs.279474 | HSPC070 protein | 2.2 | TM |
| | 303686 | AK000714 | Hs.109441 | MSTP033 protein | 1.4 | SS, |
| 20 | 310085 | R43191 | Hs.101248 | Homo sapiens clone IMAGE:32553, mRNA seq | 5.2 | other |
| | 315518 | AA808229 | Hs.167771 | ESTs | 2.3 | ? |
| | 317781 | NM_007057 | Hs.42650 | ZW10 interactor | 2.9 | ? |
| | 320836 | AI268997 | Hs.197289 | rab3 GTPase-activating protein, non-cata | 2 | other |
| | 321114 | AA902256 | Hs.78979 | Golgi apparatus protein 1 | 5.6 | SS, |
| 25 | 322221 | N24236 | Hs.179662 | nucleosome assembly protein 1-like 1 | 1.4 | ? |
| | 322474 | AF118083 | Hs.29494 | PRO1912 protein | 1.3 | other |
| | 322556 | BE041451 | Hs.177507 | hypothetical protein | 2.9 | SS, |
| | 323541 | AF292100 | Hs.104613 | RP42 homolog | 1.6 | other |
| | 407827 | BE278431 | Hs.40323 | BUB3 (budding uninhibited by benzimidazo | 1.8 | other |
| 30 | 408196 | AL034548 | Hs.43627 | SRY (sex determining region Y)-box 22 | 1.6 | other |
| | 408813 | AI580090 | Hs.48295 | RNA helicase family | 6.2 | other |
| | 409176 | R73727 | Hs.101617 | ESTs, Weakly similar to T32527 hypotheti | 5.7 | other |
| | 409487 | H19886 | | gb:yn57a05.r1 Soares adult brain N2b5HB5 | 2.7 | other |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 2.6 | ? |
| 35 | 414108 | AI267592 | Hs.75761 | SFRS protein kinase 1 | 2.4 | TM |
| | 414846 | AW304454 | Hs.77495 | UBX domain-containing 1 | 2.4 | other |
| | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone | 2.3 | other |
| | 416980 | AA381133 | Hs.80684 | high-mobility group (nonhistone chromoso | 4.2 | TM |
| | 417378 | R57256 | Hs.82037 | TATA box binding protein (TBP)-associate | 23.6 | other |
| 40 | 418283 | S79895 | Hs.83942 | cathepsin K (pseudosclerosis) | 5.8 | other |
| | 418467 | NM_006910 | Hs.85273 | retinoblastoma-binding protein 6 | 1.3 | other |
| | 420269 | U72937 | Hs.96264 | alpha thalassemia/mental retardation syn | 1.6 | ? |
| | 420802 | U22376 | Hs.1334 | v-myb avian myeloblastosis viral oncogen | 2.3 | ? |
| | 421225 | AA463798 | Hs.102696 | MCT-1 protein | 1.6 | ? |
| 45 | 421642 | AF172066 | Hs.106346 | retinoic acid repressible protein | 3.5 | other |
| | 421828 | AW891965 | Hs.279789 | histone deacetylase 3 | 5 | other |
| | 421983 | AI252640 | Hs.110364 | peptidylprolyl isomerase C (cyclophilin | 3.1 | TM |
| | 422052 | AA302744 | Hs.104518 | ESTs | 1.9 | TM |
| | 422055 | NM_014320 | Hs.111029 | putative heme-binding protein | 2.4 | other |
| 50 | 423750 | AF165883 | Hs.298229 | prefoldin 2 | 4.2 | ? |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 (PEG10; KIAA105 | 7.1 | ? |
| | 425182 | AF041259 | Hs.155040 | zinc finger protein 217 | 2.3 | other |
| | 425284 | AF155568 | Hs.155489 | NS1-associated protein 1 | 3.5 | other |
| | 426372 | BE304680 | Hs.169531 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 1.9 | ? |
| 55 | 428049 | AW183765 | Hs.182238 | GW128 protein | 7.6 | ? |
| | 428477 | AW500533 | Hs.11482 | splicing factor, arginine/serine-rich 11 | 1.7 | other |
| | 437562 | AB001636 | Hs.5683 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.4 | other |
| | 438449 | AK001333 | Hs.6216 | Homo sapiens hepatocellular carcinoma-as | 3.8 | other |
| | 441560 | F13386 | Hs.7888 | Homo sapiens clone 23736 mRNA sequence | 5.6 | other |
| 60 | 445580 | AF167572 | Hs.12912 | skb1 (S. pombe) homolog | 2 | TM |
| | 446999 | AA151520 | Hs.334822 | hypothetical protein MGC4485 | 7.6 | other |
| | 447111 | AI017574 | Hs.17409 | cysteine-rich protein 1 (intestinal) | 2.2 | other |
| | 447778 | BE620592 | Hs.71190 | ESTs, Weakly similar to S16506 hypotheti | 2.9 | other |
| | 448873 | NM_003677 | Hs.22393 | density-regulated protein | 1.8 | other |
| 65 | 449687 | W68520 | Hs.331328 | intermediate filament protein syncollin | 5.9 | other |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.7 | other |
| | 450703 | AA011202 | Hs.184771 | nuclear factor I/C (CCAAT-binding transc | 1.4 | other |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 452461 | N78223 | Hs.108106 | transcription factor | 4.8 | ? |
| | 452511 | BE408178 | Hs.285165 | Homo sapiens cDNA FLJ20845 fis, clone AD | 2.9 | other |
| | 453157 | AF077036 | Hs.31989 | DKFZP586G1722 protein | 12.1 | SS,TM |
| | 453658 | BE541906 | Hs.87819 | Homo sapiens, clone MGC:2492, mRNA, comp | 4.8 | other |
| 5 | 100685 | AA328229 | Hs.184582 | ribosomal protein L24 | 1.8 | TM |
| | 100690 | AA383256 | Hs.1657 | estrogen receptor 1 | 1.6 | other |
| | 100833 | AF135168 | Hs.108802 | N-ethylmaleimide-sensitive factor | 1.3 | other |
| | 100850 | AA836472 | Hs.297939 | cathepsin B | 1.7 | ? |
| | 101161 | NM_006262 | Hs.37044 | peripherin | 16.9 | other |
| 10 | 102481 | U50360 | | gbt:Human calcium, calmodulin-dependent p | 3.2 | other |
| | 102831 | AA262170 | Hs.80917 | adaptor-related protein complex 3, sigma | 2 | ? |
| | 103549 | BE270465 | Hs.78793 | protein kinase C, zeta | 8 | other |
| | 103749 | AL135301 | Hs.8768 | hypothetical protein FLJ10849 | 1.8 | other |
| | 104331 | AB040450 | Hs.279862 | cdk inhibitor p21 binding protein | 2 | ? |
| 15 | 104532 | AI498763 | Hs.203013 | hypothetical protein FLJ12748 | 2.1 | other |
| | 104563 | AL117403 | Hs.306189 | DKFZP434F1735 protein | 1.2 | other |
| | 105032 | AA127818 | | gb:zl12a02.s1 Soares_pregnant_uterus_NbH | 7 | ? |
| | 105039 | AA907305 | Hs.36475 | ESTs | 2.6 | ? |
| | 106531 | AA454036 | Hs.8832 | ESTs | 1.6 | other |
| 20 | 106977 | AL043152 | Hs.50421 | KIAA0203 gene product | 4.9 | other |
| | 107298 | N95657 | Hs.6820 | ESTs, Moderately similar to YOJ1_CAEEL H | 2.5 | TM |
| | 108717 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 1.3 | other |
| | 110018 | AW579842 | Hs.104557 | hypothetical protein FLJ10697 | 5.3 | TM |
| | 110330 | AI288666 | Hs.16621 | DKFZP434I116 protein | 6.3 | other |
| 25 | 111391 | NM_003896 | Hs.225939 | sialyltransferase 9 (CMP-NeuAc)lactosylc | 5.1 | SS, |
| | 111392 | W46342 | Hs.325081 | Homo sapiens, clone IMAGE:3659680, mRNA, | 8.4 | other |
| | 113554 | AW503990 | Hs.142442 | HP1-BP74 | 3.7 | TM |
| | 113722 | AV653556 | Hs.184411 | albumin | 1.3 | other |
| | 115008 | AK001827 | Hs.87889 | helicase-moi | 2 | other |
| 30 | 115062 | AA253314 | Hs.154103 | LIM protein (similar to rat protein kina | 1.5 | other |
| | 115121 | AI634549 | Hs.88155 | ESTs | 2.8 | other |
| | 117881 | AF161470 | Hs.260622 | butyrate-induced transcript 1 | 5.8 | TM |
| | 119075 | M10905 | Hs.287820 | fibronectin 1 | 5.7 | other |
| | 119615 | AL034423 | Hs.75875 | ubiquitin-conjugating enzyme E2 variant | 1.3 | other |
| 35 | 120253 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 38.9 | other |
| | 125006 | BE065136 | Hs.145696 | splicing factor (CC1.3) | 2.9 | ? |
| | 127609 | X80031 | Hs.530 | collagen, type IV, alpha 3 (Goodpasture | 1.8 | other |
| | 128868 | AA419008 | Hs.106730 | chromosome 22 open reading frame 3 | 3 | other |
| | 128891 | F34856 | Hs.292457 | Homo sapiens, clone MGC:16362, mRNA, com | 13.3 | other |
| 40 | 128959 | AI580127 | Hs.107381 | hypothetical protein FLJ11200 | 10.9 | other |
| | 129209 | R62676 | Hs.17820 | Rho-associated, coiled-coil containing p | 2.4 | other |
| | 129449 | AI096988 | Hs.111554 | ADP-ribosylation factor-like 7 | 8.2 | TM |
| | 129453 | AW974265 | Hs.111632 | Lsm3 protein | 3.3 | ? |
| | 129629 | AK000398 | Hs.11747 | hypothetical protein FLJ20391 | 3.9 | other |
| 45 | 129917 | M30773 | Hs.278540 | protein phosphatase 3 (formerly 2B), reg | 5.3 | TM |
| | 129922 | AF042379 | Hs.13386 | gamma-tubulin complex protein 2 | 4.6 | other |
| | 129989 | AB015856 | Hs.247433 | activating transcription factor 6 | 4 | SS, |
| | 130182 | BE267033 | Hs.192853 | ubiquitin-conjugating enzyme E2G 2 (homo | 4.6 | other |
| | 130365 | W56119 | Hs.155103 | eukaryotic translation initiation factor | 11 | other |
| 50 | 130471 | AL121438 | Hs.183706 | adducin 1 (alpha) | 2.7 | other |
| | 130542 | U64675 | Hs.179825 | RAN binding protein 2-like 1 | 7.9 | other |
| | 130586 | AB007891 | Hs.16349 | KIAA0431 protein | 5.6 | TM |
| | 130768 | AF258627 | Hs.211562 | ATP-binding cassette, sub-family A (ABC1 | 5.2 | other |
| | 130992 | BE398091 | Hs.74316 | desmoplakin (DPI, DPII) | 1.8 | TM |
| 55 | 131047 | H23230 | Hs.22481 | ESTs, Moderately similar to A46010 X-fin | 1.7 | ? |
| | 131135 | NM_016569 | Hs.267182 | TBX3-iso protein | 3.3 | TM |
| | 131339 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nibrin) | 2.6 | other |
| | 131760 | X76732 | Hs.3164 | nucleobindin 2 | 2.9 | TM |
| | 131774 | BE267158 | Hs.169474 | DKFZP586J0119 protein | 5.6 | other |
| 60 | 131853 | AI681917 | Hs.3321 | ESTs, Highly similar to IRX1_HUMAN IROQU | 1.3 | other |
| | 131881 | AW361018 | Hs.3383 | upstream regulatory element binding prot | 3.2 | TM |
| | 131887 | W17064 | Hs.332848 | SWI/SNF related, matrix associated, acti | 3.2 | other |
| | 132031 | AF193844 | Hs.3758 | COP9 complex subunit 7a | 5.9 | ? |
| | 132192 | AA206153 | Hs.4209 | mitochondrial ribosomal protein L37 | 2.2 | TM |
| 65 | 132203 | NM_004782 | Hs.194714 | synaptosomal-associated protein, 29kD | 7.9 | ? |
| | 132240 | AB018324 | Hs.42676 | KIAA0781 protein | 4.3 | other |
| | 132348 | AW067708 | Hs.170311 | heterogeneous nuclear ribonucleoprotein | 12.5 | other |

| | | | | | | | |
|----|----------|-----------|-----------|---|------|-------|--|
| | 132528 | T78736 | Hs.50758 | SMC4 (structural maintenance of chromoso | 7.4 | ? | |
| | 132571 | AW674699 | Hs.5169 | suppressor of G2 allele of SKP1, S. cere | 6.9 | other | |
| | 132726 | N52298 | Hs.55608 | hypothetical protein MGC955 | 14.3 | ? | |
| | 132863 | BE268048 | Hs.236494 | RAB10, member RAS oncogene family | 10.3 | other | |
| 5 | 133016 | AI439688 | Hs.6289 | hypothetical protein FLJ20886 | 4.4 | other | |
| | 133053 | AI065016 | Hs.6390 | Homo sapiens clone FLB3344 PRO0845 mRNA, | 1.8 | SS,TM | |
| | 133197 | AI275243 | Hs.180201 | hypothetical protein FLJ20671 | 1.8 | other | |
| | 133240 | AK001489 | Hs.242894 | ADP-ribosylation factor-like 1 | 1.8 | other | |
| | 133266 | AI160873 | Hs.69233 | zinc finger protein | 16.1 | other | |
| 10 | 133285 | M76477 | Hs.289082 | GM2 ganglioside activator protein | 10.4 | SS, | |
| | 133383 | BE313555 | Hs.7252 | KIAA1224 protein | 1.5 | ? | |
| | 133540 | AL037159 | Hs.74619 | proteasome (prosome, macropain) 26S subu | 1.7 | other | |
| | 133784 | BE622743 | Hs.301064 | arfaplin 1 | 12.1 | other | |
| | 133791 | M34338 | Hs.76244 | spermidine synthase | 9.7 | other | |
| 15 | 133850 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 4.2 | SS, | |
| | 133859 | U66782 | Hs.178761 | 26S proteasome-associated pad1 homolog | 2.2 | other | |
| | 133881 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 9.1 | other | |
| | 134208 | NM_000288 | Hs.79993 | peroxisomal biogenesis factor 7 | 3.2 | other | |
| | 134403 | AA334551 | Hs.82767 | sperm specific antigen 2 | 1.4 | other | |
| 20 | 134724 | AF045239 | Hs.321576 | ring finger protein 22 | 1.4 | other | |
| | 134806 | AD001528 | Hs.89718 | spermine synthase | 2.6 | other | |
| | 134859 | D26488 | Hs.90315 | KIAA0007 protein | 13.3 | other | |
| | 135193 | X95525 | Hs.96103 | TATA box binding protein (TBP)-associate | 3.1 | other | |
| | AA243007 | | | ESTs | 1.6 | ? | |
| 25 | T70541 | | | ESTs | 2.5 | SS, | |
| | X57766 | | | Human stromelysin-3 mRNA | 4.5 | other | |
| | S66431 | | | Homo sapiens clone 23592 mRNA sequence | 3.1 | other | |
| | AA453483 | | | ESTs | 4.6 | TM | |
| | R63925 | | | ESTs | 1.4 | other | |
| 30 | AA173417 | | | ESTs | 1.9 | other | |
| | AA280588 | | | ESTs | 2.2 | other | |
| | AA504223 | | | ESTs Highly similar to CHROMOSOME | 2.4 | other | |
| | AA609996 | | | ESTs Highly similar to Surf-4 protein [M.musculus] | 5.5 | ? | |
| | F02907 | | | ESTs | 2.3 | TM | |
| 35 | AA480103 | | | ESTs Weakly similar to !!!! ALU SUBFAMILY J | 2.8 | TM | |
| | AA024664 | | | Human NADH:ubiquinone oxidoreductase subunit | 6.2 | other | |
| | AA251776 | | | ESTs | 2.3 | other | |
| | AA399047 | | | ESTs | 2.4 | other | |
| | N34059 | | | EST - RC_N34059 | 3.3 | other | |
| 40 | U95367 | | | Human GABA-A receptor pi subunit mRNA complete cds | 1.7 | TM | |
| | AA490899 | | | ESTs | 3.3 | other | |
| | T54762 | | | ESTs | 2.9 | ? | |
| | Z41963 | | | Homo sapiens HP protein (HP) mRNA complete cds | 1.3 | ? | |
| | AA521186 | | | ESTs | 1.6 | TM | |
| 45 | AA400195 | | | ESTs | 1.3 | other | |
| | AA045083 | | | VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE | 2.5 | other | |
| | AA099589 | | | Homo sapiens mRNA for GDP dissociation inhibitor beta | 1.6 | TM | |
| | W85712 | | | ESTs Weakly similar to PROCOLLAGEN ALPHA 2(IV | 2.6 | TM | |
| | W45728 | | | ESTs Highly similar to HETEROGENEOUS | 3.7 | other | |
| 50 | U61232 | | | Human tubulin-folding cofactor E mRNA complete cds | 2.1 | other | |
| | AA425154 | | | ESTs | 5.3 | other | |
| | T39176 | | | ESTs Weakly similar to ZK1058.4 [C.elegans] | 2.6 | SS,TM | |
| | AA496000 | | | ESTs | 1.9 | SS, | |
| | W38150 | | | EST - RC_W38150 | 1.7 | ? | |
| 55 | T96595 | | | EST - RC_T96595 | 1.8 | TM | |
| | AA227463 | | | ESTs Weakly similar to No definition line found [C.elegans] | 1.9 | ? | |
| | R46025 | | | ESTs | 2.8 | SS, | |
| | AA233177 | | | ESTs | 2 | other | |
| | AA338760 | | | ESTs | 1.3 | ? | |
| 60 | AA412106 | | | ESTs | 6.2 | other | |
| | L47276 | | | EST - L47276 | 3.4 | other | |
| | D82307 | | | ESTs Weakly similar to TH1 protein [D.melanogaster] | 11.4 | other | |
| | AA293568 | | | ESTs | 1.5 | other | |
| | R37778 | | | ESTs | 2.4 | other | |
| 65 | AA250843 | | | Interferon regulatory factor 5 | 14.6 | ? | |
| | W49521 | | | Human prolyl 4-hydroxylase alpha (II) subunit | 6.5 | ? | |
| | D80000 | | | Human mRNA for KIAA0178 gene partial cds | 2 | other | |

| | | | | |
|----|----------|--|------|--------|
| | R99978 | ESTs Weakly similar to line-1 protein ORF2 [H.sapiens] | 6.1 | ? |
| | AA195036 | Human Ro/SSA ribonucleoprotein homolog (RoRet) | 5.3 | ? |
| | Z38501 | ESTs Weakly similar to PROBABLE E5 | 1.4 | other |
| 5 | U37547 | Human IAP homolog B (MIHB) mRNA complete cds | 3.2 | other |
| | AA479961 | ESTs | 1.7 | other |
| | X57579 | Inhibin beta A (activin A activin AB alpha polypeptide) | 15.8 | ? |
| | AA449071 | ESTs | 1.3 | TM |
| | N51855 | ESTs Moderately similar to NAD(+) ADP- | 1.3 | other |
| 10 | AA421213 | ESTs Weakly similar to F28F8.3 [C.elegans] | 3.2 | other |
| | AA355201 | ESTs | 1.2 | SS, TM |
| | N78717 | H.sapiens mRNA for translin | 1.5 | ? |
| | N73808 | ESTs | 5 | ? |
| | U86782 | Human 26S proteasome-associated pad1 | 2.2 | other |
| 15 | AA234817 | ESTs | 1.3 | other |
| | D13666 | Homo sapiens mRNA for osteoblast specific | 7.5 | SS, |
| | AA236177 | ESTs | 7.1 | ? |
| | U50648 | Protein kinase interferon-inducible double | 4.1 | ? |
| | M28211 | Homo sapiens GTP-binding protein (RAB4) | 2.9 | other |
| 20 | AA446949 | ESTs | 2.2 | other |
| | W03007 | ESTs | 1.2 | other |
| | W61011 | ESTs | 1.2 | other |
| | W87544 | ESTs | 1.2 | other |
| | X02751 | Neuroblastoma RAS viral (v-ras) oncogene homolog | 1.2 | ? |
| 25 | Z14077 | YY1 transcription factor | 1.2 | other |
| | Z38839 | ESTs | 1.2 | ? |
| | AA410894 | ESTs | 1.7 | other |
| | AA504499 | ESTs Highly similar to probable chloride channel 3 [H.sap] | 1.3 | other |

TABLE 7A

Table 7 A shows the accession numbers for those pkeys lacking unigeneID's for Table 7.

For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|------------------|------------------------|
| 102481 | 31281_-28 | U50360 |
| 105032 | genbank_AA127818 | AA127818 |
| 409487 | 1134778_1 | H19886 AW402806 T10231 |

TABLE 8: Figure 8 from BRCA 001-1 US

5 **Table 8** shows genes upregulated in tumor tissue compared to normal breast tissue. Specifically, one column shows the ratio of expression of the indicated gene in breast tumor tissue compared to other body tissues, and another column shows the ratio of expression of the indicated gene in breast tumor tissue compared to normal breast tissue.

10

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 15 R1: Ratio of tumor to normal body tissue
 R2: Ratio of tumor to normal breast tissue

| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|----|--------|-----------|-----------|---|------|------|
| 20 | 100075 | AF152333 | Hs.284160 | protocadherin gamma subfamily B, 4 | 1 | 3.8 |
| | 100229 | AV652249 | Hs.180107 | polymerase (DNA directed), beta | 1.7 | 5.3 |
| | 100262 | D38500 | Hs.278468 | postmeiotic segregation increased 2-like | 0.8 | 4.8 |
| | 100271 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 3.2 | 2.3 |
| | 100355 | AI907114 | Hs.71465 | squalene epoxidase | 3.3 | 1.4 |
| 25 | 100522 | X51501 | Hs.99949 | prolactin-induced protein | 11.9 | 0.4 |
| | 100552 | AA019521 | Hs.301946 | lysosomal | 3.8 | 1.2 |
| | 100599 | X77343 | Hs.334334 | transcription factor AP-2 alpha (activat | 9.4 | 9.4 |
| | 100676 | X02761 | Hs.287820 | fibronectin 1 | 3 | 7.8 |
| | 100690 | AA383256 | Hs.1657 | estrogen receptor 1 | 4.4 | 4.4 |
| 30 | 100895 | U01351 | Hs.75772 | nuclear receptor subfamily 3, group C, m | 1 | 3.9 |
| | 101046 | K01160 | | NM_002122:Homo sapiens major histocompat1.7 | 4 | 4 |
| | 101086 | AA382524 | Hs.250959 | histatin 1 | 0.8 | 4.1 |
| | 101148 | NM_002923 | Hs.78944 | regulator of G-protein signalling 2, 24k | 1.2 | 12 |
| | 101161 | NM_006262 | Hs.37044 | peripherin | 3.1 | 1.1 |
| 35 | 101201 | L22524 | Hs.2256 | matrix metalloproteinase 7 (MMP7; uterin | 4.4 | 0.6 |
| | 101212 | AI186220 | Hs.83164 | collagen, type XV, alpha 1 | 3.1 | 3.4 |
| | 101441 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 0.9 | 4.2 |
| | 101447 | M21305 | | gb:Human alpha satellite and satellite 3 | 29.9 | 0.3 |
| 40 | 101469 | AA310162 | Hs.169248 | cytochrome c | 0.8 | 4.9 |
| | 101567 | M33552 | Hs.56729 | lysosomal | 1 | 5.9 |
| | 101600 | BE561617 | Hs.119192 | H2A histone family, member Z | 2.8 | 4 |
| | 101624 | M55998 | | gb:Human alpha-1 collagen type I gene, 3 | 3.1 | 1.7 |
| | 101674 | NM_002291 | Hs.82124 | laminin, beta 1 | 1.5 | 4.1 |
| 45 | 101861 | AA350659 | Hs.83347 | angio-associated, migratory cell protein | 3.1 | 1.4 |
| | 101977 | AF112213 | Hs.184062 | putative Rab5-interacting protein | 1.3 | 6.9 |
| | 102193 | AL036335 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 1.9 | 4.9 |
| | 102199 | AA334592 | Hs.79914 | lumican | 2.2 | 3.8 |
| | 102304 | AF015224 | Hs.46452 | mammaglobin 1 | 4.2 | 0.7 |
| | 102345 | NM_003480 | Hs.300946 | Microfibril-associated glycoprotein-2 | 1.1 | 4.2 |
| 50 | 102457 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 4.5 | 0.5 |
| | 102534 | U96759 | Hs.198307 | von Hippel-Lindau binding protein 1 | 1.4 | 4.2 |
| | 102541 | AI379954 | Hs.79025 | KIAA0096 protein | 0.9 | 3.9 |
| | 102827 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 1.5 | 10.9 |
| | 102962 | R50032 | Hs.159263 | collagen, type VI, alpha 2 | 2.2 | 6.2 |
| 55 | 102991 | AW293542 | Hs.75309 | eukaryotic translation elongation factor | 5.6 | 5.7 |
| | 103119 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 3.7 | 0.5 |
| | 103175 | X69089 | Hs.79227 | myomesin (M-protein) 2 (165kD) | 1.3 | 4 |
| | 103286 | D38616 | Hs.54941 | phosphorylase kinase, alpha 2 (liver) | 1.3 | 3.8 |
| | 103319 | X83492 | Hs.82359 | tumor necrosis factor receptor superfam | 0.8 | 4.6 |
| 60 | 103372 | BE536700 | Hs.4888 | seryl-tRNA synthetase | 0.9 | 8 |
| | 103419 | T34708 | Hs.272927 | Sec23 (S. cerevisiae) homolog A | 1.1 | 5.1 |
| | 103471 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 3.7 | 1.2 |
| | 103546 | Z14244 | Hs.75752 | cytochrome c oxidase subunit VIIb | 0.9 | 4.4 |

| | | | | | | | |
|----|--------|-----------|-----------|---|-----|------|-----|
| | 103658 | NM_000088 | Hs.172928 | collagen, type I, alpha 1 | 3.2 | 3 | |
| | 103758 | AA084874 | | gb:zn13e04.r1 Stratagene hNT neuron (937 | 0.9 | 10 | |
| | 103774 | H24185 | Hs.92918 | hypothetical protein | 1.9 | 15.9 | |
| | 103821 | AA095971 | Hs.198793 | Homo sapiens cDNA: FLJ22463 fls, clone H | 1.2 | 3.9 | |
| 5 | 103869 | BE439604 | Hs.24322 | ATPase, H+ transporting, lysosomal (vacu | 1.4 | 3.9 | |
| | 103980 | AW130242 | Hs.293476 | hypothetical protein FKSG44 | 1.6 | 4.1 | |
| | 104054 | AK001913 | Hs.7100 | hypothetical protein | 1.5 | 4.3 | |
| | 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal | 7 | 7 | |
| | 104189 | AB040927 | Hs.301804 | KIAA1494 protein | 2 | 4.6 | |
| 10 | 104230 | AB002347 | Hs.15303 | KIAA0349 protein | 0.7 | 4.5 | |
| | 104278 | AW583693 | Hs.109253 | N-terminal acetyltransferase complex and | 3.3 | 3.3 | |
| | 104295 | AW365522 | Hs.103657 | hypothetical protein PRO2219 | 2.3 | 4.2 | |
| | 104319 | AW804296 | Hs.9950 | Sec61 gamma | 3.1 | 7 | |
| | 104425 | AF283775 | Hs.35380 | x 001 protein | 4 | 1.3 | |
| 15 | 104432 | X51501 | Hs.99949 | prolactin-induced protein | 3.8 | 0.6 | |
| | 104464 | AW966728 | Hs.54642 | methionine adenosyltransferase II, beta | 0.8 | 6.7 | |
| | 104479 | AK001731 | Hs.106390 | Homo sapiens mRNA; cDNA DKFZp586H0924 (f | 1.7 | 1.7 | 4.8 |
| | 104505 | W94824 | Hs.11565 | RIKEN cDNA 2010100O12 gene | 2 | 7.5 | |
| | 104592 | AW630488 | Hs.325820 | protease, serine, 23 | 1.9 | 7.4 | |
| 20 | 104613 | AF123303 | Hs.24713 | hypothetical protein | 1.1 | 6.3 | |
| | 104636 | R82252 | Hs.106106 | protein kinase (cAMP-dependent, catalyti | 1.2 | 4 | |
| | 104782 | AW270555 | Hs.171774 | hypothetical protein | 1.4 | 3.9 | |
| | 104792 | AA960961 | Hs.305953 | zinc finger protein 83 (HPF1) | 1.5 | 4.2 | |
| | 104848 | AA305351 | Hs.274369 | uncharacterized hypothalamus protein HAR | 1.1 | 4.1 | |
| 25 | 104849 | A1279065 | Hs.241507 | ribosomal protein S6 | 1.3 | 4.6 | |
| | 104850 | AL133035 | Hs.8728 | hypothetical protein DKFZp434G171 | 1.2 | 3.6 | |
| | 104852 | W70164 | Hs.20107 | ESTs | 0.8 | 4.2 | |
| | 104861 | AA058630 | Hs.29759 | RNA POLYMERASE I AND TRANSCRIPT RELEASE | 1.7 | 5.1 | |
| | 104873 | W03831 | Hs.20597 | host cell factor homolog | 0.8 | 5.4 | |
| 30 | 104891 | W44626 | Hs.30627 | ESTs | 0.7 | 6.8 | |
| | 104920 | AW955089 | Hs.306083 | Novel human gene mapping to chromosome 22 | 1 | 3.9 | |
| | 104926 | BE298808 | Hs.33363 | DKFZP434N093 protein | 3.3 | 3.3 | |
| | 104952 | AW076098 | Hs.74316 | desmoplakin (DPI, DP11) | 1.2 | 3.7 | |
| | 104963 | AB029020 | Hs.173694 | KIAA1097 protein | 1.1 | 5.5 | |
| 35 | 104977 | A1392640 | Hs.18272 | amino acid transporter system A1 | 3.2 | 1.4 | |
| | 105030 | BE613061 | Hs.337772 | Homo sapiens, Similar to RIKEN cDNA 0610 | 1.6 | 11.4 | |
| | 105035 | N39760 | Hs.8859 | Homo sapiens, Similar to RIKEN cDNA 5830 | 1.5 | 7.2 | |
| | 105068 | BE410438 | Hs.9006 | VAMP (vesicle-associated membrane protei | 1.1 | 3.5 | |
| | 105159 | AF146277 | Hs.265561 | CD2-associated protein | 1.2 | 10 | |
| 40 | 105178 | AA313825 | Hs.21941 | AD036 protein | 3.6 | 8.3 | |
| | 105182 | BE407961 | Hs.18271 | golgi phosphoprotein 3 | 1.7 | 6.8 | |
| | 105274 | A1554929 | Hs.281866 | ATPase, H+ transporting, lysosomal (vacu | 1.1 | 3.7 | |
| | 105303 | BE243327 | Hs.182626 | chromosome 22 open reading frame 5 | 1.5 | 4 | |
| | 105413 | A1015709 | Hs.172089 | Homo sapiens mRNA; cDNA DKFZp586I2022 (f | 1.5 | 1.5 | 14 |
| 45 | 105426 | W20027 | Hs.23439 | ESTs | 4.3 | 2.9 | |
| | 105432 | W03516 | Hs.76698 | stress-associated endoplasmic reticulum | 1.5 | 5 | |
| | 105443 | AA252372 | Hs.12144 | KIAA1033 protein | 1.2 | 3.6 | |
| | 105483 | AL137257 | Hs.23458 | Homo sapiens cDNA: FLJ23015 fls, clone L | 1.7 | 15.8 | |
| | 105492 | A1805717 | Hs.289112 | CGI-43 protein | 2 | 4.8 | |
| 50 | 105495 | AL037715 | Hs.28785 | microfibrillar-associated protein 3 | 1.3 | 3.9 | |
| | 105539 | AB040884 | Hs.109694 | KIAA1451 protein | 2.7 | 11.4 | |
| | 105594 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 1.3 | 6.1 | |
| | 105623 | BE504200 | Hs.30127 | hypothetical protein | 1.7 | 4.5 | |
| | 105807 | AA788946 | Hs.16869 | ESTs, Moderately similar to CA1C RAT COL | 3.9 | 24.6 | |
| 55 | 105812 | BE614149 | Hs.20814 | CGI-27 protein | 1.8 | 3.6 | |
| | 105823 | A1559444 | Hs.293960 | ESTs | 1.9 | 6.6 | |
| | 105831 | AA329449 | Hs.247302 | twisted gastrulation | 1.5 | 4.3 | |
| | 105851 | A1827976 | Hs.24391 | hypothetical protein FLJ13612 | 3.8 | 1.9 | |
| | 105879 | BE392914 | Hs.30503 | Homo sapiens cDNA FLJ11344 fls, clone PL | 1.7 | 4 | |
| 60 | 105918 | AW028485 | Hs.26136 | hypothetical protein MGC14156 | 1.7 | 7.4 | |
| | 105939 | AL137728 | Hs.12258 | Homo sapiens mRNA; cDNA DKFZp434B0920 (f | 1.2 | 1.2 | 3.8 |
| | 105941 | AB033075 | Hs.10669 | development and differentiation enhancin | 1.3 | 4.6 | |
| | 105969 | AB030656 | Hs.17377 | coronin, actin-binding protein, 1C | 1.1 | 5.9 | |
| | 105990 | A1690586 | Hs.29403 | hypothetical protein FLJ22060 | 2 | 4.6 | |
| 65 | 106012 | A1240665 | Hs.8895 | ESTs | 4.1 | 1.2 | |
| | 106060 | NM_001329 | Hs.171391 | C-terminal binding protein 2 | 2.6 | 7 | |
| | 106070 | T74445 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 1.4 | 10.7 | |

| | | | | | | | |
|----|--------|-----------|-----------|--|-----|------|--|
| | 106083 | H62087 | Hs.31659 | thyroid hormone receptor-associated prot | 1.5 | 3.6 | |
| | 106155 | AA425414 | Hs.33287 | nuclear factor I/B | 5.4 | 1.2 | |
| | 106255 | BE613206 | Hs.279607 | calpastatin | 1.8 | 4 | |
| 5 | 106414 | BE568205 | Hs.28827 | mitogen-activated protein kinase kinase | 5.1 | 6.1 | |
| | 106538 | AK000274 | Hs.278635 | HDCMA18P protein | 1.2 | 5.9 | |
| | 106568 | AW051564 | Hs.28285 | patched related protein translocated in | 1.8 | 5.4 | |
| | 106574 | BE044325 | Hs.227280 | U6 snRNA-associated Sm-like protein | 2.3 | 11.2 | |
| | 106613 | N88604 | Hs.30212 | thyroid receptor interacting protein 15 | 1.2 | 3.6 | |
| 10 | 106617 | H09548 | Hs.5367 | ESTs, Weakly similar to I38022 hypotheti | 0.9 | 4.4 | |
| | 106619 | AA459480 | Hs.23956 | hypothetical protein FLJ20502 | 1.3 | 3.6 | |
| | 106701 | BE387614 | Hs.25797 | splicing factor 3b, subunit 4, 49kD | 1.6 | 7.3 | |
| | 106721 | AA741038 | Hs.6670 | ESTs | 1.7 | 6.1 | |
| | 106776 | AA206079 | Hs.6693 | hypothetical protein FLJ20420 | 1 | 5.4 | |
| 15 | 106866 | AA487416 | Hs.268231 | Homo sapiens cDNA: FLJ23111 fis, clone L | 1.6 | 5.4 | |
| | 106868 | BE185536 | Hs.301183 | molecule possessing ankyrin repeats indu | 3.3 | 1.2 | |
| | 106887 | BE503373 | Hs.334335 | hypothetical protein FLJ13576 | 1.4 | 6.3 | |
| | 106940 | T85594 | Hs.339808 | hypothetical protein FLJ10120 | 3.3 | 1.8 | |
| | 106968 | AF216751 | Hs.26813 | CDA14 | 3 | 3 | |
| 20 | 107052 | BE391904 | Hs.12482 | glyceronephosphate O-acyltransferase | 1.7 | 7.6 | |
| | 107061 | BE147611 | Hs.6354 | stromal cell derived factor receptor 1 | 1.2 | 4.3 | |
| | 107149 | AI289507 | Hs.299883 | hypothetical protein FLJ23399 | 1.8 | 6.5 | |
| | 107222 | BE172058 | Hs.82689 | tumor rejection antigen (gp96) 1 | 1.2 | 6.9 | |
| | 107233 | BE267795 | Hs.22595 | hypothetical protein FLJ10637 | 1.4 | 3.5 | |
| 25 | 107295 | AA186629 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 2.6 | 4.3 | |
| | 107679 | AA011510 | Hs.60512 | ESTs | 1.8 | 4 | |
| | 107914 | AA027229 | Hs.61329 | ESTs, Weakly similar to T16370 hypotheti | 1.3 | 3.5 | |
| | 107965 | AF109219 | Hs.108787 | phosphatidylinositol glycan, class N | 1.6 | 3.5 | |
| | 108033 | AW368993 | Hs.323748 | Homo sapiens clone CDABP0086 mRNA sequen | 1.8 | 8.1 | |
| 30 | 108060 | AA291440 | Hs.73149 | paired box gene 8 | 1.1 | 3.5 | |
| | 108081 | AA093668 | Hs.28578 | muscleblind (Drosophila)-like | 0.7 | 5.6 | |
| | 108137 | AI283611 | Hs.263479 | ESTs, Weakly similar to HMGI_HUMAN HIGH | 1.2 | 5.6 | |
| | 108186 | AW068579 | Hs.7780 | Homo sapiens mRNA; cDNA DKFZp564A072 (fr | 3.1 | 6.9 | |
| | 108215 | AI879238 | Hs.299315 | collapsin response mediator protein-5; C | 1.5 | 4.6 | |
| 35 | 108297 | AA333660 | Hs.71331 | hypothetical protein MGC5350 | 1.5 | 4 | |
| | 108339 | AW151340 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 6.3 | 4.7 | |
| | 108371 | AA074374 | Hs.67639 | ESTs | 1.3 | 3.8 | |
| | 108399 | AF086070 | Hs.237519 | EST | 1 | 3.6 | |
| 40 | 108469 | AA079487 | | gb:zm97f08.s1 Stratagene colon HT29 (937 | 1.5 | 3.6 | |
| | 108470 | AA079500 | | gb:zm96h10.s1 Stratagene colon HT29 (937 | 1.1 | 4.3 | |
| | 108564 | M23114 | Hs.1526 | ATPase, Ca++ transporting, cardiac muscl | 2 | 4.9 | |
| | 108641 | AA112059 | Hs.429 | ATP synthase, H+ transporting, mitochond | 1.1 | 3.5 | |
| | 108668 | AA058522 | Hs.185751 | ESTs | 1.2 | 3.6 | |
| | 108694 | AA036725 | Hs.61847 | ESTs | 1.4 | 3.6 | |
| 45 | 108824 | AK001332 | Hs.44672 | hypothetical protein FLJ10470 | 1.4 | 3.5 | |
| | 108863 | AA133456 | Hs.102548 | glucocorticoid receptor DNA binding fact | 1.2 | 4 | |
| | 108893 | BE276891 | Hs.194691 | retinoic acid induced 3 | 1.3 | 3.6 | |
| | 108992 | AA152312 | Hs.72047 | ESTs | 1.1 | 4.1 | |
| | 109072 | AI732585 | Hs.22394 | hypothetical protein FLJ10893 | 1.2 | 3.5 | |
| 50 | 109097 | AA167512 | | gb:zp10f12.s1 Stratagene fetal retina 93 | 1.3 | 5 | |
| | 109160 | BE220601 | Hs.301997 | hypothetical protein FLJ13033 | 4 | 6.1 | |
| | 109244 | BE179030 | Hs.64239 | Human DNA sequence from clone RP5-1174N9 | 1.7 | 7.4 | |
| | 109481 | AA878923 | Hs.289069 | hypothetical protein FLJ21016 | 3.8 | 7.7 | |
| | 109484 | AA366263 | Hs.72531 | hypothetical protein FLJ11838 | 1.9 | 4 | |
| 55 | 109795 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 3.7 | 1.3 | |
| | 110009 | BE075297 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 p | 4.6 | 7.4 | |
| | 110107 | AW151660 | Hs.31444 | ESTs | 1.2 | 3.5 | |
| | 110411 | AW001579 | Hs.9645 | Homo sapiens mRNA for KIAA1741 protein, | 3.7 | 3.3 | |
| | 110731 | NM_014899 | Hs.188006 | KIAA0878 protein | 2.8 | 3.7 | |
| 60 | 110756 | N21207 | Hs.182999 | ESTs | 1.6 | 3.5 | |
| | 110930 | BE242691 | Hs.14947 | ESTs | 3.1 | 1.2 | |
| | 110935 | AI753230 | Hs.323562 | hypothetical protein DKFZp564K142 | 1.9 | 7.5 | |
| | 111051 | AI681293 | Hs.12186 | hypothetical protein FLJ22558 | 2 | 4 | |
| | 111110 | AK001566 | Hs.23618 | hypothetical protein FLJ10704 | 1.1 | 3.8 | |
| 65 | 111356 | BE301871 | Hs.4867 | mannosyl (alpha-1,3-)-glycoprotein beta- | 1 | 8.2 | |
| | 111357 | BE314949 | Hs.87128 | hypothetical protein FLJ23309 | 3.3 | 6.1 | |
| | 111770 | R27975 | Hs.269401 | ESTs, Moderately similar to S65657 alpha | 1.2 | 5.4 | |
| | 111900 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 3.2 | 0.8 | |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 111903 | NM_014906 | Hs.166351 | KIAA1072 protein | 1 | 5.4 |
| | 111951 | NM_014927 | Hs.100527 | KIAA0902 protein | 1 | 3.8 |
| | 112141 | AW137198 | Hs.278682 | Phosphatidylglycerophosphate Synthase | 1.4 | 3.5 |
| | 112193 | R49499 | Hs.138238 | ESTs | 1.5 | 3.6 |
| 5 | 112197 | NM_003655 | Hs.5637 | ESTs | 4.6 | 2 |
| | 112610 | AW500106 | Hs.23643 | serine/threonine protein kinase MASK | 3.3 | 10.5 |
| | 112971 | Z42387 | Hs.83883 | transmembrane, prostate androgen induced | 3.2 | 3 |
| | 112984 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 3.7 | 10.8 |
| | 113056 | AF019226 | Hs.8036 | glioblastoma overexpressed | 4.5 | 3.7 |
| 10 | 113449 | AW160683 | Hs.158006 | hypothetical protein | 1.2 | 4.4 |
| | 113497 | AF143321 | Hs.15572 | hypothetical protein IMAGE 109914 | 0.9 | 3.6 |
| | 113508 | AL042936 | Hs.211571 | holocytochrome c synthase (cytochrome c | 1.1 | 3.5 |
| | 113531 | AK001898 | Hs.16740 | hypothetical protein FLJ11036 | 1.2 | 3.9 |
| | 113604 | AI075407 | Hs.296083 | ESTs, Moderately similar to I54374 gene | 1.7 | 5.3 |
| 15 | 113674 | NM_014214 | Hs.5753 | inositol(myo)-1(or 4)-monophosphatase 2 | 0.8 | 6.1 |
| | 113841 | W30681 | Hs.146233 | Homo sapiens cDNA: FLJ22130 fis, clone H | 1.7 | 6.2 |
| | 113857 | AW243158 | Hs.5297 | DKFZP564A2416 protein | 1.2 | 4.6 |
| | 113931 | BE255499 | Hs.3496 | hypothetical protein MGC15749 | 1.5 | 4 |
| | 113936 | W17056 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 3.8 | 1 |
| 20 | 113987 | AA345519 | Hs.9641 | complement component 1, q subcomponent, | 1.2 | 4.7 |
| | 114132 | AI342493 | Hs.24192 | Homo sapiens cDNA FLJ20767 fis, clone CO | 0.3 | 4.3 |
| | 114156 | BE179882 | Hs.336920 | glutathione peroxidase 3 (plasma) | 1.1 | 4.3 |
| | 114213 | N58309 | Hs.19575 | CGI-11 protein | 1.6 | 9.2 |
| | 114636 | AA075488 | | gb:zm88d01.s1 Stratagene ovarian cancer | 1.6 | 3.7 |
| 25 | 114760 | AI929382 | Hs.252692 | hypothetical protein FLJ20343 | 1.4 | 4 |
| | 114781 | T10446 | Hs.95388 | ESTs | 1 | 4.3 |
| | 114795 | AB037858 | Hs.173484 | hypothetical protein FLJ10337 | 1.6 | 9.2 |
| | 114901 | AV660012 | Hs.196437 | hypothetical protein FLJ10788 | 1.4 | 5.2 |
| | 115086 | AI683069 | Hs.175319 | ESTs | 3.7 | 1 |
| 30 | 115518 | BE541042 | Hs.23240 | Homo sapiens cDNA: FLJ21848 fis, clone H | 3.2 | 4.2 |
| | 115646 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glu | 1.5 | 3.9 |
| | 115764 | AW582256 | Hs.91011 | anterior gradient 2 (Xenopus laevis) hom | 1.3 | 5.9 |
| | 115802 | AW410233 | Hs.206521 | YME1 (S.cerevisiae)-like 1 | 1.7 | 6.6 |
| | 115994 | AB037836 | Hs.109315 | KIAA1415 protein | 1.5 | 9.1 |
| 35 | 116032 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 0.9 | 4.3 |
| | 116046 | BE395293 | Hs.94491 | hypothetical protein FLJ20297 | 1.6 | 5.5 |
| | 116274 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 3.2 | 2.4 |
| | 116310 | Z24854 | Hs.42299 | ESTs | 0.8 | 4.7 |
| | 116356 | AI371223 | Hs.288671 | Homo sapiens cDNA FLJ11997 fis, clone HE | 2.4 | 3.9 |
| 40 | 116429 | AF191018 | Hs.279923 | putative nucleotide binding protein, est | 5.5 | 5.5 |
| | 116461 | AA313607 | Hs.58633 | Homo sapiens cDNA: FLJ22145 fis, clone H | 5 | 1.3 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 8.7 | 4.5 |
| | 116578 | D21262 | Hs.75337 | nucleolar and coiled-body phosphoprotein | 3.2 | 6.9 |
| | 116579 | AW888411 | Hs.81915 | leukemia-associated phosphoprotein p18 (| 3.2 | 3 |
| 45 | 116589 | AI557212 | Hs.17132 | ESTs, Moderately similar to I54374 gene | 3.1 | 8.3 |
| | 116786 | H25836 | Hs.301527 | ESTs, Moderately similar to unknown [H.s | 3.2 | 4.5 |
| | 117170 | N25929 | Hs.42500 | ADP-ribosylation factor-like 5 | 7 | 5.5 |
| | 117215 | N20066 | Hs.133207 | PTPRF interacting protein, binding prote | 1.2 | 6.2 |
| | 117280 | M18217 | Hs.172129 | Homo sapiens cDNA: FLJ21409 fis, clone C | 4.5 | 2.4 |
| 50 | 117576 | AI383467 | Hs.44597 | ESTs | 1.4 | 4.2 |
| | 117667 | U59305 | Hs.44708 | Ser-Thr protein kinase related to the my | 4.3 | 0.5 |
| | 117881 | AF161470 | Hs.260622 | butyrate-induced transcript 1 | 2.1 | 5.7 |
| | 118336 | BE327311 | Hs.47166 | HT021 | 3.6 | 7.7 |
| | 118475 | N66845 | | gb:za46c11.s1 Soares fetal liver spleen | 4.2 | 0.5 |
| 55 | 118493 | AL353944 | Hs.50115 | Homo sapiens mRNA; cDNA DKFZp761J1112 (f | 3.5 | 3.3 |
| | 118505 | N67343 | | gb:yz50b07.s1 Morton Fetal Cochlea Homo | 2.1 | 3.8 |
| | 119159 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 3.7 | 1.5 |
| | 119307 | BE048061 | Hs.37054 | ephrin-A3 | 3 | 1.1 |
| | 119355 | BE218319 | Hs.5807 | GTPase Rab14 | 1.1 | 5.6 |
| 60 | 119462 | BE041667 | Hs.314544 | Homo sapiens cervical cancer suppressor- | 1.4 | 4.3 |
| | 119771 | AI905687 | Hs.2533 | EST | 3.2 | 1 |
| | 119940 | AL050097 | Hs.272531 | DKFZP586B0319 protein- | 4.3 | 0.7 |
| | 119943 | BE565849 | Hs.14158 | copine III | 3.5 | 1.9 |
| | 120407 | AA235207 | Hs.250456 | hypothetical protein DKFZp762F2011 | 1.5 | 3.7 |
| 65 | 120493 | AW968080 | Hs.152939 | Homo sapiens clone 24630 mRNA sequence | 4 | 1.4 |
| | 120677 | AF150208 | Hs.108327 | damage-specific DNA binding protein 1 (1 | 1.6 | 6.8 |
| | 120867 | AA350781 | Hs.96967 | ESTs | 1.1 | 3.6 |

| | | | | | | | |
|----|--------|----------|-----------|--|------|------|--|
| | 121368 | BE262956 | Hs.178292 | KIAA0180 protein | 1.5 | 4.1 | |
| | 121603 | AA416785 | Hs.249495 | heterogeneous nuclear ribonucleoprotein | 2.2 | 5.5 | |
| | 121723 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 3.4 | 3.2 | |
| 5 | 122223 | AF169797 | Hs.27413 | adaptor protein containing pH domain, PT | 3.9 | 3.9 | |
| | 122378 | AB032948 | Hs.21356 | hypothetical protein DKFZp762K2015 | 1.4 | 7.1 | |
| | 122946 | AI718702 | Hs.308026 | major histocompatibility complex, class | 1.4 | 3.7 | |
| | 123155 | AF121856 | Hs.284291 | sorting nexin 6 | 1.2 | 4.9 | |
| | 123158 | AF161426 | Hs.218329 | hypothetical protein | 2.4 | 3.6 | |
| | 123327 | AA421581 | Hs.178443 | ESTs | 0.9 | 5.2 | |
| 10 | 123495 | W28673 | Hs.106747 | serine carboxypeptidase 1 precursor prot | 1.3 | 5.1 | |
| | 123526 | AA608657 | | gb:ae55d04.s1 Stratagene lung carcinoma | 2.1 | 5.2 | |
| | 123533 | AA608751 | | gb:ae56h07.s1 Stratagene lung carcinoma | 2.1 | 9.3 | |
| | 123768 | AI932318 | Hs.188762 | ESTs, Moderately similar to H2BL_HUMAN H | 1.1 | 3.6 | |
| | 123961 | AL050184 | Hs.21610 | DKFZP434B203 protein | 1.1 | 3.5 | |
| 15 | 123999 | AF084555 | Hs.7351 | cyclic AMP phosphoprotein, 19 kD | 1.4 | 3.8 | |
| | 124000 | BE563957 | Hs.74861 | activated RNA polymerase II transcriptio | 1.9 | 11.2 | |
| | 124038 | AB037860 | Hs.173933 | nuclear factor I/A | 1.5 | 4.4 | |
| | 124059 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 14.8 | 11.5 | |
| | 124083 | AW195237 | Hs.7734 | hypothetical protein FLJ22174 | 1.2 | 6.2 | |
| 20 | 124148 | BE300094 | Hs.227751 | lectin, galactoside-binding, soluble, 1 | 2.5 | 12.7 | |
| | 124153 | AU077333 | Hs.160483 | erythrocyte membrane protein band 7.2 (s | 1 | 4.1 | |
| | 124252 | BE613340 | Hs.334725 | Homo sapiens, Similar to RIKEN cDNA 9430 | 1.5 | 8.4 | |
| | 124314 | AK001552 | Hs.215766 | GTP-binding protein | 1.8 | 10.2 | |
| | 124375 | D87454 | Hs.192966 | KIAA0265 protein | 1.1 | 4.8 | |
| 25 | 124432 | N39016 | Hs.268869 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 1.3 | 4.1 | |
| | 124447 | N48000 | | gb:yy98e12.s1 Soares_multiple_sclerosis_ | 2.7 | 4.3 | |
| | 124539 | D54120 | Hs.146409 | cell division cycle 42 (GTP-binding prot | 2.1 | 5.7 | |
| | 124543 | AI393320 | Hs.104573 | ESTs | 1 | 4.1 | |
| | 124564 | H66409 | Hs.108275 | ESTs | 1.4 | 4 | |
| 30 | 124574 | AL036596 | Hs.42322 | A kinase (PRKA) anchor protein 2 | 0.7 | 4 | |
| | 124605 | AA749315 | Hs.77171 | minichromosome maintenance deficient (S. | 1.1 | 3.5 | |
| | 124639 | H60193 | Hs.21143 | DKFZP586C1324 protein | 1.4 | 3.6 | |
| | 124659 | AI680737 | Hs.289068 | Homo sapiens cDNA FLJ11918 fis, clone HE | 1.5 | 9.9 | |
| | 124737 | BE270465 | Hs.78793 | protein kinase C, zeta | 0.7 | 4 | |
| 35 | 124760 | AW408586 | Hs.91052 | ESTs, Moderately similar to ALU5_HUMAN A | 0.9 | 3.6 | |
| | 124763 | BE410405 | Hs.76288 | calpain 2, (mII) large subunit | 1.3 | 3.9 | |
| | 124792 | R44357 | Hs.48712 | hypothetical protein FLJ20736 | 1.8 | 4.2 | |
| | 124842 | R56485 | | gb:yg93h09.s1 Soares infant brain 1NIB H | 1 | 3.6 | |
| | 124940 | AF068846 | Hs.103804 | heterogeneous nuclear ribonucleoprotein | 3.2 | 3.4 | |
| 40 | 124949 | AI903210 | Hs.336780 | tubulin, beta polypeptide | 1 | 4.4 | |
| | 124960 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 0.9 | 5.2 | |
| | 124995 | T52700 | Hs.110044 | ESTs | 0.9 | 3.5 | |
| | 125030 | AA610577 | Hs.187775 | ESTs | 1.2 | 5 | |
| | 125034 | BE548446 | Hs.5167 | Homo sapiens mRNA; cDNA DKFZp434F152 (fr | 1.5 | 3.7 | |
| 45 | 125058 | T83731 | Hs.3343 | phosphoglycerate dehydrogenase | 0.9 | 6 | |
| | 125076 | AA973971 | | gb:ox02h08.s1 NCI_CGAP_Lu5 Homo sapiens | 1 | 3.7 | |
| | 125090 | T91518 | | gb:ye20f05.s1 Stratagene lung (937210) H | 3.2 | 2.5 | |
| | 125103 | AA570056 | Hs.122730 | ESTs, Moderately similar to KIAA1215 pro | 5.3 | 6.6 | |
| | 125154 | W38419 | | gb:zc78a07.s1 Pancreatic Islet Homo sapi | 0.9 | 6.1 | |
| 50 | 125155 | AA837043 | Hs.143669 | ESTs | 1.1 | 4.3 | |
| | 125159 | AK000669 | Hs.274428 | TRF2-interacting telomeric RAP1 protein | 1.1 | 4.1 | |
| | 125170 | AL020996 | Hs.8518 | selenoprotein N | 1.1 | 3.8 | |
| | 125181 | R40815 | Hs.12396 | ESTs, Weakly similar to 2004399A chromos | 1 | 3.6 | |
| | 125193 | W67577 | Hs.84298 | CD74 antigen (invariant polypeptide of m | 1.2 | 7.8 | |
| 55 | 125260 | H05635 | Hs.294030 | topoisomerase-related function protein 4 | 1 | 4.9 | |
| | 125262 | AW884980 | Hs.171957 | triple functional domain (PTPRF interact | 1.3 | 4.8 | |
| | 125272 | BE612888 | Hs.180224 | myosin regulatory light chain | 1.1 | 16.1 | |
| | 125388 | W27235 | Hs.64311 | a disintegrin and metalloproteinase doma | 1.4 | 5.3 | |
| | 125824 | Z45258 | Hs.286013 | short coiled-coil protein | 2.4 | 8.7 | |
| 60 | 125852 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 1.8 | 4.6 | |
| | 125970 | AW504721 | Hs.177516 | high density lipoprotein binding protein | 1.9 | 3.8 | |
| | 126192 | AW160399 | Hs.30376 | hypothetical protein | 1.4 | 4.1 | |
| | 126469 | BE384361 | Hs.182885 | ESTs, Weakly similar to JC5024 UDP-galac | 2 | 3.7 | |
| | 126510 | AA057593 | Hs.334762 | hypothetical protein FLJ14735 | 1.3 | 4.1 | |
| 65 | 127095 | AA340277 | Hs.10248 | Homo sapiens cDNA FLJ20167 fis, clone CO | 1.3 | 5 | |
| | 127524 | AI243596 | Hs.94830 | ESTs, Moderately similar to T03094 A-kin | 4.3 | 0.9 | |
| | 128312 | J04182 | Hs.150101 | lysosomal | 1.5 | 4.7 | |

| | | | | | | | |
|----|--------|-----------|-----------|--|-----|------|--|
| | 128453 | X02761 | Hs.287820 | fibronectin 1 | 1.2 | 4.3 | |
| | 128460 | T16206 | Hs.237164 | ESTs, Highly similar to LDHH_HUMAN L-LAC | 3.1 | 44.4 | |
| | 128491 | H08379 | Hs.165563 | hypothetical protein DKFZp434N1429 | 0.6 | 13.1 | |
| | 128495 | NM_005904 | Hs.100602 | MAD (mothers against decapentaplegic, Dr | 1.3 | 4 | |
| 5 | 128546 | NM_003478 | Hs.101299 | cullin 5 | 1 | 5.1 | |
| | 128574 | AI185977 | Hs.38260 | ubiquitin specific protease 18 | 0.8 | 4 | |
| | 128611 | NM_014721 | Hs.102471 | KIAA0680 gene product | 1.3 | 3.7 | |
| | 128652 | AA432202 | Hs.103147 | hypothetical protein FLJ21347 | 1.4 | 3.9 | |
| | 128653 | D87432 | Hs.10315 | solute carrier family 7 (cationic amino | 1.2 | 3.6 | |
| 10 | 128655 | AI246669 | Hs.324275 | WW domain-containing protein 1 | 0.8 | 4.1 | |
| | 128684 | BE246444 | Hs.283685 | hypothetical protein FLJ20396 | 3 | 1.6 | |
| | 128717 | AK001564 | Hs.104222 | hypothetical protein FLJ10702 | 2.8 | 4.8 | |
| | 128774 | AA476220 | Hs.54457 | CD81 antigen (target of antiproliferativ | 1.1 | 10.6 | |
| | 128790 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 1 | 3.8 | |
| 15 | 128805 | AA194554 | Hs.183434 | ATPase, H+ transporting, lysosomal (vacu | 5.3 | 5.3 | |
| | 128827 | AI638184 | Hs.106334 | Homo sapiens clone 23836 mRNA sequence | 2.2 | 5.3 | |
| | 128840 | AI917602 | Hs.106440 | ESTs | 1 | 4.5 | |
| | 128869 | AA768242 | Hs.80618 | hypothetical protein | 0.8 | 3.6 | |
| | 128889 | D60985 | Hs.106909 | DKFZP566D193 protein | 4.6 | 3.7 | |
| 20 | 128890 | AI222020 | Hs.182364 | CocoaCrisp | 3 | 1.5 | |
| | 128915 | AK000140 | Hs.107139 | hypothetical protein | 0.2 | 3.9 | |
| | 128920 | AA622037 | Hs.166468 | programmed cell death 5 | 2.5 | 15.2 | |
| | 128926 | AF155096 | Hs.107213 | hypothetical protein FLJ20585 | 4 | 4 | |
| | 128930 | AA298958 | Hs.10724 | MDS023 protein | 1.2 | 4.5 | |
| 25 | 128942 | AW247536 | Hs.10729 | hypothetical protein | 1.4 | 5 | |
| | 128948 | AW953622 | Hs.223025 | RAB31, member RAS oncogene family | 2.3 | 5.6 | |
| | 128953 | AB020716 | Hs.107362 | KIAA0909 protein | 0.9 | 3.9 | |
| | 128979 | AW271217 | Hs.281434 | Homo sapiens cDNA FLJ14028 fis, clone HE | 1.5 | 3.6 | |
| | 128980 | AA258924 | Hs.10758 | NM_002495: Homo sapiens NADH dehydrogena | 0.8 | 3.8 | |
| 30 | 129005 | AI770025 | Hs.13323 | hypothetical protein FLJ22059 | 1.2 | 5.7 | |
| | 129009 | C15105 | Hs.330716 | Homo sapiens cDNA FLJ14368 fis, clone HE | 2.1 | 9.9 | |
| | 129013 | AA371156 | Hs.107942 | DKFZP564M112 protein | 2.4 | 3.8 | |
| | 129068 | AI634522 | Hs.152925 | KIAA1268 protein | 1.2 | 3.8 | |
| | 129106 | AW504486 | Hs.108689 | sterol regulatory element binding transc | 1.2 | 5.5 | |
| 35 | 129113 | BE543205 | Hs.288771 | DKFZP586A0522 protein | 0.5 | 3.7 | |
| | 129125 | AB002450 | Hs.278391 | CGI-109 protein | 1 | 5.2 | |
| | 129126 | AW881089 | Hs.108806 | Homo sapiens mRNA; cDNA DKFZp566M0947 (f | 1.5 | 7 | |
| | 129151 | N23018 | Hs.171391 | C-terminal binding protein 2 | 2.1 | 9.7 | |
| | 129230 | AA335362 | Hs.109646 | Empirically selected from AFFX single pr | 0.9 | 8.6 | |
| 40 | 129234 | M18916 | Hs.282997 | glucosidase, beta; acid (includes glucos | 1.1 | 3.5 | |
| | 129238 | BE542214 | Hs.109697 | ESTs | 1.1 | 12.8 | |
| | 129239 | W57656 | Hs.109701 | ubiquitin-like 5 | 3.2 | 5.1 | |
| | 129241 | AI878857 | Hs.109706 | hematological and neurological expressed | 1.9 | 5.7 | |
| | 129243 | BE169531 | Hs.109727 | TAK1-binding protein 2; KIAA0733 protein | 1.2 | 6.6 | |
| 45 | 129247 | R49920 | Hs.109733 | CGI-131 protein | 1.5 | 3.5 | |
| | 129250 | AA344367 | Hs.109760 | Empirically selected from multiple AFFX | 1 | 5.4 | |
| | 129258 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 1.3 | 4.1 | |
| | 129260 | AF077200 | Hs.279813 | hypothetical protein | 1.6 | 3.9 | |
| | 129270 | AA357185 | Hs.109918 | ras homolog gene family, member H | 1.8 | 4.2 | |
| 50 | 129277 | AB007896 | Hs.110 | putative L-type neutral amino acid trans | 1.1 | 6.1 | |
| | 129284 | AA318224 | Hs.296141 | ESTs | 2.5 | 4.8 | |
| | 129300 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 1.6 | 5.1 | |
| | 129318 | AF189062 | Hs.285976 | tumor metastasis-suppressor | 1.8 | 6.5 | |
| | 129352 | AW511656 | Hs.170177 | Meis1 (mouse) homolog | 0.9 | 4 | |
| 55 | 129362 | U30246 | Hs.110736 | solute carrier family 12 (sodium/potassi | 1.4 | 9.2 | |
| | 129379 | BE278964 | Hs.11085 | CGI-111 protein | 1 | 4.8 | |
| | 129390 | AA318271 | Hs.250905 | hypothetical protein | 1 | 4.1 | |
| | 129416 | AA016188 | Hs.111244 | hypothetical protein | 1.8 | 10.7 | |
| | 129427 | AI498631 | Hs.111334 | femtin, light polypeptide | 1.1 | 4.8 | |
| 60 | 129470 | W92931 | Hs.250899 | heat shock factor binding protein 1 | 1.8 | 9.3 | |
| | 129472 | AL050260 | Hs.323817 | DKFZP547E1010 protein | 1 | 5 | |
| | 129475 | NM_004477 | Hs.203772 | FSDH region gene 1 | 1.1 | 4.2 | |
| | 129498 | AA449789 | Hs.75511 | connective tissue growth factor | 1.9 | 6.8 | |
| | 129501 | AI631811 | Hs.180403 | STRIN protein | 1.1 | 9.7 | |
| 65 | 129527 | AA769221 | Hs.270847 | delta-tubulin | 1.1 | 4.3 | |
| | 129545 | R18087 | Hs.323769 | cisplatin resistance related protein CRR | 1 | 4.2 | |
| | 129579 | AW517695 | Hs.286218 | junctional adhesion molecule 1 | 2.3 | 3.5 | |

| | | | | | | |
|----|--------|-------------|-----------|--|-----|------|
| | 129606 | AW968941 | Hs.166254 | hypothetical protein DKFZp566i133 | 2.4 | 4.4 |
| | 129619 | AA209534 | Hs.284243 | tetraspan NET-6 protein | 3.2 | 13 |
| | 129620 | D79338 | Hs.239720 | CCR4-NOT transcription complex, subunit | 1.6 | 4.6 |
| | 129621 | AL110212 | Hs.301005 | purine-rich element binding protein B | 1.1 | 5.7 |
| 5 | 129634 | AB020335 | Hs.181300 | sel-1 (suppressor of lin-12, C.elegans)- | 0.9 | 4.3 |
| | 129663 | AI207406 | Hs.11866 | translocase of inner mitochondrial membr | 1.9 | 4.8 |
| | 129679 | AW889132 | Hs.11916 | ribokinase | 0.9 | 4.1 |
| | 129688 | U53209 | Hs.24937 | transformer-2 alpha (htra-2 alpha) | 1.3 | 4.7 |
| | 129691 | M26939 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 4.7 | 3.7 |
| 10 | 129712 | U46386 | Hs.12102 | sorting nexin 3 | 1.2 | 3.6 |
| | 129747 | AL050272 | Hs.12305 | DKFZP566B183 protein | 1 | 8.9 |
| | 129788 | BE397454 | Hs.124969 | Homo sapiens clone 24707 mRNA sequence | 1.4 | 3.6 |
| | 129796 | BE218319 | Hs.5807 | GTPase Rab14 | 2.9 | 5.1 |
| | 129797 | M62839 | Hs.1252 | apolipoprotein H (beta-2-glycoprotein I) | 0.3 | 5.1 |
| 15 | 129800 | AF052112 | Hs.12540 | lysosomal | 1.6 | 8.8 |
| | 129834 | AL080084 | Hs.296155 | CGI-100 protein | 0.9 | 5.3 |
| | 129836 | AW410233 | Hs.206521 | YME1 (S.cerevisiae)-like 1 | 1.8 | 9.9 |
| | 129843 | NM_014840 | Hs.200598 | KIAA0537 gene product | 0.9 | 3.6 |
| | 129874 | AA626837 | Hs.181551 | hypothetical protein MGC2594 | 1.4 | 9.5 |
| 20 | 129878 | Z43161 | Hs.283714 | 30 kDa protein | 1.1 | 6.3 |
| | 129904 | AL119499 | Hs.13285 | neuronal potassium channel alpha subunit | 1 | 3.5 |
| | 129917 | M30773 | Hs.278540 | protein phosphatase 3 (formerly 2B), reg | 2 | 5.1 |
| | 129976 | X14008 | Hs.234734 | lysosomal | 0.9 | 4.9 |
| | 129982 | Z14221 | | gb:H.sapiens germline transcript of Ig h | 1.2 | 3.6 |
| 25 | 130007 | R15917 | Hs.142570 | Homo sapiens clone 24629 mRNA sequence | 4.3 | 1.3 |
| | 130060 | BE277024 | Hs.146381 | RNA binding motif protein, X chromosome | 1.6 | 3.8 |
| | 130064 | X57815.comp | | Empirically selected from AFFX single pr | 1.2 | 8.2 |
| | 130068 | M93143 | Hs.262869 | plasminogen-like | 1.4 | 7.9 |
| | 130090 | H97878 | Hs.132390 | zinc finger protein 36 (KOX 18) | 1.4 | 12.3 |
| 30 | 130095 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 0.2 | 4.6 |
| | 130102 | W61005 | Hs.14896 | DHHC1 protein | 1 | 4.1 |
| | 130112 | AA916785 | Hs.180610 | splicing factor proline/glutamine rich (| 1.2 | 5.3 |
| | 130115 | T47294 | Hs.149923 | X-box binding protein 1 | 3.8 | 0.8 |
| | 130123 | NM_005095 | Hs.150390 | zinc finger protein 262 | 1 | 4.2 |
| 35 | 130150 | BE094848 | Hs.15113 | homogentisate 1,2-dioxygenase (homogenti | 0.5 | 4 |
| | 130161 | R42678 | Hs.151385 | KIAA0564 protein | 1 | 3.7 |
| | 130210 | M23115 | Hs.1526 | ATPase, Ca++ transporting, cardiac muscl | 0.4 | 4.4 |
| | 130213 | BE278370 | Hs.15265 | heterogeneous nuclear ribonucleoprotein | 1.7 | 7.5 |
| | 130215 | BE301883 | Hs.152707 | glioblastoma amplified sequence | 1 | 5.6 |
| 40 | 130232 | U29463 | | gb:Human cytochrome b561 gen | 1.2 | 4.2 |
| | 130252 | U92014 | Hs.153527 | Homo sapiens pTM5 mariner-like transposo | 1.3 | 3.6 |
| | 130281 | W78907 | Hs.15395 | similar to arginyl-tRNA synthetase (argi | 1.5 | 4.4 |
| | 130343 | AB040914 | Hs.278628 | KIAA1481 protein | 2.9 | 7.5 |
| | 130385 | AW067800 | Hs.155223 | stanniocalcin 2 | 3.2 | 0.2 |
| 45 | 130414 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 1.4 | 10.6 |
| | 130417 | AW163518 | Hs.155485 | huntingtin interacting protein 2 | 1.7 | 11.7 |
| | 130440 | AA852868 | Hs.132853 | KIAA0171 gene product | 1.1 | 5 |
| | 130442 | NM_006245 | Hs.118244 | protein phosphatase 2, regulatory subuni | 1.4 | 4.3 |
| | 130465 | AW362955 | Hs.15641 | Homo sapiens cDNA FLJ14415 fis, clone HE | 1.6 | 7.6 |
| 50 | 130479 | R44163 | Hs.12457 | hypothetical protein FLJ10814 | 0.9 | 4.1 |
| | 130499 | AB007915 | Hs.158286 | KIAA0446 gene product | 1 | 3.8 |
| | 130546 | AI598022 | Hs.193989 | TAR DNA binding protein | 1.3 | 4.7 |
| | 130568 | AA232119 | Hs.16085 | putative G-protein coupled receptor | 1.2 | 9.4 |
| | 130606 | AI652143 | Hs.288382 | hypothetical protein FLJ13111 | 1 | 4.1 |
| 55 | 130612 | BE242873 | Hs.16677 | WD repeat domain 15 | 1.1 | 3.6 |
| | 130616 | AL049963 | Hs.284205 | up-regulated by BCG-CWS | 0.6 | 3.8 |
| | 130623 | AL045128 | Hs.1691 | glucan (1,4-alpha-), branching enzyme 1 | 0.9 | 6.6 |
| | 130629 | AL042896 | Hs.1697 | ATPase, H+ transporting, lysosomal (vacu | 0.9 | 3.9 |
| | 130632 | AW073971 | Hs.238954 | ESTs, Weakly similar to KIAA1204 protein | 0.9 | 6.9 |
| 60 | 130639 | AI557212 | Hs.17132 | ESTs, Moderately similar to I54374 gene | 2.6 | 3.9 |
| | 130641 | AF158555 | Hs.239189 | glutaminase | 1.2 | 13.8 |
| | 130653 | AI861791 | Hs.278479 | TSPY-like | 1.3 | 4 |
| | 130655 | AI831962 | Hs.17409 | cysteine-rich protein 1 (intestinal) | 2.5 | 4 |
| | 130666 | AL117508 | Hs.194035 | KIAA0737 gene product | 1.3 | 6.2 |
| 65 | 130669 | AI928985 | Hs.17680 | hypothetical protein MGC1314 similar to | 1.4 | 3.9 |
| | 130693 | R68537 | Hs.17962 | ESTs | 3.2 | 0.8 |
| | 130694 | NM_014827 | Hs.17969 | KIAA0663 gene product | 1.1 | 4.8 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|---|
| 5 | 130696 | AA325308 | Hs.18016 | Homo sapiens mRNA; cDNA DKFZp586H0324 (f | 1.8 | 5 |
| | 130701 | Z98883 | Hs.18079 | phosphatidylinositol glycan, class Q | 1.1 | |
| | 130707 | AW190925 | Hs.203559 | hypothetical protein FLJ12701 | 1.2 | |
| | 130731 | AI932971 | Hs.18593 | Homo sapiens cDNA: FLJ21449 fis, clone C | 1.4 | |
| | 130787 | AF072813 | Hs.252831 | reticulin 3 | 1.2 | |
| 10 | 130796 | AA088809 | Hs.19525 | hypothetical protein FLJ22794 | 1.8 | |
| | 130808 | NM_001761 | Hs.1973 | cyclin F | 1.3 | |
| | 130863 | Y10805 | Hs.20521 | HMT1 (hnRNP methyltransferase, S. cerevi | 3.2 | |
| | 130902 | AB037750 | Hs.21061 | KIAA1329 protein | 1 | |
| | 130908 | AW195747 | Hs.21122 | hypothetical protein FLJ11830 similar to | 1.3 | |
| 15 | 130911 | BE409769 | Hs.21189 | DnaJ (Hsp40) homolog, subfamily A, membe | 2.7 | |
| | 130913 | BE390905 | Hs.21198 | translocase of outer mitochondrial membr | 1.9 | |
| | 130923 | H96115 | Hs.21293 | UDP-N-acetylglucosamine pyrophosphorylas | 1.9 | |
| | 130959 | AB023182 | Hs.184523 | KIAA0965 protein | 1.5 | |
| | 130967 | AA393071 | Hs.182579 | leucine aminopeptidase | 1.4 | |
| 20 | 130975 | AA099923 | Hs.283728 | PEST-containing nuclear protein | 1.3 | |
| | 131037 | BE243101 | Hs.22391 | chromosome 20open reading frame 3 | 1.9 | |
| | 131039 | D87436 | Hs.166318 | lipin 2 | 1.6 | |
| | 131060 | AA194422 | Hs.22564 | myosin VI | 4.5 | |
| | 131097 | AL137682 | Hs.22937 | I-kappa-B-interacting Ras-like protein 2 | 2 | |
| 25 | 131101 | BE387561 | Hs.22981 | DKFZP586M1523 protein | 1.6 | |
| | 131104 | W27770 | Hs.301756 | ESTs, Weakly similar to T31475 hypotheti | 0.9 | |
| | 131107 | BE620886 | Hs.75354 | GCN1 (general control of amino-acid synt | 2.1 | |
| | 131109 | BE564123 | Hs.23060 | DKFZP564F0522 protein | 1.1 | |
| | 131136 | AB033099 | Hs.23413 | KIAA1273 protein | 1.2 | |
| 30 | 131148 | AW953575 | Hs.303125 | p53-induced protein PIGPC1 | 4.5 | |
| | 131150 | X77753 | Hs.23582 | tumor-associated calcium signal transduc | 3.4 | |
| | 131156 | AI472209 | Hs.323117 | ESTs | 0.8 | |
| | 131164 | AW013807 | Hs.182265 | keratin 19 | 3.3 | |
| | 131181 | H25094 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 0.6 | |
| 35 | 131194 | AW864222 | Hs.24083 | KIAA0997 protein | 1.4 | |
| | 131199 | AW979155 | Hs.298275 | amino acid transporter 2 | 1.2 | |
| | 131215 | AL050107 | Hs.24341 | transcriptional co-activator with PDZ-bi | 0.7 | |
| | 131216 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 2.1 | |
| | 131233 | D89053 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 1.7 | |
| 40 | 131237 | AW956868 | Hs.24608 | DKFZP564D177 protein | 1.3 | |
| | 131262 | AU077158 | Hs.24930 | tubulin-specific chaperone a | 1.6 | |
| | 131263 | AU077002 | Hs.24950 | regulator of G-protein signalling 5 | 1.4 | |
| | 131367 | AI750575 | Hs.173933 | nuclear factor I/A | 3.3 | |
| | 131372 | AW293399 | Hs.144904 | nuclear receptor co-repressor 1 | 1.6 | |
| 45 | 131373 | NM_006052 | Hs.26146 | Down syndrome critical region gene 3 | 1 | |
| | 131388 | NM_014810 | Hs.92200 | KIAA0480 gene product | 5 | |
| | 131492 | AI452601 | Hs.288869 | nuclear receptor subfamily 2, group F, m | 0.9 | |
| | 131493 | AW960146 | Hs.284137 | hypothetical protein FLJ12888 | 1 | |
| | 131514 | BE270734 | Hs.2795 | lactate dehydrogenase A | 2 | |
| 50 | 131524 | AB040927 | Hs.301804 | KIAA1494 protein | 1.5 | |
| | 131528 | AU076408 | Hs.28309 | UDP-glucose dehydrogenase | 1.3 | |
| | 131534 | AF157326 | Hs.184786 | TBP-interacting protein | 1.3 | |
| | 131555 | T47364 | Hs.278613 | interferon, alpha-inducible protein 27 | 1.5 | |
| | 131578 | AA936296 | Hs.234265 | DKFZP586G011 protein | 1.8 | |
| 55 | 131589 | C18825 | Hs.29191 | epithelial membrane protein 2 | 1.3 | |
| | 131609 | D83032 | Hs.169984 | nuclear protein | 2.8 | |
| | 131626 | BE514605 | Hs.289092 | Homo sapiens cDNA: FLJ22380 fis, clone H | 1.3 | |
| | 131670 | H03514 | Hs.10130 | ESTs | 1.3 | |
| | 131697 | C19034 | Hs.288613 | Homo sapiens cDNA FLJ14175 fis, clone NT | 3.2 | |
| 60 | 131701 | AF103798 | Hs.30819 | hypothetical protein | 1.3 | |
| | 131703 | AW160865 | Hs.30888 | cytochrome c oxidase subunit VIIa polype | 1.3 | |
| | 131739 | AF017986 | Hs.31386 | secreted frizzled-related protein 2 | 10.6 | |
| | 131764 | AI805664 | Hs.31731 | peroxiredoxin 5 | 1.1 | |
| | 131781 | AF077036 | Hs.31989 | DKFZP586G1722 protein | 1.6 | |
| 65 | 131791 | X62111 | | gbH.sapiens VII-5 gene for immunoglobul | 1.1 | |
| | 131853 | AI681917 | Hs.3321 | ESTs, Highly similar to IRX1_HUMAN IROQU | 5.3 | |
| | 131870 | NM_014874 | Hs.3363 | KIAA0214 gene product | 0.6 | |
| | 131903 | NM_004642 | Hs.3436 | deleted in oral cancer (mouse, homolog) | 2.4 | |
| | 131913 | AW207440 | Hs.185973 | degenerative spermatocyte (homolog Droso | 2.4 | |
| | 131930 | AA772603 | Hs.69476 | Homo sapiens cDNA FLJ12758 fis, clone NT | 1.7 | |
| | 131941 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 0.5 | |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|--|
| | 131947 | AI123939 | Hs.182997 | ESTs | 0.7 | 4.1 | |
| | 131961 | AA129782 | Hs.3576 | Homo sapiens mRNA full length insert cDN | 0.9 | 4.8 | |
| | 131964 | AW381148 | Hs.198365 | 2,3-bisphosphoglycerate mutase | 1.1 | 6.1 | |
| 5 | 131974 | AF208856 | Hs.268122 | hypothetical protein | 1.3 | 3.9 | |
| | 131983 | AF119665 | Hs.184011 | pyrophosphatase (inorganic) | 3.3 | 6.9 | |
| | 131997 | AF229181 | Hs.136644 | CS box-containing WD protein | 0.9 | 5.2 | |
| | 132006 | AW162336 | Hs.3709 | low molecular mass ubiquinone-binding pr | 1.2 | 3.6 | |
| | 132063 | BE277910 | Hs.3833 | 3'-phosphoadenosine 5'-phosphosulfate sy | 3.2 | 1.8 | |
| | 132065 | BE379335 | Hs.211594 | proteasome (prosome, macropain) 26S subu | 1.2 | 3.6 | |
| 10 | 132071 | AF217798 | Hs.3850 | LIS1-interacting protein NUDEL; endoolig | 0.7 | 5.2 | |
| | 132079 | AI701457 | Hs.38694 | ESTs | 2 | 5.3 | |
| | 132094 | NM_016045 | Hs.3945 | CGI-107 protein | 1.2 | 4.3 | |
| | 132116 | AW960474 | Hs.40289 | ESTs | 3.1 | 3.1 | |
| | 132164 | AI752235 | Hs.41270 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.8 | 3.7 | |
| 15 | 132181 | AW961231 | Hs.16773 | Homo sapiens clone TCCCIA00427 mRNA sequ | 1.2 | 5 | |
| | 132208 | AL031709 | Hs.241575 | hypothetical protein CAB56184 | 1.4 | 4.2 | |
| | 132258 | AA306325 | Hs.4311 | SUMO-1 activating enzyme subunit 2 | 2 | 10.3 | |
| | 132303 | BE177330 | Hs.325093 | Homo sapiens cDNA: FLJ21210 fis, clone C | 1.2 | 4.1 | |
| | 132316 | U28831 | Hs.44566 | KIAA1641 protein | 5.9 | 1.6 | |
| 20 | 132358 | NM_003542 | Hs.46423 | H4 histone family, member G | 5.8 | 1.5 | |
| | 132384 | AA312135 | Hs.46967 | HSPCO34 protein | 2.1 | 9.3 | |
| | 132397 | AA021160 | Hs.4750 | hypothetical protein DKFZp564K0822 | 1.3 | 4.6 | |
| | 132413 | AW361383 | Hs.260116 | metalloprotease 1 (pitrilysin family) | 2 | 4.9 | |
| | 132442 | AW970859 | Hs.313503 | ESTs | 1.2 | 5 | |
| 25 | 132534 | BE388673 | Hs.5086 | hypothetical protein MGC10433 | 2 | 3.9 | |
| | 132540 | BE396290 | Hs.5097 | synaptogyrin 2 | 1.4 | 5.1 | |
| | 132554 | AF065391 | Hs.194718 | zinc finger protein 265 | 1.2 | 4 | |
| | 132575 | AV660538 | Hs.284162 | 60S ribosomal protein L30 isolog | 3 | 1.7 | |
| | 132585 | AF029750 | Hs.179600 | TAP binding protein (tapasin) | 1.8 | 4.7 | |
| 30 | 132602 | AW606927 | Hs.5306 | hypothetical protein DKFZp586F1122 simil | 1.6 | 4.9 | |
| | 132608 | AA353044 | Hs.5321 | ARP3 (actin-related protein 3, yeast) ho | 1.8 | 8.1 | |
| | 132718 | NM_004600 | Hs.554 | Sjogren syndrome antigen A2 (60kD, ribon | 4.2 | 2 | |
| | 132719 | AI264357 | Hs.55405 | hypothetical protein MGC16212 | 1.1 | 5.3 | |
| | 132730 | AK000868 | Hs.5570 | hypothetical protein FLJ10006 | 1.4 | 5.2 | |
| 35 | 132765 | BE222975 | Hs.56205 | insulin induced gene 1 | 1.1 | 5.8 | |
| | 132782 | F07424 | Hs.279840 | zinc finger protein 222 | 1.3 | 3.7 | |
| | 132793 | AB020713 | Hs.56966 | KIAA0906 protein | 2.3 | 6.3 | |
| | 132805 | AW975748 | Hs.5724 | sclerostin | 0.7 | 7.7 | |
| 40 | 132863 | BE268048 | Hs.236494 | RAB10, member RAS oncogene family | 1.8 | 6.2 | |
| | 132894 | D63209 | Hs.5944 | solute carrier family 11 (proton-coupled | 1.5 | 20.8 | |
| | 132930 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21028 fis, clone C | 1 | 3.8 | |
| | 132932 | AW118826 | Hs.6093 | Homo sapiens cDNA: FLJ22783 fis, clone K | 0.7 | 5.4 | |
| | 132933 | BE263252 | Hs.6101 | hypothetical protein MGC3178 | 1.6 | 4.1 | |
| | 132965 | AI248173 | Hs.191460 | hypothetical protein MGC12936 | 1 | 4.2 | |
| 45 | 132984 | BE539199 | Hs.62112 | zinc finger protein 207 | 1.5 | 4.4 | |
| | 132990 | X77343 | Hs.334334 | transcription factor AP-2 alpha (activat | 13.9 | 0.8 | |
| | 132998 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor t | 0.6 | 4.6 | |
| | 133002 | AW499985 | Hs.42915 | ARP2 (actin-related protein 2, yeast) ho | 1.5 | 11.1 | |
| | 133011 | NM_006379 | Hs.171921 | sema domain, Immunoglobulin domain (Ig), | 3.5 | 1 | |
| 50 | 133012 | AA847843 | Hs.62711 | Homo sapiens, clone IMAGE:3351295, mRNA1 | 1 | 4.5 | |
| | 133040 | AW502761 | Hs.30909 | KIAA0430 gene product | 0.9 | 5.5 | |
| | 133056 | H12028 | Hs.6396 | jumping translocation breakpoint | 1.7 | 5.3 | |
| | 133063 | AI654133 | Hs.30212 | thyroid receptor interacting protein 15 | 0.6 | 4.9 | |
| | 133067 | AK000708 | Hs.169764 | hypothetical protein FLJ20701 | 1.2 | 3.5 | |
| 55 | 133080 | AF089816 | Hs.6454 | chromosome 19 open reading frame 3 | 1.2 | 17.5 | |
| | 133110 | AA808177 | Hs.65228 | ESTs | 0.9 | 5.1 | |
| | 133150 | AV655783 | Hs.661 | Empirically selected from AFFX single pr | 1.1 | 4.5 | |
| | 133175 | AW955632 | Hs.66666 | ESTs, Weakly similar to S19560 proline-r | 1.5 | 4.8 | |
| | 133199 | AF231981 | Hs.250175 | homolog of yeast long chain polyunsatura | 5.5 | 5.9 | |
| 60 | 133203 | AA464362 | Hs.6748 | hypothetical protein PP1665 | 1.2 | 3.7 | |
| | 133206 | AB037773 | Hs.6762 | hypothetical protein | 1.6 | 8.6 | |
| | 133221 | W32474 | Hs.301746 | RAP2A, member of RAS oncogene family | 2.4 | 4.8 | |
| | 133229 | AL137480 | Hs.6834 | KIAA1014 protein | 1 | 4.2 | |
| | 133241 | AW796524 | Hs.68644 | Homo sapiens microsomal signal peptidase | 1.3 | 3.9 | |
| 65 | 133257 | BE617892 | Hs.6895 | actin related protein 2/3 complex, subun | 1.4 | 5.4 | |
| | 133271 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 3.1 | 0.7 | |
| | 133273 | N27672 | Hs.69469 | dendritic cell protein | 2.5 | 6.5 | |

| | | | | | | | |
|----|--------|-------------|-----------|--|-----|------|-----|
| 5 | 133287 | AW797437 | Hs.69771 | B-factor, properdin | 1.3 | 4 | |
| | 133291 | BE297855 | Hs.69855 | NRAS-related gene | 1.4 | 5 | |
| | 133292 | AA304961 | Hs.699 | peptidylprolyl isomerase B (cyclophilin | 2.2 | 6.8 | |
| | 133294 | AJ001388 | Hs.69997 | zinc finger protein 238 | 1.5 | 4.3 | |
| | 133300 | AF116666 | Hs.70333 | hypothetical protein MGC10753 | 1.4 | 6.3 | |
| 10 | 133302 | X04898 | Hs.237658 | apolipoprotein A-II | 0.2 | 3.6 | |
| | 133308 | U56979 | Hs.250651 | H factor 1 (complement) | 0.6 | 5 | |
| | 133347 | BE257758 | Hs.71475 | acid cluster protein 33 | 1.2 | 4.2 | |
| | 133370 | AF245505 | Hs.72157 | DKFZP564I1922 protein | 3.7 | 5.8 | |
| | 133404 | AB007916 | Hs.214646 | KIAA0447 gene product | 1.4 | 5.1 | |
| 15 | 133408 | AI738719 | Hs.198427 | hexokinase 2 | 0.9 | 6.3 | |
| | 133422 | AB033061 | Hs.73287 | KIAA1235 protein | 1.2 | 3.7 | |
| | 133442 | AL137663 | Hs.7378 | Homo sapiens mRNA; cDNA DKFZp434G227 (fr | 0.7 | 0.7 | 4.8 |
| | 133448 | M27749 | Hs.288168 | immunoglobulin lambda-like polypeptide 1 | 1.1 | 4.3 | |
| | 133449 | AF038962 | Hs.7381 | voltage-dependent anion channel 3 | 0.7 | 4.2 | |
| 20 | 133501 | AI962602 | Hs.74284 | hypothetical protein MGC2714 | 3.1 | 5.9 | |
| | 133504 | NM_004415 | Hs.74316 | desmoplakin (DPI, DPII) | 4.3 | 11.5 | |
| | 133506 | BE562958 | Hs.74346 | hypothetical protein MGC14353 | 1.8 | 19.7 | |
| | 133532 | D87452 | Hs.74579 | KIAA0263 gene product | 1.2 | 5.4 | |
| | 133574 | H97991 | Hs.193313 | Empirically selected from AFFX single pr | 1.4 | 3.9 | |
| 25 | 133586 | AI929645 | Hs.225936 | synapsin I | 0.8 | 4.9 | |
| | 133589 | L37368 | Hs.75104 | RNA-binding protein S1, serine-rich doma | 2 | 10.8 | |
| | 133591 | AI423369 | Hs.75111 | protease, serine, 11 (IGF binding) | 2.1 | 4.5 | |
| | 133606 | U10564 | Hs.75188 | wee1+ (S. pombe) homolog | 3.3 | 1.1 | |
| | 133617 | BE244334 | Hs.75249 | ADP-ribosylation factor-like 6 interacti | 2.3 | 5.6 | |
| 30 | 133651 | AI301740 | Hs.173381 | dihydropyrimidinase-like 2 | 0.8 | 13.5 | |
| | 133660 | H14843 | Hs.303154 | popeye protein 3 | 1 | 9.1 | |
| | 133663 | AJ006239 | Hs.75438 | quinoid dihydropteridine reductase | 0.5 | 5.8 | |
| | 133668 | L77964 | Hs.271980 | mitogen-activated protein kinase 6 | 1.1 | 6.9 | |
| | 133671 | AW503116 | Hs.301819 | zinc finger protein 146 | 1.8 | 3.8 | |
| 35 | 133681 | AI352558 | Hs.75544 | tyrosine 3-monooxygenase/tryptophan 5-mo | 1.5 | 11.1 | |
| | 133694 | W17187.comp | Hs.232400 | heterogeneous nuclear ribonucleoprotein | 2 | 3.9 | |
| | 133708 | AI018666 | Hs.75667 | synaptophysin | 0.6 | 3.5 | |
| | 133737 | AW001130 | Hs.75824 | KIAA0174 gene product | 1.2 | 7.2 | |
| | 133743 | AI929587 | Hs.75847 | CREBBP/EP300 inhibitory protein 1 | 1.5 | 5 | |
| 40 | 133750 | BE410769 | Hs.75873 | zyxin | 1.2 | 4.8 | |
| | 133765 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 3.2 | 4.1 | |
| | 133776 | BE268649 | Hs.177766 | ADP-ribosyltransferase (NAD+; poly (ADP- | 2.1 | 3.8 | |
| | 133799 | W24087 | Hs.76285 | DKFZP564B167 protein | 1.9 | 12.6 | |
| | 133800 | AF075337 | Hs.76293 | thymosin, beta 10 | 2.6 | 6.6 | |
| 45 | 133802 | AW239400 | Hs.76297 | G protein-coupled receptor kinase 6 | 1 | 4.9 | |
| | 133806 | D25969 | Hs.76325 | step II splicing factor SLU7 | 0.5 | 3.8 | |
| | 133817 | AW578716 | Hs.7644 | H1 histone family, member 2 | 1.5 | 4.5 | |
| | 133829 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 3.7 | 5.6 | |
| | 133841 | AA345824 | Hs.76688 | carboxylesterase 1 (monocyte/macrophage | 0.3 | 4.4 | |
| 50 | 133845 | AA147026 | Hs.76704 | ESTs | 5.5 | 2.9 | |
| | 133863 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 0.6 | 4.8 | |
| | 133887 | X07767 | Hs.77271 | protein kinase, cAMP-dependent, catalyti | 1 | 10.2 | |
| | 133892 | AW859528 | Hs.301497 | arginyltransferase 1 | 0.9 | 4.8 | |
| | 133913 | AU076964 | Hs.7753 | calumenin | 2.8 | 10.5 | |
| 55 | 133914 | AI458213 | Hs.77542 | ESTs | 1.8 | 5.6 | |
| | 133917 | AL031177 | Hs.7756 | proteasome (prosome, macropain) 26S subu | 1.5 | 6.6 | |
| | 133947 | L41066 | Hs.77810 | nuclear factor of activated T-cells, cyt | 1.5 | 3.8 | |
| | 133986 | M54968 | Hs.184050 | v-Ki-ras2 Kirsten rat sarcoma 2 viral on | 0.9 | 4.3 | |
| | 133987 | L15409 | Hs.174007 | von Hippel-Lindau syndrome | 2.3 | 4.3 | |
| 60 | 133989 | AL040328 | Hs.78202 | SWI/SNF related, matrix associated, acti | 3.3 | 3.4 | |
| | 133990 | R48316 | Hs.7822 | Homo sapiens mRNA; cDNA DKFZp564C1216 (f | 1.3 | 1.3 | 5.7 |
| | 134029 | BE150882 | Hs.143601 | hypothetical protein hCLA-Iso | 1 | 6.5 | |
| | 134040 | NM_003470 | Hs.78683 | ubiquitin specific protease 7 (herpes vi | 1.7 | 3.6 | |
| | 134042 | AI027881 | Hs.7869 | lysosomal | 1 | 7.5 | |
| 65 | 134049 | AF117236 | Hs.78825 | matrin 3 | 1.2 | 4 | |
| | 134095 | NM_004354 | Hs.79069 | cyclin G2 | 2.7 | 4.8 | |
| | 134098 | BE513171 | Hs.79086 | mitochondrial ribosomal protein L3 | 3.3 | 2.1 | |
| | 134207 | Z43039 | Hs.170198 | KIAA0009 gene product | 1.3 | 3.5 | |
| | 134210 | AF035606 | Hs.80019 | programmed cell death 6 | 1.7 | 6.9 | |
| | 134218 | U77735 | Hs.80205 | pim-2 oncogene | 0.8 | 5.3 | |
| | 134270 | X68194 | Hs.80919 | synaptophysin-like protein | 1.4 | 11.4 | |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 134277 | NM_004369 | Hs.80988 | collagen, type VI, alpha 3 | 2.6 | 3.5 |
| | 134280 | NM_000712 | Hs.81029 | biliverdin reductase A | 1.8 | 5.8 |
| | 134288 | AI022650 | Hs.81117 | erbB2-Interacting protein ERBIN | 1.1 | 3.6 |
| 5 | 134296 | R00603 | Hs.81128 | phosphatidylserine decarboxylase | 1.1 | 5.9 |
| | 134300 | NM_001430 | Hs.81136 | endothelial PAS domain protein 1 | 0.5 | 4.8 |
| | 134310 | AL037800 | Hs.81148 | selenoprotein T | 1.7 | 7.9 |
| | 134343 | D50683 | Hs.82028 | transforming growth factor, beta recepto | 0.8 | 7.6 |
| | 134364 | X76534 | Hs.82226 | glycoprotein (transmembrane) nmb | 2.2 | 3.6 |
| | 134374 | N22687 | Hs.8236 | ESTs | 1.9 | 3.6 |
| 10 | 134378 | AL035786 | Hs.82425 | actin related protein 2/3 complex, subun | 1.5 | 8.3 |
| | 134382 | BE512856 | Hs.109051 | SH3 domain binding glutamic acid-rich pr | 1.1 | 3.6 |
| | 134415 | AI750762 | Hs.82911 | protein tyrosine phosphatase type IVA, m | 1.9 | 4.6 |
| | 134417 | NM_006416 | Hs.82921 | solute carrier family 35 (CMP-sialic aci | 1.2 | 7.5 |
| | 134421 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 6.6 | 8.7 |
| 15 | 134439 | Z23024 | Hs.138860 | Rho GTPase activating protein 1 | 2 | 3.9 |
| | 134454 | NM_013230 | Hs.286124 | CD24 antigen (small cell lung carcinoma | 3.5 | 1.1 |
| | 134494 | D86981 | Hs.84084 | amyloid beta precursor protein (cytoplas | 1.5 | 4.4 |
| | 134501 | W84869 | Hs.211568 | eukaryotic translation initiation factor | 1.2 | 5.7 |
| | 134505 | AW960673 | Hs.177530 | ATP synthase, H+ transporting, mitochond | 1.3 | 3.9 |
| 20 | 134520 | BE091005 | Hs.74861 | activated RNA polymerase II transcriptio | 1.8 | 4.3 |
| | 134528 | M23161 | Hs.84775 | Human transposon-like element mRNA | 0.8 | 5.6 |
| | 134545 | AI902899 | Hs.85155 | butyrate response factor 1 (EGF-response | 1.4 | 5 |
| | 134553 | AI203545 | Hs.296169 | S-phase response (cyclin-related) | 0.8 | 3.9 |
| | 134573 | NM_016142 | Hs.279617 | steroid dehydrogenase homolog | 1.3 | 5.7 |
| 25 | 134576 | AB033017 | Hs.8594 | KIAA1191 protein | 0.9 | 3.7 |
| | 134577 | BE244323 | Hs.85951 | exportin, tRNA (nuclear export receptor | 4 | 6.8 |
| | 134579 | AW936928 | Hs.85963 | DKFZP564M182 protein | 2.2 | 4.3 |
| | 134582 | AA927177 | Hs.86041 | CGG triplet repeat binding protein 1 | 1.6 | 3.6 |
| | 134600 | AF078859 | Hs.86347 | hypothetical protein | 2.1 | 3.5 |
| 30 | 134655 | AF265208 | Hs.123090 | SWI/SNF related, matrix associated, acti | 1.7 | 4.2 |
| | 134700 | AK000606 | Hs.8868 | golgi SNAP receptor complex member 1 | 4.4 | 0.9 |
| | 134737 | D17530 | Hs.89434 | drebrin 1 | 3.1 | 1.6 |
| | 134762 | T51986 | Hs.283108 | hemoglobin, gamma G | 0.5 | 4.6 |
| 35 | 134843 | AA428520 | Hs.90061 | progesterone binding protein | 1.3 | 3.7 |
| | 134854 | J03464 | Hs.179573 | collagen, type I, alpha 2 | 8.7 | 17.3 |
| | 134865 | AA587775 | Hs.66295 | multi-PDZ-domain-containing protein | 1.7 | 4 |
| | 134868 | AB020689 | Hs.90419 | KIAA0882 protein | 3.4 | 0.9 |
| | 134874 | AI803761 | Hs.90458 | serine palmitoyltransferase, long chain | 1.3 | 6.9 |
| | 134885 | AJ002030 | Hs.9071 | progesterone membrane binding protein | 1.4 | 9.6 |
| 40 | 134891 | R51083 | Hs.90787 | ESTs | 1 | 10.1 |
| | 134908 | BE089782 | Hs.9877 | hypothetical protein | 1.9 | 3.9 |
| | 134934 | AF005043 | Hs.91390 | poly (ADP-ribose) glycohydrolase | 1 | 4.3 |
| | 134970 | BE560779 | Hs.284233 | NICE-5 protein | 1.4 | 10.4 |
| | 134982 | AK002085 | Hs.92308 | Homo sapiens cDNA FLJ11223 fls, clone PL | 1.6 | 4.1 |
| 45 | 135011 | AB037835 | Hs.92991 | KIAA1414 protein | 1.2 | 5.6 |
| | 135032 | AW301984 | Hs.173685 | hypothetical protein FLJ12619 | 1.7 | 7.6 |
| | 135035 | AL034344 | Hs.284186 | forkhead box C1 | 3.2 | 0.6 |
| | 135051 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 4.2 | 4.1 |
| 50 | 135060 | AK001887 | Hs.259842 | protein kinase, AMP-activated, gamma 2 n | 1.3 | 4.8 |
| | 135062 | AK000967 | Hs.93872 | KIAA1682 protein | 2 | 3.7 |
| | 135077 | AW503733 | Hs.9414 | KIAA1488 protein | 2.8 | 3.7 |
| | 135082 | AB017363 | Hs.94234 | frizzled (Drosophila) homolog 1 | 2.4 | 4.8 |
| | 135107 | T97257 | Hs.337531 | ESTs, Moderately similar to I38022 hypot | 1.4 | 5.8 |
| 55 | 135143 | AA132813 | Hs.69559 | KIAA1096 protein | 1.8 | 8.5 |
| | 135156 | BE563088 | Hs.9552 | binder of Arl Two | 1.2 | 6.8 |
| | 135172 | AB028956 | Hs.12144 | KIAA1033 protein | 3.1 | 1.4 |
| | 135181 | BE250865 | Hs.279529 | px19-like protein | 1.3 | 7.5 |
| | 135222 | AA534009 | Hs.183487 | Interferon stimulated gene (20kD) | 1.3 | 3.8 |
| | 135232 | AL038812 | Hs.96800 | ESTs, Moderately similar to ALU7_HUMAN A | 2.1 | 3.9 |
| 60 | 135289 | AW372569 | Hs.9788 | hypothetical protein MGC10924 similar to | 0.9 | 8.4 |
| | 135290 | AA331901 | Hs.184736 | hypothetical protein FLJ10097 | 1 | 3.8 |
| | 135291 | T83882 | Hs.97927 | ESTs | 1.2 | 3.5 |
| | 135349 | AA114212 | Hs.9930 | serine (or cysteine) proteinase inhibito | 2.6 | 8.9 |
| | 135357 | AI565004 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 2.5 | 5.4 |
| 65 | 135398 | M16029 | Hs.287270 | ret proto-oncogene (multiple endocrine n | 0.4 | 7.9 |
| | 135399 | W79431 | Hs.326249 | ribosomal protein L22 | 1.5 | 4.5 |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 3.2 | 1.8 |

| | | | | | | | |
|----|--------|---------------|-----------|--|-----|------|--|
| | 302665 | R99693 | Hs.224410 | Homo sapiens cDNA FLJ12843 fis, clone NT | 3.6 | 3.6 | |
| | 302892 | AW176909 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 3.3 | 1.6 | |
| | 302963 | AW673106 | Hs.151945 | mitochondrial ribosomal protein L43 | 0.9 | 4.2 | |
| | 303131 | AW081061 | Hs.103180 | DC2 protein | 3 | 17.3 | |
| 5 | 303150 | AA887146 | Hs.8217 | stromal antigen 2 | 6.2 | 4 | |
| | 310125 | AA147979 | Hs.285005 | mitochondrial import receptor Tom22 | 1.2 | 6.6 | |
| | 312662 | AA233808 | Hs.286241 | protein kinase, cAMP-dependent, regulato | 1 | 3.5 | |
| | 319429 | BE616412 | Hs.286218 | junctional adhesion molecule 1 | 1.5 | 4.7 | |
| | 320591 | AA054761 | Hs.169149 | karyopherin alpha 1 (importin alpha 5) | 1.2 | 5.6 | |
| 10 | 406779 | AA412048 | Hs.279574 | CGI-39 protein; cell death-regulatory pr | 1.3 | 3.5 | |
| | 410691 | AW239226 | Hs.65450 | reticulon 4 | 1.2 | 13.9 | |
| | 410763 | AF279145 | Hs.8966 | hypothetical protein FLJ21776 | 2 | 5.1 | |
| | 415738 | BE539367 | Hs.295953 | ESTs, Weakly similar to AF220049 1 uncha | 1.3 | 3.9 | |
| | 420186 | NM_015925 | Hs.95697 | liver-specific bHLH-Zip transcription fa | 1.5 | 6.2 | |
| 15 | 422055 | NM_014320 | Hs.111029 | putative heme-binding protein | 2 | 11.3 | |
| | 425815 | R94023 | Hs.337531 | ESTs, Moderately similar to I38022 hypot | 1.7 | 3.6 | |
| | 426218 | AF119043 | Hs.168005 | Homo sapiens cDNA FLJ13372 fis, clone PL | 3.3 | 2.8 | |
| | 427397 | AI929685 | Hs.177656 | calmodulin 1 (phosphorylase kinase, delt | 1.3 | 4.7 | |
| | 427466 | AA523543 | Hs.7678 | cellular retinoic acid-binding protein 1 | 1.1 | 3.7 | |
| 20 | 427505 | AA361562 | Hs.178761 | 26S proteasome-associated pad1 homolog | 3.2 | 2.5 | |
| | 427723 | AI355260 | Hs.279789 | histone deacetylase 3 | 2.8 | 22 | |
| | 428673 | AW601325 | Hs.324278 | Homo sapiens mRNA; cDNA DKFZp566M063 (fr | 1.1 | 5.2 | |
| | 430219 | X99209 | Hs.235887 | HMT1 (hnRNP methyltransferase, S. cerevi | 1.8 | 8.8 | |
| | 430450 | R23553 | Hs.241489 | hypothetical protein | 1.1 | 5.6 | |
| 25 | 432866 | BE395875 | Hs.279609 | mitochondrial carrier homolog 2 | 1.5 | 6.1 | |
| | 433423 | BE407127 | Hs.8997 | heat shock 70kD protein 1A | 1.3 | 7.6 | |
| | 437562 | AB001636 | Hs.5683 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 1.6 | 6.5 | |
| | 437667 | BE616412 | Hs.286218 | junctional adhesion molecule 1 | 1.3 | 3.5 | |
| | 437754 | R60366 | Hs.5822 | Homo sapiens cDNA: FLJ22120 fis, clone H | 2 | 5.7 | |
| 30 | 440252 | BE513940 | Hs.6101 | hypothetical protein MGC3178 | 1.1 | 6.2 | |
| | 441471 | AL042986 | Hs.7857 | erythrocyte membrane protein band | 0.5 | 3.7 | |
| | 448292 | BE281316 | Hs.47334 | hypothetical protein FLJ14495 | 2.5 | 4.9 | |
| | 449404 | H51066 | Hs.23581 | leptin receptor gene-related protein | 1.1 | 3.6 | |
| | 449964 | AW001741 | Hs.273193 | hypothetical protein FLJ10706 | 1.4 | 3.5 | |
| 35 | 451389 | N73222 | Hs.279009 | matrix Gla protein | 4 | 11.2 | |
| | 452685 | AI634651 | Hs.30250 | v-maf musculoaponeurotic fibrosarcoma (a | 0.8 | 5.6 | |
| | | RC_H15847_s | | peptidylprolyl isomerase B (cyclophilin B) | 1.8 | 4.8 | |
| | | RC_W84712 | | calumenin | 3.5 | 4.6 | |
| 40 | | X14008_ma1_f | | lysozyme (renal amyloidosis) | 0.9 | 4.5 | |
| | | RC_H86543_f | | ESTs | 1.8 | 6.6 | |
| | | H07011 | | ESTs; Weakly similar to SAS [H.sapiens] | 1.8 | 3.9 | |
| | | RC_AA164586_s | | ESTs | 6.2 | 0.8 | |
| | | RC_AA070485 | | Homo sapiens clone 23967 | 3.4 | 2.6 | |
| | | RC_H98714_s | | ESTs | 1.6 | 3.5 | |
| 45 | | RC_AA406145_f | | ESTs | 4.6 | 3 | |
| | | AA458584 | | SRY (sex determining region Y)-box 4 | 3.4 | 0.4 | |
| | | AA031548 | | cell division cycle 42 (GTP-binding protein; 25kD) | 3.1 | 3.9 | |
| | | X02761 | | fibronectin 1 | 3.6 | 15.2 | |
| 50 | | RC_AA487193 | | secreted frizzled-related protein 4 | 4.7 | 4 | |
| | | R25326 | | Homo sapiens mRNA for putative vacuolar | 0.9 | 5 | |
| | | RC_AA393805 | | ESTs; Weakly similar to (define not | 1.1 | 8.4 | |
| | | RC_AA449333 | | ESTs | 2.9 | 4.6 | |
| | | RC_AA287681_s | | ESTs | 1.3 | 4 | |
| | | RC_AA490864 | | ESTs; Highly similar to heat shock factor | 1.4 | 5 | |
| 55 | | RC_C14243_f | | ESTs; Highly similar to heat shock factor | 1.7 | 5 | |
| | | R21443 | | ESTs | 1.6 | 3.7 | |
| | | RC_AA251902 | | Homo sapiens lysophospholipase (LPL1) | 2.2 | 3.8 | |
| | | M21121_s | | small inducible cytokine A5 (RANTES) | 0.9 | 9.9 | |
| | | C00038_s | | ESTs | 2.8 | 4.8 | |
| 60 | | Y00503 | | keratin 19 | 3.1 | 1.1 | |
| | | RC_R27006_f | | ESTs | 1.6 | 3.7 | |
| | | RC_AA416886 | | ESTs; Weakly similar to predicted using | 3.1 | 3.1 | |
| | | RC_AA460450 | | fibroblast growth factor receptor 2 (bacteria- | 1.5 | 3.7 | |
| | | RC_AA488433 | | ESTs; Weakly similar to deduced amino acid | 1.1 | 4 | |
| 65 | | RC_AA278400_f | | Homo sapiens HRIHFB2115 mRNA; partial cds | 1.5 | 3.6 | |
| | | U28831 | | Human protein immuno-reactive with anti-PTH4.4 | 0.6 | | |
| | | RC_AA199588 | | Homo sapiens actin-related protein Arp3 (ARP3) | 1.8 | 4.7 | |

| | | | | |
|----|-------------------------|--|-----|------|
| 5 | AF006082 | Homo sapiens actin-related protein Arp2 (ARP2) | 1.6 | 10.9 |
| | RC_H90899 | desmoplakin (DPI; DP11) | 5.4 | 5.5 |
| | RC_W95070 | desmoplakin (DPI; DP11) | 5 | 2.6 |
| | RC_T90946_f | Human mRNA for KIAA263 gene; complete cds | 1.1 | 3.9 |
| | D87258 | protease; serine; 11 (IGF binding) | 2.4 | 3.5 |
| 10 | AA313414_s | ESTs; Weakly similar to cDNA EST EMBL:T1157 | 1.5 | 5.3 |
| | RC_H73484_s | ESTs; Weakly similar to similar to Yeast | 1.3 | 6.3 |
| | AFFX-HUMISGF3A/M97935_3 | | 2.3 | 13.5 |
| | AFFX-HUMRGE/M10098_5 | | 1.1 | 7.9 |
| | AFFX-M27830_5 | | 0.5 | 7.4 |
| | AFFX-M27830_5 | | 0.6 | 5.4 |
| | RC_AA063431_f | ESTs | 0.8 | 4.1 |
| | RC_T63769_f | ferritin; light polypeptide | 1.1 | 3.7 |

TABLE 8A

Table 8A shows the accession numbers for those pkeys lacking unigeneID's for Table 8. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15

| Pkey | CAT number | Accessions |
|--------|---------------------|--|
| 108469 | 116761_1 | AA079487 AA128547 AA128291 AA079587 AA079600 |
| 125076 | 190299_1 | AA973971 T88817 AA253263 |
| 114636 | 109698_1 | AA075488 AA129081 AA074851 AA082852 AA074732 AA084908 AA084751 AA076042 AA131172 AA085374 AA079519 AA074510 AA113824 AA102437 AA070833 AA070143 AA084693 AA084389 AA076373 AA075492 AA062834 AA084335 AA078829 AA079344 AA069916 AA079275 AA070914 AA654069 AA081976 AA080957 AA083115 AA070942 AA085296 |
| 123526 | genbank_AA608657 | AA608657 |
| 123533 | genbank_AA608751 | AA608751 |
| 125090 | genbank_T91518 | T91518 |
| 125154 | genbank_W38419 | W38419 |
| 118475 | genbank_N66845 | N66845 |
| 118505 | genbank_N67343 | N67343 |
| 101046 | entrez_K01160K01160 | |
| 129982 | 221_267 | Z14221 AW381862 M97920 AW401444 Z66542 M29470 AW406502 X61011 M34024 AA327072 Z14166 Z14167 Z14165 AW403806 Z14200 AA383972 Z14205 Z14201 M18513 Z14202 AW403684 X14584 AF062221 U43760 X65892 X65883 X62107 Z80847 X65885 X65893 AF062142 X65891 X17675 Z47274 Z47277 Z47276 X65888 Z47275 X62109 AF062140 L01278 AF062134 AF062139 X81723 Z80840 X81733 X81743 X81744 X81732 Z80843 AW402942 AW403516 X65919 AF062190 AF062177 AF062222 AF062115 Z47240 AF062263 AF062261 AF062223 AF062211 Z47238 AW401714 AW404008 AW404991 AF062280 M99595 Z47214 Z47232 Z47218 M26995 AF062184 X65895 L38433 X81731 Z11946 Z47226 AF062205 AF174012 L01276 AF062168 AF062136 X81755 X81748 AF174019 AF062285 L06924 L11699 AW402665 L09070 L28049 L08090 AW407843 Z14171 AW402944 L08083 AW405627 L33035 L26907 M17750 L28052 M17751 AJ239360 U19885 L14821 X56526 AB014341 L12087 L12098 U68231 L12184 AF062242 AF022000 U64499 U00570 AI268604 Y15773 X64239 X62969 U00506 X73605 X99360 U00577 D83677 AB021539 AF035796 Z33899 U00588 AJ239353 AF174062 Z33901 X98899 AF174058 X63080 D83676 AB021529 Z18318 U00488 L01412 X81746 U21262 U21272 U00560 AF174060 U00547 U00561 Z18321 S73957 M26435 AF115130 AF115117 Z92896 U21254 Z92895 AF115112 AF062290 T28938 Y09386 AF174067 U27189 Y09384 U77373 AF174057 M17749 X69692 AF174038 U64478 U64486 AF174098 X99365 AF174077 AF174083 AF174089 AF015133 AF127792 AJ006171 U00510 U58144 AF004323 AF115109 AF004324 AF015130 AF090414 AF090418 AB021536 AB021519 Z96957 AF021986 Z92898 Z96956 L34164 AF062251 AF052524 U00549 U00541 D83687 AF052522 AF087420 AF052520 AF022011 L43085 U00536 L19915 L43083 AF090420 AB021530 AB021534 Z96955 Z96954 Z33903 X62964 AF103282 U00509 AF062298 AF062289 AF062307 AW408326 L33037 L04337 L04328 X81742 L04336 L03385 AF032360 S56184 AF062191 AF191092 AI906954 AF103184 L04343 AW364860 AF001424 AF103163 Z98717 AF103143 AJ008250 L04323 AF103321 AF103335 L04342 L03818 L03817 AW404978 AW403690 U86801 AF103150 AJ010334 AF035027 AJ007327 AF103115 AF017458 AJ008207 AJ008183 AJ008196 AJ008241 AJ008208 AF103210 AF068668 AF068670 AF068671 AF068664 AF068669 AF068666 AF068665 AF068672 AW371244 AW403670 AW408074 AW404575 AW362153 AW403803 AW406702 AW351514 D78345 T29140 J00231 NM_002179 AW405146 AA301091 X04646 H64660 AW402990 AW406534 T93007 AI857980 AW368899 AI905833 AW406586 AA482084 AI872299 AA715266 AW404328 AI831674 AI709348 AA603112 AW514864 AA485775 H64492 AW404789 AA487630 AA715498 AA295885 T27613 T98113 |
| 108470 | genbank_AA079500 | AA079500 |
| 101447 | entrez_M21305 | M21305 |
| 124447 | genbank_N48000 | N48000 |
| 101624 | entrez_M55998 | M55998 |
| 131791 | 221_260 | X62111 S67984 AJ131056 Z47243 Z47235 AF062268 Z47237 AJ131058 AF062130 AF062282 X62108 AA385989 AA464794 X69861 AW402964 M90808 Z98735 Z98734 Z98736 AF035018 X79161 U00545 AF174046 AF174071 U00552 U96288 AF021989 AF062255 AF174061 S73953 AF062135 AF062155 X64147 U00555 AF174070 AF129754 U86789 Z98714 Z98738 S75886 AJ008175 AJ008186 AJ008188 Y08403 H15753 H22208 AA327241 AW405737 H42300 H39677 H26239 H26903 |

60

5 H45128 R86072 AA327565 AI660584 AW361537 AW383759 S71043 H15014 H45570 H42819 H45523 H45134 R72043
H24543 H27636 H27610 T28147 H25496 AW364071 AW364072 H45561 H45556 H42605 AI735017 T47421 R48719 H27570
H44599 AI459598 H42347 H41938 H24993 AA345888 H22339 AI538691 AJ012264 AA664201 AI880450 AA327310 AI991250
AI833028 AW001210 AI956075 H30467 AA326915 H41943 AI749266 AI744441 AA327377 AW512326 AI735170 H01634
AI587047 AI571623 AA327486 AA327103 AA327195 AA326973 T28143
124842 217726_1 R56485 R37248 R59992
103758 AA084874_f_at AA084874_f
130064 221_264 X57815 L29157 AA367448 AW328098 AW404536 L29156 L29163 H27683 R83195 AA295096 AW327822 H25458 AW404692
10 X57819 X57823 AW405604 AW404447 Z34914 AW406542 AA427726 AA604389 AW405606 AW405918 AW405117
AW407182 L03632 AW405058 L03627 AW407470 R72738 L21959 AW375738 X87888 AF124166 AF054638 AJ241406
U09902 AW405284 M12025 AA360219 L03631 L03629 AW327727 AF194810 AF058076 AF194686 AF063774 AF063737
AF063755 AF063740 AF063739 AF063738 S73129 L43088 AF063775 L33026 AF060138 AF194813 AF194812 AF194811
AF194809 AF194814 AF194808 AF064505 AF064503 AF063765 AF063757 AF063752 AF063716 AF063736 AF194806
15 AF058077 AF063747 AF063772 AF063781 AF060137 AF194805 AF060134 AF060132 AF058074 AF063754 AF063704
U38589 Z18332 AF060122 AF194807 AF060135 AF064506 AF064504 AF063773 L26540 AF058072 AF060131 AF064500
AF060136 AF064513 AF194683 AF194711 AF058075 AF063717 Z19546 AF194581 X72746 U96393 U09890 X98897
AF194592 M80916 AJ241405 AF194632 AJ388659 AF194625 Z74694 AF194588 AF194601 U09901 U09911 U09892
AJ010336 AJ006162 AJ249377 AJ241414 AA327392 U97248 X72747 Z46850 X95739 AW406701 AJ243109 AF194609
S80758 AF194595 AF194596 L22483 Z70262 D84141 AW405758 AF001788 AF194580 D84143 U76684 AF194593 L03630
20 X87892 X91134 U21249 Z46346 AJ132426 AF103659 AJ233718 AF021038 AJ233727 H24657 U09882 S75627 AA573599
AF047231 AF047232 AF103616 AW404484 Z46848 S76132 AF103663 AF103713 Y17940 AF047216 AF103595 Y17956
AF052799 AF052797 AF052802 AF052798 AF052801 AF052794 AF052796 AF047218 AF052800 AF047217 AF052795
AF032351 AF103701 AF103708 AF103710 AF103706 S62232 AF103645 AF103632 AF103647 AF103644 AF103640
AF103692 AF093581 AF103620 AW405934 AI445389 AW383753 AA360256 AF099676 H21654 H39501 AI820828 H53689
25 W26785 AW384496 AW407708 AA541663 AA911602 AI821461 AA588300 AA327050 H42717 AI951280 AA421322 AI923193
AA864302 H25133 D87023 J03011 M61771 D87017 AA526865 AA253450
130232 18831_2 U29463 U06715 W24970 AA584303 T39581 AA155603 AA305043 AA429426 W05664 AA102382 AA482044 W24487 AA319060
T88946 F10106 AA232161 AA243117 AA158937 AA100864
109097 genbank_AA167512 AA167512

TABLE 9: Figure 9 from BRCA 001-2 US

5 **Table 9** depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

| | | | | |
|----|----------------|---|-----------|--|
| 10 | Pkey: | Unique Eos probeset identifier number | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | |
| | UnigeneID: | Unigene number | | |
| | Unigene Title: | Unigene gene title | | |
| 15 | Pkey | ExAccn | UnigeneID | UnigeneTitle |
| | 100690 | AA383256 | Hs.1657 | estrogen receptor 1 |
| | 102211 | BE314524 | Hs.78776 | putative transmembrane protein |
| | 103587 | BE270266 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein |
| | 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal syndrome I |
| | 105038 | AW503733 | Hs.9414 | KIAA1488 protein |
| 20 | 105500 | AW602166 | Hs.222399 | CEGP1 protein |
| | 105990 | AI690586 | Hs.29403 | hypothetical protein FLJ22060 |
| | 106155 | AA425414 | Hs.33287 | nuclear factor I/B |
| | 106373 | AW503807 | Hs.21907 | histone acetyltransferase |
| | 106414 | BE568205 | Hs.28827 | mitogen-activated protein kinase kinase kinase 2 |
| 25 | 110009 | BE075297 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 precursor, Intestinal |
| | 111900 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence |
| | 114540 | AI904232 | Hs.75323 | prohibitin |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 |
| | 117280 | M18217 | Hs.172129 | Homo sapiens cDNA: FLJ21409 fis, clone COL03924 |
| 30 | 119771 | AI905687 | Hs.2533 | EST |
| | 121723 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 |
| | 124059 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothetical protein YGL050w |
| | 131148 | AW953575 | Hs.303125 | p53-induced protein PIGPC1 |
| | 132371 | AA235448 | Hs.46677 | PRO2000 protein |
| 35 | 134169 | AI690916 | Hs.178137 | transducer of ERBB2, 1 |
| | 302235 | AL049987 | Hs.166361 | Homo sapiens mRNA; cDNA DKFZp564F112 |
| | 452410 | AL133619 | Hs.29383 | Homo sapiens mRNA; cDNA DKFZp434 |

TABLE 10: Figure 10 from BRCA 001-3 PCT

5 **Table 10 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.**

10 Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue
 R2: Ratio of 90th percentile tumor to body
 R3: Ratio of 75th percentile body to tumor
 R4: Ratio of tumor to normal breast tissue

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 | R3 | R4 |
|--------|-----------|-----------|--|------|------|-----|------|
| 10082 | AA130080 | Hs.4295 | proteasome (prosome, macropain) 26S subu | 4.2 | 152 | 36 | 12.2 |
| 100103 | AA380887 | Hs.5085 | dolichyl-phosphate mannosyltransferase p | 9.8 | 123 | 13 | 5 |
| 100131 | D12485 | Hs.11951 | ectonucleotide pyrophosphatase/phosphodi | 13.2 | 244 | 19 | 9.9 |
| 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fasciclin | 15.7 | 1030 | 66 | 5 |
| 100154 | H60720 | Hs.81892 | KIAA0101 gene product | 4.1 | 320 | 78 | 10.6 |
| 100157 | D14661 | Hs.119 | Wilms' tumour 1-associating protein | 4.7 | 119 | 26 | 3 |
| 100169 | AL037228 | Hs.82043 | D123 gene product | 5.1 | 106 | 21 | 9.2 |
| 100203 | BE242284 | Hs.172199 | adenylate cyclase 7 | 4.7 | 47 | 1 | 4.3 |
| 100210 | D26361 | Hs.3104 | KIAA0042 gene product | 4.7 | 47 | 4 | 0.7 |
| 100219 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 3.8 | 350 | 93 | 1.9 |
| 100234 | D29677 | Hs.3085 | KIAA0054 gene product Helicase | 4.1 | 64 | 16 | 3 |
| 100248 | NM_015156 | Hs.78398 | KIAA0071 protein | 3.4 | 77 | 23 | 5.9 |
| 100252 | NM_006207 | Hs.170040 | platelet-derived growth factor receptor- | 4.5 | 45 | 4 | 4 |
| 100260 | D38491 | Hs.322478 | KIAA0117 protein | 5.9 | 59 | 1 | 2.6 |
| 100279 | D42084 | Hs.82007 | KIAA0094 protein | 3.5 | 96 | 28 | 1.3 |
| 100286 | BE247550 | Hs.86859 | growth factor receptor-bound protein 7 | 3.1 | 306 | 98 | 1.5 |
| 100294 | AA331881 | Hs.75454 | peroxiredoxin 3 | 12.8 | 128 | 1 | 11.7 |
| 100335 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 4.2 | 187 | 44 | 5.4 |
| 100365 | AI878927 | Hs.79284 | mesoderm specific transcript (mouse) hom | 4.5 | 129 | 29 | 3.1 |
| 100375 | D80004 | Hs.75909 | KIAA0182 protein | 3.5 | 78 | 23 | 4.8 |
| 100409 | D86957 | Hs.80712 | KIAA0202 protein | 10.2 | 102 | 1 | 4.8 |
| 100410 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 4 | 40 | 1 | 3.8 |
| 100414 | NM_014735 | Hs.82292 | KIAA0215 gene product | 3.2 | 32 | 2 | 2.9 |
| 100418 | D86978 | Hs.84790 | KIAA0225 protein | 3.6 | 36 | 7 | 3.2 |
| 100438 | AA013051 | Hs.91417 | topoisomerase (DNA) II binding protein | 5.6 | 76 | 14 | 2 |
| 100439 | AA347720 | Hs.122669 | KIAA0264 protein | 3.5 | 35 | 9 | 3.1 |
| 100448 | AF234887 | Hs.57652 | cadherin, EGF LAG seven-pass G-type rece | 5.5 | 145 | 27 | 2.2 |
| 100449 | D87470 | Hs.75400 | KIAA0280 protein | 3.4 | 34 | 1 | 1.2 |
| 100522 | X51501 | Hs.99949 | prolactin-induced protein | 22.7 | 760 | 34 | 1.4 |
| 100552 | AA019521 | Hs.301946 | lysosomal | 14.4 | 144 | 9 | 4.7 |
| 100643 | NM_005032 | Hs.4114 | plastin 3 (T isoform) | 4.1 | 259 | 63 | 1.9 |
| 100661 | BE623001 | Hs.132748 | Homo sapiens ribosomal protein L39 mRNA, | 3.3 | 116 | 36 | 2.2 |
| 100666 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 8.5 | 85 | 1 | 3.2 |
| 100667 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 3 | 594 | 201 | 2.3 |
| 100745 | BE207168 | Hs.144630 | nuclear receptor subfamily 2, group F, m | 5 | 82 | 17 | 0.9 |
| 100774 | J05581 | Hs.89603 | mucin 1, transmembrane | 3.5 | 37 | 11 | 2.8 |
| 100783 | AF078847 | Hs.191356 | general transcription factor IIH, polype | 9.7 | 97 | 10 | 7.2 |
| 100821 | M26460 | | gb:Homo sapiens (clone 104) retinoblasto | 3.3 | 33 | 1 | 0.8 |
| 100864 | BE563957 | Hs.74861 | activated RNA polymerase II transcriptio | 3.7 | 477 | 130 | 3.1 |
| 100877 | X80821 | Hs.27973 | KIAA0874 protein | 6.3 | 63 | 4 | 5.7 |
| 100892 | BE245294 | Hs.180789 | S164 protein | 4.7 | 47 | 1 | 4.2 |
| 101038 | BE297139 | Hs.79411 | replication protein A2 (32kD) | 3.8 | 115 | 30 | 7.1 |
| 101046 | K01160 | | NM_002122:Homo sapiens major histocompat | 3.9 | 390 | 100 | 11.1 |
| 101079 | BE264901 | Hs.250502 | carbonic anhydrase VIII | 3.9 | 39 | 8 | 3.6 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| | 101084 | AW409934 | Hs.75528 | nucleolar GTPase | 4.1 | 53 | 13 | 4 |
| | 101104 | AW862258 | Hs.169266 | neuropeptide Y receptor Y1 | 15.3 | 153 | 1 | 14.1 |
| | 101185 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 11.3 | 113 | 8 | 3.9 |
| 5 | 101188 | L20320 | Hs.184298 | cyclin-dependent kinase 7 (homolog of Xe | 3.1 | 118 | 38 | 2 |
| | 101201 | L22524 | Hs.2256 | matrix metalloproteinase 7 (MMP7; uterin | 8.2 | 396 | 48 | 0.9 |
| | 101232 | AU077288 | Hs.242894 | ADP-ribosylation factor-like 1 | 4 | 110 | 28 | 10.7 |
| | 101275 | BE545277 | Hs.3273 | Ts translation elongation factor, mitoch | 4.2 | 50 | 12 | 4.4 |
| | 101300 | BE535511 | Hs.74137 | transmembrane trafficking protein | 6.6 | 135 | 21 | 13.1 |
| 10 | 101396 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 6.4 | 249 | 39 | 22.4 |
| | 101447 | M21305 | | gb:Human alpha satellite and satellite 3 | 6.5 | 878 | 135 | 0.8 |
| | 101448 | NM_000424 | Hs.195850 | keratin 5 (epidermolysis bullosa simplex | 4.8 | 622 | 130 | 0.7 |
| | 101470 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 5.1 | 97 | 19 | 9.3 |
| | 101478 | NM_002890 | Hs.758 | RAS p21 protein activator (GTPase activa | 9.6 | 96 | 1 | 8.5 |
| 15 | 101484 | AA053486 | Hs.20315 | interferon-induced protein with tetratri | 11.2 | 112 | 8 | 5.9 |
| | 101507 | X16896 | Hs.82112 | interleukin 1 receptor, type I | 3.9 | 39 | 2 | 3.5 |
| | 101621 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 3.6 | 36 | 1 | 2.6 |
| | 101624 | M55998 | | gb:Human alpha-1 collagen type I gene, 3 | 3.1 | 2898 | 923 | 2.2 |
| | 101684 | AA436989 | Hs.121017 | H2A histone family, member A | 6.9 | 103 | 15 | 8.4 |
| 20 | 101684 | M63256 | Hs.75124 | cerebellar degeneration-related protein | 6.4 | 64 | 2 | 4.9 |
| | 101724 | L11690 | Hs.620 | bullous pemphigoid antigen 1 (230/240kD) | 9.4 | 94 | 1 | 0.3 |
| | 101754 | S70114 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-bi | 8.9 | 89 | 5 | 8 |
| | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 3.6 | 824 | 227 | 1.4 |
| | 101791 | M83822 | Hs.62354 | cell division cycle 4-like | 9 | 144 | 16 | 13 |
| 25 | 101794 | M84605 | Hs.957 | putative opioid receptor, neuromedin K (| 3.3 | 36 | 11 | 2.4 |
| | 101803 | AW024390 | Hs.155691 | pre-B-cell leukemia transcription factor | 5.4 | 180 | 34 | 15.9 |
| | 101809 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 12 | 120 | 8 | 9 |
| | 101839 | AA446644 | Hs.692 | GA733-2 antigen; epithelial glycoprotein | 3.1 | 353 | 116 | 2.8 |
| | 101888 | AL049610 | Hs.95243 | transcription elongation factor A (SII)- | 7.3 | 73 | 1 | 5.3 |
| 30 | 101960 | AL036287 | Hs.194662 | calponin 3, acidic | 3.8 | 399 | 105 | 3.3 |
| | 102009 | BE245149 | Hs.82643 | protein tyrosine kinase 9 | 4.6 | 148 | 32 | 11.3 |
| | 102095 | U11313 | Hs.75760 | sterol carrier protein 2 | 9.5 | 95 | 4 | 8.8 |
| | 102123 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 4.2 | 42 | 7 | 3.4 |
| | 102125 | NM_006456 | Hs.288215 | sialyltransferase | 9.3 | 93 | 4 | 3 |
| 35 | 102139 | NM_004419 | Hs.2128 | dual specificity phosphatase 5 | 5.4 | 137 | 26 | 2.5 |
| | 102162 | AA450274 | Hs.1592 | CDC16 (cell division cycle 16, S. cerevi | 4.6 | 151 | 33 | 2 |
| | 102165 | BE313280 | Hs.159627 | death associated protein 3 | 9.3 | 93 | 5 | 8 |
| | 102193 | AL036335 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 45.7 | 457 | 1 | 39.7 |
| | 102211 | BE314524 | Hs.78776 | putative transmembrane protein | 3.9 | 442 | 114 | 1.3 |
| 40 | 102221 | NM_006769 | Hs.3844 | LIM domain only 4 | 4.9 | 49 | 1 | 3.6 |
| | 102242 | U27185 | Hs.82547 | retinoic acid receptor responder (tazaro | 3.1 | 31 | 1 | 1.3 |
| | 102258 | NM_001546 | Hs.34853 | Inhibitor of DNA binding 4, dominant neg | 3.8 | 163 | 43 | 0.5 |
| | 102302 | AA306342 | Hs.69171 | protein kinase C-like 2 | 4.5 | 45 | 1 | 3.6 |
| | 102304 | AF015224 | Hs.46452 | mammaglobin 1 | 8.5 | 2058 | 243 | 1.4 |
| 45 | 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 6.4 | 428 | 67 | 2.3 |
| | 102369 | U39840 | Hs.299867 | hepatocyte nuclear factor 3, alpha | 6.7 | 67 | 9 | 6.3 |
| | 102407 | AW602154 | Hs.82143 | E74-like factor 2 (ets domain transcript | 5.3 | 53 | 1 | 4.8 |
| | 102409 | BE300330 | Hs.118725 | selenophosphate synthetase 2 | 3.3 | 111 | 34 | 7.5 |
| | 102457 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 20.2 | 202 | 5 | 1.3 |
| 50 | 102544 | NM_003937 | Hs.169139 | kynureninase (L-kynurenine hydrolase) | 3.8 | 38 | 1 | 1.5 |
| | 102567 | U63830 | Hs.146847 | TRAF family member-associated NFKB activ | 8.2 | 82 | 1 | 6.8 |
| | 102580 | U60808 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 4.1 | 41 | 1 | 3.3 |
| | 102618 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 10.2 | 628 | 62 | 17.2 |
| | 102638 | U67319 | Hs.9216 | caspase 7, apoptosis-related cysteine pr | 5 | 66 | 13 | 5.3 |
| 55 | 102663 | NM_002270 | Hs.168075 | karyopherin (importin) beta 2 | 6.1 | 126 | 21 | 2.4 |
| | 102669 | U71207 | Hs.29279 | eyes absent (Drosophila) homolog 2 | 4.5 | 45 | 1 | 2.8 |
| | 102742 | U79293 | Hs.159264 | Human clone 23948 mRNA sequence | 4.1 | 41 | 1 | 2.4 |
| | 102784 | U85658 | Hs.61796 | transcription factor AP-2 gamma (activat | 4.4 | 255 | 58 | 1.6 |
| | 102805 | U90304 | Hs.25351 | Iroquois homeobox protein 5 | 3.6 | 142 | 39 | 1.6 |
| 60 | 102813 | BE242035 | Hs.151461 | embryonic ectoderm development | 3.5 | 35 | 1 | 2.7 |
| | 102823 | D85390 | Hs.5057 | carboxypeptidase D | 5.6 | 56 | 1 | 5.3 |
| | 102825 | BE262386 | Hs.7137 | clones 23667 and 23775 zinc finger prote | 4.2 | 42 | 7 | 3.7 |
| | 102899 | AI815559 | Hs.75730 | signal recognition particle receptor (d | 3.2 | 58 | 18 | 5 |
| | 102913 | NM_002275 | Hs.80342 | keratin 15 | 5.8 | 753 | 131 | 0.4 |
| 65 | 102927 | BE512730 | Hs.65114 | keratin 18 | 3.1 | 815 | 266 | 1.7 |
| | 102961 | AL119505 | Hs.198166 | activating transcription factor 2 | 3.2 | 32 | 4 | 2.6 |
| | 102968 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase | 5.7 | 251 | 44 | 6.6 |
| | 103003 | AI910275 | Hs.1406 | trefoil factor 1 (pS2) | 5.6 | 1346 | 239 | 5.4 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| | 103023 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 5.8 | 218 | 38 | 13 |
| | 103024 | NM_002343 | Hs.105938 | lactotransferrin | 3.7 | 1421 | 388 | 1.9 |
| | 103036 | M13509 | Hs.83169 | matrix metalloproteinase 1 (MMP1; inters | 3.1 | 94 | 30 | 5.8 |
| | 103038 | AA926960 | Hs.334883 | CDC28 protein kinase 1 | 3.5 | 332 | 94 | 3.1 |
| 5 | 103119 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 4.8 | 312 | 65 | 30.9 |
| | 103134 | X65724 | Hs.2839 | Norie disease (pseudoglioma) | 5.2 | 331 | 64 | 1.5 |
| | 103134 | X65724 | Hs.2839 | Norie disease (pseudoglioma) | 4.9 | 49 | 5 | 3.8 |
| | 103171 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 3.3 | 1497 | 458 | 2.1 |
| | 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 3.5 | 796 | 228 | 3.2 |
| 10 | 103208 | AW411340 | Hs.31314 | retinoblastoma-binding protein 7 | 5.6 | 191 | 34 | 3.5 |
| | 103226 | X75042 | Hs.44313 | v-rel avian reticuloendotheliosis viral | 4.1 | 53 | 13 | 4.9 |
| | 103333 | AA206186 | Hs.79889 | monocyte to macrophage differentiation-a | 3.4 | 34 | 8 | 2.3 |
| | 103346 | X87613 | Hs.5464 | thyroid hormone receptor coactivating pr | 3.9 | 43 | 11 | 1 |
| | 103352 | H09366 | Hs.78853 | uracil-DNA glycosylase | 9.3 | 93 | 8 | 8.2 |
| 15 | 103375 | NM_005982 | Hs.54416 | sine oculis homeobox (Drosophila) homolo | 9.7 | 97 | 1 | 9.3 |
| | 103376 | AL036166 | Hs.323378 | coated vesicle membrane protein | 6.3 | 98 | 16 | 9.1 |
| | 103391 | X94453 | Hs.114366 | pyrroline-5-carboxylate synthetase (glut | 4.3 | 77 | 18 | 7.2 |
| | 103438 | AW175781 | Hs.152720 | M-phase phosphoprotein 6 | 4.9 | 153 | 31 | 2.4 |
| | 103453 | AI878922 | Hs.180139 | SMT3 (suppressor of mit two 3, yeast) ho | 4.9 | 261 | 53 | 3.7 |
| 20 | 103471 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 3.5 | 564 | 162 | 1.7 |
| | 103500 | AW408009 | Hs.22580 | alkylglycerone phosphate synthase | 3.9 | 49 | 13 | 2.5 |
| | 103557 | AL133415 | Hs.297753 | vimentin | 7.5 | 136 | 18 | 3.4 |
| | 103587 | BE270266 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein | 7.9 | 79 | 2 | 6.9 |
| | 103605 | BE409838 | Hs.194657 | cadherin 1, type 1, E-cadherin (epitheli | 3.3 | 745 | 229 | 1.8 |
| 25 | 103606 | AW403814 | Hs.41714 | BCL2-associated athanogene | 3.2 | 41 | 13 | 2.8 |
| | 103613 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 7.3 | 73 | 1 | 5.2 |
| | 103658 | NM_000088 | Hs.172928 | collagen, type I, alpha 1 | 3.8 | 1612 | 429 | 3.1 |
| | 103666 | NM_003528 | Hs.2178 | H2B histone family, member Q | 3.2 | 32 | 5 | 2.8 |
| | 103988 | AA314389 | Hs.42500 | ADP-ribosylation factor-like 5 | 3.2 | 32 | 9 | 2.7 |
| 30 | 103990 | AB033112 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.9 | 49 | 1 | 4.2 |
| | 104052 | NM_002407 | Hs.97644 | mammaglobin 2 | 7.2 | 498 | 69 | 9.3 |
| | 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal | 29 | 290 | 1 | 26.8 |
| | 104129 | H63349 | Hs.98806 | hypothetical protein | 3.7 | 37 | 7 | 2.1 |
| | 104146 | AW880614 | Hs.146381 | RNA binding motif protein, X chromosome | 5.2 | 52 | 1 | 4.3 |
| 35 | 104147 | BE081342 | Hs.283037 | HSPC039 protein | 8 | 84 | 11 | 6.3 |
| | 104209 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 5.8 | 58 | 1 | 3.2 |
| | 104239 | AB002367 | Hs.21355 | doublecortin and CaM kinase-like 1 | 6.4 | 64 | 8 | 3 |
| | 104278 | AW583693 | Hs.109253 | N-terminal acetyltransferase complex ard | 4.7 | 229 | 49 | 7.9 |
| | 104309 | AI337300 | Hs.284123 | hypothetical protein MGC4604 | 3.2 | 32 | 7 | 2.4 |
| 40 | 104394 | AA129551 | Hs.172129 | Homo sapiens cDNA: FLJ21409 fis, clone C | 5.3 | 144 | 27 | 13.1 |
| | 104432 | X51501 | Hs.99949 | prolactin-induced protein | 6.9 | 1494 | 218 | 1.3 |
| | 104558 | R56678 | Hs.88959 | hypothetical protein MGC4816 | 7.7 | 77 | 8 | 6.9 |
| | 104567 | AA040620 | Hs.5672 | hypothetical protein AF140225 | 3.7 | 37 | 5 | 2.5 |
| 45 | 104590 | AW373062 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 6.1 | 493 | 81 | 0.7 |
| | 104602 | H47610 | | gb:yp75f03.s1 Soares fetal liver spleen | 3.8 | 38 | 4 | 1.2 |
| | 104613 | AF123303 | Hs.24713 | hypothetical protein | 4.8 | 231 | 49 | 7.3 |
| | 104633 | H00820 | Hs.30977 | ESTs, Weakly similar to B34087 hypotheti | 3.4 | 154 | 46 | 3 |
| | 104636 | R82252 | Hs.106106 | protein kinase (cAMP-dependent, catalyti | 5 | 468 | 94 | 4.7 |
| | 104660 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (fr | 3.8 | 82 | 22 | 3.1 |
| 50 | 104667 | AI239923 | Hs.30098 | ESTs | 14.9 | 149 | 1 | 6.4 |
| | 104766 | BE244072 | Hs.20815 | macrophage erythroblast attacher | 6.3 | 165 | 26 | 3.2 |
| | 104787 | AA027317 | | gb:ze97d11.s1 Soares_fetal_heart_NbHH19W | 3.8 | 40 | 11 | 3.8 |
| | 104804 | AI858702 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapien | 7.7 | 77 | 1 | 5.1 |
| 55 | 104807 | AI139058 | Hs.125790 | leucine-rich repeat-containing 2 | 7 | 70 | 1 | 6.5 |
| | 104846 | AI250789 | Hs.32478 | ESTs | 4.7 | 201 | 43 | 4.5 |
| | 104896 | AW015318 | Hs.23165 | ESTs | 7.4 | 74 | 1 | 6 |
| | 104919 | AA026880 | Hs.25252 | prolactin receptor | 3.9 | 280 | 72 | 3.3 |
| | 104926 | BE298808 | Hs.33363 | DKFZP434N093 protein | 4.2 | 135 | 32 | 4 |
| | 104943 | AF072873 | Hs.114218 | frizzled (Drosophila) homolog 6 | 16.2 | 162 | 1 | 4.2 |
| 60 | 104968 | AI249502 | Hs.29669 | ESTs | 3.8 | 38 | 1 | 2.4 |
| | 104977 | AI392640 | Hs.18272 | amino acid transporter system A1 | 3.2 | 522 | 165 | 1.9 |
| | 104997 | AA121686 | Hs.10692 | ESTs | 3.2 | 32 | 4 | 2.9 |
| | 105029 | AI122691 | Hs.13268 | ESTs | 3.7 | 157 | 43 | 3.6 |
| | 105038 | AW503733 | Hs.9414 | KIAA1488 protein | 5.5 | 55 | 1 | 5.2 |
| 65 | 105041 | AB037716 | Hs.26204 | KIAA1295 protein | 10.3 | 103 | 1 | 3.9 |
| | 105086 | AA148710 | Hs.79914 | lumican | 6.6 | 66 | 1 | 5.4 |
| | 105088 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PL | 3.1 | 31 | 1 | 2.5 |

| | | | | | | | | |
|----|--------|-----------|-----------|---|------|-----|------|------|
| | 105091 | AA148859 | Hs.179909 | hypothetical protein FLJ22995 | 3.2 | 32 | 1 | 3 |
| | 105143 | AI368836 | Hs.24808 | ESTs, Weakly similar to I38022 hypotheti | 7.3 | 73 | 1 | 3.8 |
| | 105154 | AA307279 | Hs.35947 | methyl-CpG binding domain protein 4 | 4.2 | 90 | 22 | 2.8 |
| 5 | 105162 | AL133033 | Hs.4084 | KIAA1025 protein | 6 | 60 | 6 | 4.6 |
| | 105167 | AW612147 | Hs.32058 | Homo sapiens C1orf19 mRNA, partial cds | 3.8 | 38 | 2 | 3.2 |
| | 105178 | AA313825 | Hs.21941 | AD036 protein | 9.3 | 436 | 47 | 5.8 |
| | 105195 | AA975096 | Hs.19522 | hypothetical protein PRO2849 | 5.7 | 57 | 8 | 5.3 |
| | 105200 | AA328102 | Hs.24641 | cytoskeleton associated protein 2 | 4.5 | 45 | 1 | 3.6 |
| 10 | 105248 | AW952479 | Hs.22826 | tropomodulin 3 (ubiquitous) | 4.3 | 43 | 1 | 3.9 |
| | 105252 | AB039670 | Hs.9728 | ALEX1 protein | 8 | 80 | 6 | 7.3 |
| | 105253 | AW997484 | Hs.5003 | KIAA0456 protein | 3.9 | 39 | 6 | 3.2 |
| | 105280 | AA894638 | Hs.14600 | ESTs | 3.5 | 35 | 7 | 2.7 |
| | 105288 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DNAJ | 4.5 | 45 | 10 | 0.5 |
| 15 | 105309 | AK000796 | Hs.4104 | hypothetical protein | 3.8 | 93 | 25 | 7.5 |
| | 105329 | AA234561 | Hs.22862 | ESTs | 2.8 | 131 | 47 | 3.9 |
| | 105344 | AF151073 | Hs.8645 | hypothetical protein | 3.9 | 79 | 20 | 6.5 |
| | 105376 | AW994032 | Hs.8768 | hypothetical protein FLJ10849 | 5.1 | 181 | 36 | 15.8 |
| | 105386 | AW500718 | Hs.8115 | Homo sapiens, clone MGC:16169, mRNA, com | 4.1 | 41 | 2 | 3.3 |
| 20 | 105400 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 6.2 | 62 | 6 | 5.6 |
| | 105426 | W20027 | Hs.23439 | ESTs | 3.3 | 206 | 63 | 2.2 |
| | 105483 | AL137257 | Hs.23458 | Homo sapiens cDNA: FLJ23015 fis, clone L | 3.2 | 466 | 146 | 8.4 |
| | 105496 | AL117441 | Hs.301997 | hypothetical protein FLJ13033 | 16.6 | 166 | 8 | 12.7 |
| | 105500 | AW602166 | Hs.222399 | CEGP1 protein | 25.4 | 508 | 20 | 3 |
| 25 | 105508 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f9 | 117 | 13 | 10.6 | |
| | 105511 | AB037829 | Hs.3862 | regulator of nonsense transcripts 2; DKF | 3.2 | 32 | 6 | 1.5 |
| | 105516 | AK001269 | Hs.30738 | hypothetical protein FLJ10407 | 8.3 | 83 | 3 | 1.8 |
| | 105539 | AB040884 | Hs.109694 | KIAA1451 protein | 3.5 | 73 | 21 | 1.6 |
| | 105564 | BE616694 | Hs.288042 | hypothetical protein FLJ14299 | 5.8 | 336 | 58 | 2 |
| 30 | 105610 | AA280072 | Hs.99872 | fetal Alzheimer antigen | 3.2 | 32 | 1 | 1 |
| | 105616 | R35343 | Hs.24968 | Human DNA sequence from clone RP1-233G16 | 4.8 | 79 | 17 | 5.2 |
| | 105627 | AA281279 | Hs.23317 | hypothetical protein FLJ14681 | 4 | 75 | 19 | 1.7 |
| | 105640 | AA001021 | Hs.6685 | thyroid hormone receptor interactor 8 | 4.5 | 45 | 1 | 3.7 |
| | 105645 | AW294631 | Hs.11325 | ESTs | 3.6 | 36 | 1 | 0.1 |
| 35 | 105674 | AI609530 | Hs.279789 | histone deacetylase 3 | 6.4 | 64 | 8 | 6 |
| | 105687 | NM_014517 | Hs.28423 | upstream binding protein 1 (LBP-1a) | 4.7 | 152 | 33 | 5.3 |
| | 105691 | AI680737 | Hs.289068 | Homo sapiens cDNA FLJ11918 fis, clone HE | 5.7 | 57 | 8 | 4.1 |
| | 105730 | AW377314 | Hs.5364 | DKFZP564I052 protein | 6.9 | 69 | 1 | 4.4 |
| | 105731 | AA834664 | Hs.29131 | nuclear receptor coactivator 2 | 3.4 | 34 | 1 | 3.1 |
| 40 | 105743 | BE246502 | Hs.9598 | sema domain, immunoglobulin domain (Ig), | 3 | 30 | 10 | 0.9 |
| | 105759 | AI123118 | Hs.15159 | chemokine-like factor, alternatively spl | 5.4 | 54 | 1 | 4.4 |
| | 105772 | H57111 | Hs.221132 | ESTs | 5.3 | 67 | 13 | 5.3 |
| | 105774 | AW369278 | Hs.23412 | hypothetical protein FLJ20160 | 4.9 | 49 | 1 | 4.5 |
| | 105784 | W84446 | Hs.226434 | hypothetical protein MGC4643 | 3.3 | 98 | 30 | 4.7 |
| 45 | 105795 | AA878183 | Hs.17448 | Homo sapiens cDNA FLJ13618 fis, clone PL | 3.2 | 143 | 46 | 3.6 |
| | 105806 | AF206019 | Hs.110347 | REV1 (yeast homolog)-like | 4 | 40 | 3 | 3.2 |
| | 105807 | AA788946 | Hs.16869 | ESTs, Moderately similar to CA1C RAT COL | 4.7 | 747 | 158 | 5.7 |
| | 105823 | AI559444 | Hs.293960 | ESTs | 3.9 | 371 | 94 | 4.8 |
| | 105832 | AW802282 | Hs.22265 | pyruvate dehydrogenase phosphatase | 3.6 | 68 | 19 | 6 |
| 50 | 105840 | AA601518 | Hs.22209 | secreted modular calcium-binding protein | 4.8 | 134 | 28 | 3.2 |
| | 105851 | AI827976 | Hs.24391 | hypothetical protein FLJ13612 | 4.3 | 772 | 179 | 1.7 |
| | 105864 | AI640775 | Hs.28332 | Homo sapiens cDNA: FLJ21560 fis, clone C | 4.3 | 43 | 1 | 3.7 |
| | 105870 | AW021691 | Hs.101067 | GCN5 (general control of amino-acid synt | 3.6 | 36 | 7 | 3.1 |
| | 105875 | AK001708 | Hs.32271 | hypothetical protein FLJ10846 | 3.4 | 34 | 8 | 2.9 |
| 55 | 105886 | AK001735 | Hs.22983 | UDP-glucose:glycoprotein glucosyltransfe | 3.6 | 45 | 13 | 1.3 |
| | 105906 | N25986 | Hs.22380 | ESTs | 3.4 | 34 | 1 | 1.5 |
| | 106012 | AI240665 | Hs.8895 | ESTs | 21.2 | 212 | 6 | 17.4 |
| | 106020 | AA043039 | Hs.7870 | hypothetical protein | 3.9 | 47 | 12 | 4.4 |
| | 106024 | AL122072 | Hs.103804 | heterogeneous nuclear ribonucleoprotein | 4.4 | 174 | 40 | 1.6 |
| 60 | 106034 | AW952005 | Hs.14928 | hypothetical protein FLJ12903 | 4.7 | 47 | 1 | 4 |
| | 106036 | AA382267 | Hs.10653 | ESTs | 3.4 | 49 | 15 | 4.4 |
| | 106055 | AA417034 | | gb:zu04f10.s1 Soares_testis_NHT Homo sap | 3.5 | 53 | 15 | 1.2 |
| | 106057 | BE614474 | Hs.289074 | F-box only protein 22 | 3.4 | 116 | 35 | 2.2 |
| | 106060 | NM_001329 | Hs.171391 | C-terminal binding protein 2 | 3.6 | 444 | 125 | 4.6 |
| | 106070 | T74445 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 3.6 | 365 | 103 | 6.9 |
| 65 | 106095 | AF115402 | Hs.11713 | E74-like factor 5 (ets domain transcript | 26.3 | 356 | 14 | 1 |
| | 106096 | AW379378 | Hs.170121 | protein tyrosine phosphatase, receptor t | 3.2 | 267 | 83 | 2.3 |
| | 106126 | AA576953 | Hs.22972 | hypothetical protein FLJ13352 | 3.8 | 38 | 1 | 3.3 |

| | | | | | | | | |
|----|--------|-----------|-----------|---|------|-----|-----|------|
| 5 | 106155 | AA425414 | Hs.33287 | nuclear factor I/B | 9.9 | 483 | 49 | 1.8 |
| | 106157 | W37943 | Hs.34892 | KIAA1323 protein | 6.7 | 94 | 14 | 8 |
| | 106198 | AI244563 | Hs.325531 | Homo sapiens clone 015h12 My015 protein | 3.3 | 95 | 29 | 4.4 |
| | 106236 | AB040896 | Hs.21104 | KIAA1463 protein | 3.8 | 83 | 22 | 7.5 |
| | 106286 | AI765107 | Hs.274422 | hypothetical protein FLJ20550 | 3.3 | 97 | 30 | 6.4 |
| 10 | 106290 | AW961393 | Hs.16364 | hypothetical protein FLJ10955 | 4.5 | 116 | 26 | 4.5 |
| | 106310 | R98185 | Hs.17240 | ESTs | 7 | 70 | 3 | 1.3 |
| | 106323 | AB007866 | Hs.158249 | KIAA0406 gene product | 3.2 | 37 | 12 | 2.6 |
| | 106330 | AW977397 | Hs.35580 | ESTs | 3.8 | 38 | 1 | 1.9 |
| | 106383 | AA447453 | Hs.27860 | Homo sapiens mRNA; cDNA DKFZp586M0723 (f16 | 255 | 16 | 6.6 | |
| 15 | 106389 | AW748420 | Hs.6236 | Homo sapiens cDNA: FLJ21487 fis, clone C | 4.9 | 337 | 70 | 2.7 |
| | 106394 | Z42993 | Hs.25320 | Homo sapiens clone 25142 mRNA sequence | 3.1 | 72 | 23 | 5 |
| | 106432 | AK000310 | Hs.17138 | hypothetical protein FLJ20303 | 3.1 | 165 | 54 | 1.6 |
| | 106459 | AA789081 | Hs.4029 | glioma-amplified sequence-41 | 3.1 | 31 | 1 | 2.6 |
| | 106503 | AB033042 | Hs.29679 | cofactor required for Sp1 transcription | 5.5 | 147 | 27 | 4.4 |
| 20 | 106508 | AI205785 | Hs.30348 | ESTs | 4.4 | 222 | 51 | 1.8 |
| | 106565 | NM_014892 | Hs.227602 | KIAA1116 protein | 7.4 | 74 | 3 | 1.7 |
| | 106586 | AA243837 | Hs.57787 | ESTs | 15.2 | 152 | 1 | 12.6 |
| | 106589 | AK000933 | Hs.28661 | Homo sapiens cDNA FLJ10071 fis, clone HE | 3.8 | 263 | 69 | 3.9 |
| | 106596 | AA452379 | Hs.293552 | ESTs, Moderately similar to ALU7_HUMAN A | 4.9 | 49 | 1 | 4.1 |
| 25 | 106611 | R49131 | Hs.26267 | ATP-dependant interferon response protei | 5.8 | 58 | 5 | 3.1 |
| | 106628 | AW188205 | Hs.12311 | Homo sapiens clone 23570 mRNA sequence | 5.3 | 166 | 32 | 14.9 |
| | 106650 | AL049951 | Hs.22370 | Homo sapiens mRNA; cDNA DKFZp564O0122 (f5.4 | 75 | 14 | 0.8 | |
| | 106683 | BE296396 | Hs.14512 | DIPB protein | 3.6 | 210 | 58 | 4.7 |
| | 106698 | N28524 | Hs.29403 | hypothetical protein FLJ22060 | 5.7 | 57 | 10 | 4.8 |
| 30 | 106710 | N38902 | Hs.334437 | hypothetical protein MGC4248 | 4.4 | 371 | 84 | 3.2 |
| | 106717 | AA600357 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-bi | 4.3 | 101 | 24 | 1.6 |
| | 106747 | NM_007118 | Hs.171957 | triple functional domain (PTPRF interact | 4.6 | 46 | 1 | 4. |
| | 106834 | AL044182 | Hs.28070 | KIAA0753 gene product | 3.5 | 58 | 17 | 1.6 |
| | 106846 | AB037744 | Hs.34892 | KIAA1323 protein | 5.4 | 192 | 36 | 4.4 |
| 35 | 106868 | BE185536 | Hs.301183 | molecule possessing ankyrin repeats indu | 3.3 | 696 | 214 | 1.8 |
| | 106882 | AA149537 | Hs.26994 | hypothetical protein FLJ20477 | 3.8 | 38 | 1 | 1.6 |
| | 106893 | AA835868 | Hs.25253 | mannosidase, alpha, class 1A, member 1 | 4.3 | 43 | 10 | 2.2 |
| | 106895 | AK001826 | Hs.25245 | hypothetical protein FLJ11269 | 3.6 | 36 | 1 | 1.2 |
| | 106897 | AF039023 | Hs.167496 | RAN binding protein 6 | 4.5 | 45 | 1 | 3.8 |
| 40 | 106916 | AA134329 | Hs.24170 | Homo sapiens, clone IMAGE:3685398, mRNA, | 5.7 | 94 | 17 | 7.3 |
| | 106962 | AI868648 | Hs.22315 | ESTs | 3.5 | 180 | 52 | 2.3 |
| | 106968 | AF216751 | Hs.26813 | CDA14 | 5.5 | 130 | 24 | 12.5 |
| | 106990 | AA280722 | Hs.24758 | ESTs, Weakly similar to I38022 hypotheti | 3.2 | 266 | 83 | 1.8 |
| | 107008 | AL157479 | Hs.23740 | KIAA1598 protein | 5.1 | 298 | 59 | 4.4 |
| 45 | 107014 | AA598820 | | gb:ae36h12.s1 Gessler Wilms tumor Homo s | 3.3 | 228 | 69 | 2.8 |
| | 107032 | AV650537 | Hs.247309 | succinate-CoA ligase, GDP-forming, beta | 3.1 | 55 | 18 | 3.8 |
| | 107056 | AW401864 | Hs.18720 | programmed cell death 8 (apoptosis-induc | 3.1 | 75 | 24 | 2.2 |
| | 107071 | AW385224 | Hs.35198 | ectonucleotide pyrophosphatase/phosphodi | 3.1 | 367 | 119 | 2.3 |
| | 107080 | AL122043 | Hs.19221 | hypothetical protein DKFZp566G1424 | 3.9 | 98 | 25 | 8.6 |
| 50 | 107102 | AB037765 | Hs.30652 | KIAA1344 protein | 6.3 | 63 | 1 | 5.4 |
| | 107109 | AA249096 | Hs.32793 | ESTs | 4.6 | 71 | 16 | 3.6 |
| | 107136 | AV661958 | Hs.8207 | GK001 protein | 2.5 | 392 | 155 | 4.3 |
| | 107151 | AW378065 | Hs.8687 | ESTs | 15.6 | 156 | 7 | 10.8 |
| | 107217 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 4.8 | 48 | 8 | 3.1 |
| 55 | 107222 | BE172058 | Hs.82689 | tumor rejection antigen (gp96) 1 | 3.4 | 251 | 74 | 23.7 |
| | 107240 | AI290284 | Hs.159872 | ESTs | 3.6 | 36 | 6 | 0.5 |
| | 107248 | AW263124 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 5.4 | 483 | 90 | 4 |
| | 107295 | AA186629 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 4.6 | 199 | 44 | 19.2 |
| | 107299 | BE277457 | Hs.30661 | hypothetical protein MGC4606 | 12.5 | 156 | 13 | 2.9 |
| 60 | 107316 | T63174 | Hs.193700 | Homo sapiens mRNA; cDNA DKFZp586I0324 (f | 3.2 | 110 | 35 | 9.6 |
| | 107318 | T74445 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 3.5 | 35 | 1 | 2.6 |
| | 107485 | AL042613 | Hs.262476 | S-adenosylmethionine decarboxylase 1 | 5.8 | 151 | 26 | 11.4 |
| | 107612 | AI498986 | Hs.60090 | Homo sapiens cDNA FLJ13595 fis, clone PL | 3.2 | 32 | 5 | 2.1 |
| | 107638 | AI580492 | Hs.42743 | hypothetical protein | 4.4 | 73 | 17 | 6.2 |
| 65 | 107727 | AA149707 | Hs.173091 | ubiquitin-like 3 | 3.5 | 282 | 80 | 3.7 |
| | 107859 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 5.7 | 85 | 15 | 7.8 |
| | 107876 | AW372451 | Hs.61184 | CGI-79 protein | 3.5 | 35 | 1 | 1 |
| | 107884 | AA054949 | Hs.61307 | ESTs | 4.3 | 43 | 10 | 2.7 |
| | 107886 | AA025782 | Hs.61284 | ESTs | 3.1 | 31 | 9 | 2.2 |
| | 107908 | AF087999 | Hs.42826 | ESTs | 4.7 | 47 | 4 | 4.3 |
| | 107922 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 9 | 90 | 1 | 5.5 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|-----|-----|------|
| | 107994 | AA036811 | Hs.48469 | LIM domains containing 1 | 4.5 | 45 | 1 | 3.8 |
| | 108040 | AL121031 | Hs.159971 | SWI/SNF related, matrix associated, acti | 6.5 | 65 | 2 | 6 |
| | 108055 | AJ404672 | Hs.334483 | hypothetical protein FLJ23571 | 7.4 | 74 | 8 | 6 |
| | 108063 | BE548479 | Hs.14838 | hypothetical protein FLJ10773 | 3.4 | 34 | 1 | 2.3 |
| 5 | 108339 | AW151340 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 18.7 | 187 | 1 | 17 |
| | 108467 | AI478658 | Hs.94631 | brefeldin A-inhibited guanine nucleotide | 3.8 | 38 | 1 | 3.2 |
| | 108539 | AA084677 | Hs.54558 | hypothetical protein FLJ22222 | 5.7 | 57 | 1 | 4.9 |
| | 108634 | AW022410 | Hs.69507 | ESTs | 3.2 | 32 | 5 | 1.7 |
| | 108647 | BE546947 | Hs.44276 | homeo box C10 | 8.7 | 247 | 29 | 5.7 |
| 10 | 108695 | AB029000 | Hs.70823 | KIAA1077 protein | 3.7 | 625 | 168 | 3.8 |
| | 108778 | AF133123 | Hs.90847 | general transcription factor IIIC, polyp | 3.7 | 37 | 1 | 3.2 |
| | 108806 | AF070578 | Hs.71168 | Homo sapiens clone 24674 mRNA sequence | 3.4 | 34 | 1 | 2.8 |
| | 108807 | AI652236 | Hs.49376 | hypothetical protein FLJ20644 | 3.5 | 35 | 1 | 3.2 |
| | 108810 | AW295647 | Hs.71331 | hypothetical protein MGC5350 | 5.3 | 53 | 1 | 2.8 |
| 15 | 108846 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 4.8 | 96 | 20 | 6.5 |
| | 108857 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 5.4 | 54 | 1 | 4 |
| | 108893 | BE276891 | Hs.194691 | retinoic acid induced 3 | 3.1 | 529 | 170 | 4.1 |
| | 108917 | AI380268 | Hs.173648 | ESTs, Weakly similar to Zinc-finger prot | 3.3 | 33 | 5 | 1.7 |
| | 109010 | NM_007240 | Hs.44229 | dual specificity phosphatase 12 | 3.4 | 34 | 1 | 2.6 |
| 20 | 109060 | BE062109 | Hs.241551 | chloride channel, calcium activated, fam | 3.1 | 31 | 8 | 2 |
| | 109101 | AW608930 | Hs.52184 | hypothetical protein FLJ20618 | 3.4 | 71 | 21 | 2.4 |
| | 109112 | AW419196 | Hs.257924 | hypothetical protein FLJ13782 | 4.1 | 334 | 82 | 3.4 |
| | 109124 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 3.3 | 33 | 1 | 2.9 |
| | 109128 | H89083 | Hs.181915 | ESTs | 4 | 40 | 7 | 1.1 |
| 25 | 109160 | BE220601 | Hs.301997 | hypothetical protein FLJ13033 | 3.8 | 233 | 62 | 3.8 |
| | 109166 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rakbines | 8.8 | 199 | 23 | 16.1 |
| | 109173 | AA179962 | Hs.73643 | EST | 3.2 | 32 | 1 | 2.2 |
| | 109178 | AW976516 | Hs.283707 | Homo sapiens cDNA: FLJ21354 fis, clone C | 3.2 | 32 | 10 | 2.9 |
| | 109235 | AI381800 | Hs.300684 | calcitonin gene-related peptide-receptor | 4.9 | 121 | 25 | 10.4 |
| 30 | 109273 | AA375752 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 2.9 | 114 | 39 | 9.9 |
| | 109292 | AW975746 | Hs.188662 | KIAA1702 protein | 7.1 | 71 | 1 | 6.5 |
| | 109391 | AL096858 | Hs.184245 | KIAA0929 protein Msx2 interacting nuclea | 6.9 | 69 | 5 | 6.2 |
| | 109411 | R98881 | Hs.109655 | sex comb on midleg (Drosophila)-like 1 | 3.3 | 39 | 12 | 1.5 |
| | 109412 | BE543313 | Hs.209473 | hypothetical protein FLJ10520 | 4.2 | 56 | 14 | 2.2 |
| 35 | 109415 | U80736 | Hs.110826 | trinucleotide repeat containing 9 | 12.3 | 123 | 1 | 11.3 |
| | 109481 | AA878923 | Hs.289069 | hypothetical protein FLJ21016 | 3.2 | 286 | 91 | 5.7 |
| | 109517 | AI631874 | Hs.155140 | casein kinase 2, alpha 1 polypeptide | 8.3 | 83 | 8 | 1.9 |
| | 109597 | AA989362 | Hs.293780 | ESTs | 5.9 | 59 | 10 | 4.2 |
| | 109729 | F10024 | Hs.268740 | ESTs | 3.2 | 41 | 13 | 3.3 |
| 40 | 109795 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 5.9 | 208 | 36 | 1.8 |
| | 109799 | AW965076 | Hs.180378 | hypothetical protein 669 | 5 | 50 | 5 | 4.1 |
| | 109883 | R68827 | Hs.95011 | syntrophin, beta 1 (dystrophin-associate | 3.7 | 37 | 4 | 2 |
| | 109912 | AW390822 | Hs.301528 | L-kynurenine/alpha-aminoadipate aminotra | 14.2 | 142 | 1 | 9.5 |
| | 109937 | AI084066 | Hs.20072 | myosin regulatory light chain interactin | 4.1 | 41 | 7 | 1.7 |
| 45 | 109958 | AA001266 | Hs.133521 | ESTs | 4.2 | 58 | 14 | 0.8 |
| | 109984 | AI796320 | Hs.10299 | Homo sapiens cDNA FLJ13545 fis, clone PL | 3.2 | 136 | 43 | 3.6 |
| | 110009 | BE075297 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 p | 6.3 | 693 | 110 | 7.2 |
| | 110240 | AI668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 4.6 | 913 | 199 | 2.9 |
| | 110369 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 3.8 | 38 | 7 | 2.8 |
| 50 | 110426 | AI610702 | Hs.28212 | ESTs, Weakly similar to TRHY_HUMAN TRICH | 6.7 | 78 | 12 | 3 |
| | 110478 | H11236 | Hs.31034 | peroxisomal biogenesis factor 11A | 3.7 | 37 | 1 | 2.1 |
| | 110481 | AF075089 | Hs.36823 | ESTs | 3.6 | 36 | 10 | 2.5 |
| | 110581 | H61560 | | gb:yr22g03.s1 Soares fetal liver spleen | 3.3 | 33 | 1 | 1.8 |
| | 110674 | AA071276 | Hs.19469 | KIAA0859 protein | 3.5 | 35 | 8 | 1.9 |
| 55 | 110705 | AB007902 | Hs.32168 | KIAA0442 protein | 3.6 | 282 | 79 | 1.7 |
| | 110721 | H97678 | Hs.31319 | ESTs | 4.4 | 103 | 24 | 3.8 |
| | 110731 | NM_014899 | Hs.188006 | KIAA0878 protein | 3.3 | 138 | 42 | 3.6 |
| | 110769 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 13.5 | 135 | 1 | 5.1 |
| | 110775 | N22414 | | gb:yr39a07.s1 Weizmann Olfactory Epithel | 5.4 | 54 | 1 | 3.7 |
| 60 | 110787 | AA831267 | Hs.12244 | hypothetical protein FLJ20097 | 4.7 | 47 | 4 | 4.2 |
| | 110799 | AI089660 | Hs.323401 | dpy-30-like protein | 5 | 50 | 1 | 4.3 |
| | 110818 | AL157503 | Hs.27552 | Homo sapiens mRNA; cDNA DKFZp586N2424 (f | 3.1 | 31 | 1 | 2.7 |
| | 110839 | AF153330 | Hs.30246 | solute carrier family 19 (thiamine trans | 8.4 | 84 | 1 | 5.3 |
| | 110844 | AI740792 | Hs.167531 | methylcrotonoyl-Coenzyme A carboxylase 2 | 10.5 | 105 | 4 | 7.1 |
| 65 | 110854 | BE612992 | Hs.27931 | hypothetical protein FLJ10607 similar to | 7.9 | 79 | 1 | 6.2 |
| | 110882 | AW963705 | Hs.301183 | molecule possessing ankyrin repeats indu | 3.9 | 353 | 90 | 1.2 |
| | 110908 | AI433165 | Hs.9856 | ESTs | 3.1 | 31 | 1 | 1.3 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|-----|-----|------|
| 5 | 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 20.9 | 209 | 1 | 19.5 |
| | 110930 | BE242691 | Hs.14947 | ESTs | 3.4 | 115 | 34 | 2.4 |
| | 110970 | Y19062 | Hs.96870 | staufer (Drosophila, RNA-binding protein | 3.5 | 35 | 9 | 3.2 |
| | 111084 | H44186 | Hs.15456 | PDZ domain containing 1 | 4.3 | 43 | 1 | 2 |
| | 111125 | N63823 | Hs.269115 | ESTs, Moderately similar to Z195_HUMAN Z | 5.4 | 54 | 1 | 4.3 |
| | 111132 | AB037807 | Hs.83293 | hypothetical protein | 7.2 | 72 | 10 | 6.1 |
| | 111164 | N46180 | Hs.122489 | Homo sapiens cDNA FLJ13289 fis, clone OV | 7.7 | 77 | 1 | 5 |
| | 111179 | AK000136 | Hs.10760 | asporin (LRR class 1) | 25.1 | 288 | 12 | 6.7 |
| | 111184 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 3.9 | 146 | 37 | 9.8 |
| 10 | 111190 | AK002055 | Hs.151046 | hypothetical protein FLJ11193 | 6.3 | 63 | 1 | 5.8 |
| | 111221 | AB037782 | Hs.151119 | KIAA1361 protein | 3.7 | 119 | 33 | 6.7 |
| | 111223 | AA852773 | Hs.334838 | KIAA1866 protein | 3.6 | 402 | 112 | 4.9 |
| | 111229 | AW389845 | Hs.110855 | ESTs | 4.3 | 43 | 1 | 1 |
| | 111234 | AA902656 | Hs.21943 | NIF3 (Ngg1 interacting factor 3, S.pombe | 3.3 | 33 | 1 | 1.1 |
| 15 | 111241 | AA345644 | Hs.288880 | PAN2 protein | 4.8 | 61 | 13 | 5.6 |
| | 111345 | AW263155 | Hs.14559 | hypothetical protein FLJ10540 | 4.3 | 43 | 5 | 2.2 |
| | 111353 | W20090 | Hs.6616 | ESTs | 4.1 | 41 | 1 | 2.6 |
| | 111357 | BE314949 | Hs.87128 | hypothetical protein FLJ23309 | 3.8 | 425 | 111 | 4 |
| | 111378 | AW160993 | Hs.326292 | hypothetical gene DKFZp434A1114 | 4.3 | 65 | 15 | 5.7 |
| 20 | 111389 | AK000987 | Hs.169111 | oxidation resistance 1 | 3.4 | 314 | 91 | 2.4 |
| | 111540 | U82670 | Hs.9786 | zinc finger protein 275 | 3.5 | 35 | 1 | 2.1 |
| | 111806 | BE071382 | Hs.279008 | hypothetical protein FLJ20170 | 3.5 | 105 | 30 | 9.6 |
| | 111884 | AW502285 | Hs.127236 | hypothetical protein FLJ12879 | 3.2 | 37 | 12 | 3.5 |
| | 111923 | BE383234 | Hs.25925 | Homo sapiens, clone MGC:15393, mRNA, com | 6.2 | 62 | 2 | 5.9 |
| 25 | 111929 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | 8.1 | 328 | 41 | 1.7 |
| | 111942 | R40576 | Hs.21590 | hypothetical protein DKFZp564O0523 | 4.2 | 125 | 30 | 7.4 |
| | 111987 | NM_015310 | Hs.6763 | KIAA0942 protein | 6.5 | 65 | 10 | 1.5 |
| | 112092 | R44538 | | gb:yg29c02.s1 Soares Infant brain 1NIB H | 3.3 | 33 | 10 | 2.3 |
| | 112134 | R41823 | Hs.7413 | ESTs; calyntenin-2 | 6.1 | 185 | 31 | 6.6 |
| 30 | 112197 | NM_003655 | Hs.5637 | ESTs | 3.5 | 507 | 145 | 3.3 |
| | 112198 | AI432672 | Hs.288539 | hypothetical protein FLJ22191 | 3.5 | 40 | 12 | 2.5 |
| | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 5.7 | 567 | 100 | 6.7 |
| | 112253 | R51818 | | gb:yg77h12.s1 Soares Infant brain 1NIB H | 4 | 70 | 18 | 6.8 |
| | 112269 | R53734 | Hs.25978 | ESTs, Weakly similar to 2109260A B cell | 3.7 | 37 | 1 | 3 |
| 35 | 112275 | AW972635 | Hs.301904 | hypothetical protein FLJ12671 | 4.3 | 45 | 11 | 4.4 |
| | 112280 | AA863360 | Hs.26040 | ESTs, Weakly similar to fatty acid omega | 2.8 | 751 | 270 | 1.3 |
| | 112305 | AK000914 | Hs.26244 | hypothetical protein FLJ10052 | 3.5 | 41 | 12 | 3.7 |
| | 112483 | AW969785 | Hs.285885 | Homo sapiens cDNA FLJ11321 fis, clone PL | 4.2 | 42 | 6 | 3.6 |
| | 112513 | R68425 | Hs.13809 | hypothetical protein FLJ10648 | 4.7 | 54 | 12 | 4.5 |
| 40 | 112571 | AA412205 | Hs.140996 | ESTs | 4.8 | 48 | 2 | 3.4 |
| | 112971 | Z42387 | Hs.83883 | transmembrane, prostate androgen induced | 4.5 | 390 | 87 | 5.3 |
| | 113023 | AL134324 | Hs.7312 | ESTs | 3.2 | 99 | 31 | 3.1 |
| | 113047 | AI571940 | Hs.7549 | ESTs | 9.6 | 124 | 13 | 9 |
| | 113073 | N39342 | Hs.103042 | microtubule-associated protein 1B | 9.1 | 91 | 6 | 8.3 |
| 45 | 113083 | AA283057 | Hs.266957 | hypothetical protein FLJ14281 | 6.5 | 65 | 6 | 4.8 |
| | 113287 | T66847 | Hs.194040 | ESTs, Weakly similar to I38022 hypotheti | 3.5 | 35 | 1 | 1.4 |
| | 113296 | AW449560 | Hs.89576 | inner mitochondrial membrane peptidase 2 | 3.5 | 35 | 4 | 3.3 |
| | 113523 | AI791905 | Hs.95549 | hypothetical protein | 7.6 | 76 | 1 | 4.2 |
| | 113604 | AI075407 | Hs.296083 | ESTs, Moderately similar to I54374 gene | 3.1 | 453 | 148 | 7 |
| 50 | 113617 | AI869372 | Hs.17207 | Homo sapiens cDNA FLJ11922 fis, clone HE | 3.6 | 36 | 4 | 2.6 |
| | 113702 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen | 12.3 | 129 | 11 | 11.7 |
| | 113783 | AL359588 | Hs.7041 | hypothetical protein DKFZp762B226 | 4.6 | 46 | 4 | 4.3 |
| | 113791 | AI269096 | Hs.135578 | chilobiase, di-N-acetyl- | 3.6 | 36 | 1 | 1.2 |
| | 113794 | T62849 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 3.3 | 744 | 227 | 2.5 |
| 55 | 113804 | BE247683 | Hs.14611 | dual specificity phosphatase 11 (RNA/RNP | 3.3 | 180 | 54 | 2.1 |
| | 113808 | W44735 | Hs.9286 | Homo sapiens cDNA: FLJ21278 fis, clone C | 5.1 | 51 | 5 | 4.5 |
| | 113847 | NM_005032 | Hs.4114 | plastin 3 (T isoform) | 3.2 | 238 | 75 | 2.1 |
| | 113849 | AA457211 | Hs.8858 | bromodomain adjacent to zinc finger doma | 4.3 | 43 | 8 | 3.6 |
| | 113867 | AW002834 | Hs.24095 | ESTs | 6.1 | 110 | 18 | 10.2 |
| 60 | 113886 | W76027 | Hs.23920 | hypothetical protein FLJ11105 | 4 | 48 | 12 | 4 |
| | 113923 | AW953484 | Hs.3849 | hypothetical protein FLJ22041 similar to | 3.7 | 239 | 65 | 3.6 |
| | 113936 | W17056 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 4.3 | 819 | 191 | 1.2 |
| | 113950 | AI267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 10.7 | 123 | 12 | 7 |
| | 114030 | AI825386 | Hs.164478 | hypothetical protein FLJ21939 similar to | 4.4 | 44 | 6 | 2.3 |
| 65 | 114051 | AB026436 | Hs.177534 | dual specificity phosphatase 10 | 4.5 | 45 | 4 | 2.6 |
| | 114057 | AF116653 | Hs.34192 | Homo sapiens PRO0823 mRNA, complete cds | 3.5 | 35 | 6 | 3.2 |
| | 114082 | AK001612 | Hs.26962 | Homo sapiens cDNA FLJ10750 fis, clone NT | 3.1 | 31 | 5 | 1.5 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|-----|-----|------|
| 5 | 114124 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 24.2 | 242 | 10 | 5.6 |
| | 114138 | AW384793 | Hs.15740 | Homo sapiens mRNA; cDNA DKFZp434E033 (fr | 6.7 | 67 | 1 | 6.3 |
| | 114162 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 3.8 | 73 | 19 | 1.8 |
| | 114196 | AF017445 | Hs.150926 | fucose-1-phosphate guanylyltransferase | 4.4 | 104 | 24 | 5.1 |
| | 114208 | AL049466 | Hs.7859 | ESTs | 5.7 | 57 | 1 | 4.9 |
| 10 | 114239 | AL137667 | Hs.267445 | Homo sapiens mRNA; cDNA DKFZp434B231 (fr | 3.3 | 33 | 1 | 2.4 |
| | 114251 | H15261 | Hs.21948 | ESTs | 4.2 | 46 | 11 | 1.4 |
| | 114306 | AF100143 | Hs.6540 | fibroblast growth factor 13 | 4.5 | 45 | 2 | 3 |
| | 114460 | AF183810 | Hs.26102 | trichorhinophalangeal syndrome I | 4.4 | 44 | 1 | 3 |
| | 114542 | AW970128 | Hs.91011 | anterior gradient 2 (Xenopus laevis) hom | 4.7 | 770 | 166 | 5.8 |
| 15 | 114652 | AI521936 | Hs.107149 | novel protein similar to archaeal, yeast | 5.2 | 52 | 3 | 2.3 |
| | 114767 | AI859865 | Hs.154443 | minichromosome maintenance deficient (S. | 4.6 | 196 | 43 | 10 |
| | 114768 | AF212848 | Hs.182339 | ets homologous factor | 13.7 | 137 | 1 | 8.9 |
| | 114774 | AV656017 | Hs.184325 | CGI-76 protein | 3.3 | 168 | 51 | 7.3 |
| | 114798 | AA159181 | Hs.54900 | serologically defined colon cancer antig | 7.4 | 137 | 19 | 1.8 |
| 20 | 114821 | AI648602 | Hs.55468 | ESTs | 4.7 | 57 | 12 | 4.7 |
| | 114860 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 9.1 | 91 | 1 | 7.6 |
| | 114918 | BE165762 | Hs.23518 | hypothetical protein from BCRA2 region | 10.1 | 111 | 11 | 10.2 |
| | 114940 | BE092696 | Hs.75928 | ESTs | 6.4 | 67 | 11 | 5 |
| | 114965 | AI733881 | Hs.72472 | BMP-R1B | 35.9 | 359 | 10 | 29.7 |
| 25 | 114969 | AW162998 | Hs.24684 | KIAA1376 protein | 9.4 | 94 | 8 | 7.3 |
| | 114988 | AA251089 | | gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens | 11.5 | 115 | 1 | 6.9 |
| | 115004 | AA329340 | Hs.4867 | mannosyl (alpha-1,3-)-glycoprotein beta- | 4.2 | 42 | 9 | 1.1 |
| | 115054 | AW265668 | Hs.87729 | hypothetical protein FLJ12428 | 5.1 | 51 | 1 | 4.2 |
| | 115061 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 4.5 | 290 | 65 | 3.7 |
| 30 | 115140 | NM_014158 | Hs.279938 | HSPC067 protein | 4.8 | 48 | 1 | 4.4 |
| | 115142 | AI623693 | Hs.191533 | ESTs | 3.2 | 49 | 16 | 4.2 |
| | 115188 | AK000219 | Hs.88367 | hypothetical protein FLJ20212 | 3.3 | 33 | 1 | 3 |
| | 115206 | AW183695 | Hs.186572 | ESTs | 5.8 | 58 | 1 | 5 |
| | 115221 | AW365434 | Hs.79741 | hypothetical protein FLJ10116 | 5.5 | 343 | 62 | 2.5 |
| 35 | 115262 | AI422867 | Hs.88594 | ESTs | 11.2 | 112 | 1 | 10.3 |
| | 115291 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 4.5 | 96 | 21 | 7.8 |
| | 115536 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 5.9 | 59 | 1 | 4.2 |
| | 115583 | NM_012317 | Hs.45231 | leucine zipper, down-regulated in cancer | 9.8 | 98 | 1 | 8.8 |
| | 115600 | AA081395 | Hs.42173 | Homo sapiens cDNA FLJ10366 fis, clone NT | 4.6 | 46 | 2 | 1.8 |
| 40 | 115622 | AI088691 | Hs.208414 | Homo sapiens mRNA; cDNA DKFZp564D0472 (f | 4.4 | 44 | 7 | 1.1 |
| | 115646 | N36110 | Hs.305971 | solute carrier family 2 (facilitated glu | 3.2 | 372 | 115 | 2.1 |
| | 115674 | AW992356 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 10.2 | 506 | 50 | 2.8 |
| | 115675 | W87707 | Hs.82065 | interleukin 6 signal transducer (gp130, | 5.2 | 405 | 78 | 10.1 |
| | 115719 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 7.6 | 144 | 19 | 13.9 |
| 45 | 115725 | AW899053 | Hs.76917 | F-box only protein 8 | 3.1 | 58 | 19 | 2.5 |
| | 115764 | AW582256 | Hs.91011 | anterior gradient 2 (Xenopus laevis) hom | 5.7 | 368 | 65 | 28.5 |
| | 115821 | AW338063 | Hs.130965 | zinc-finger protein ZBRK1 | 3.9 | 39 | 8 | 2.2 |
| | 115825 | R50956 | Hs.159993 | glycosyltransferase | 4.2 | 79 | 19 | 1.9 |
| | 115839 | BE300266 | Hs.28935 | transducin-like enhancer of split 1, hom | 5.8 | 58 | 1 | 4.4 |
| 50 | 115844 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 6.2 | 62 | 1 | 5.4 |
| | 115892 | AA291377 | Hs.50831 | ESTs | 3.2 | 40 | 13 | 0.7 |
| | 115967 | AI745379 | Hs.42911 | ESTs | 8.4 | 101 | 12 | 8.7 |
| | 116093 | AW673312 | Hs.50848 | hypothetical protein FLJ20331 | 3.6 | 36 | 1 | 2 |
| | 116097 | AI198719 | Hs.176376 | ESTs | 5.1 | 51 | 1 | 2 |
| 55 | 116107 | AL133916 | Hs.172572 | hypothetical protein FLJ20093 | 3.4 | 34 | 8 | 1 |
| | 116127 | AF126743 | Hs.279884 | DNAJ domain-containing | 3.5 | 35 | 8 | 3.3 |
| | 116129 | AF189011 | Hs.49163 | putative ribonuclease III | 4.5 | 45 | 9 | 3.4 |
| | 116204 | AW861622 | Hs.108646 | Homo sapiens cDNA FLJ14934 fis, clone PL | 5.2 | 52 | 4 | 3.9 |
| | 116226 | AW976438 | Hs.17428 | RBP1-like protein | 3.8 | 38 | 7 | 2.1 |
| 60 | 116238 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 5.1 | 198 | 39 | 17.9 |
| | 116250 | N76712 | Hs.44829 | ESTs, Weakly similar to I38022 hypotheti | 13.3 | 133 | 8 | 3.2 |
| | 116256 | AA328153 | Hs.88201 | ESTs, Weakly similar to A Chain A, Cryst | 3.3 | 106 | 33 | 9.8 |
| | 116298 | AI955411 | Hs.94109 | Homo sapiens cDNA FLJ13634 fis, clone PL | 4.8 | 179 | 38 | 2.8 |
| | 116336 | AL133033 | Hs.4084 | KIAA1025 protein | 3.2 | 173 | 55 | 3 |
| 65 | 116351 | AL133623 | Hs.82501 | similar to mouse Xn1 / Dh2 protein | 3.7 | 37 | 1 | 1.8 |
| | 116365 | N50174 | Hs.46765 | ESTs | 3.9 | 39 | 10 | 0.6 |
| | 116379 | AA448588 | Hs.71252 | hypothetical protein DKFZp761C169 | 5.6 | 106 | 19 | 9 |
| | 116429 | AF191018 | Hs.279923 | putative nucleotide binding protein, est | 3.6 | 256 | 72 | 3.7 |
| | 116450 | AI654450 | Hs.47274 | Homo sapiens mRNA; cDNA DKFZp564B176 (fr | 3.1 | 119 | 39 | 2 |
| | 116461 | AA313607 | Hs.58633 | Homo sapiens cDNA: FLJ22145 fis, clone H | 5.5 | 315 | 58 | 3.1 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.4 | 496 | 144 | 1.6 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| | 116507 | AI418366 | Hs.68501 | ESTs | 3.1 | 31 | 4 | 1.9 |
| | 116579 | AW888411 | Hs.81915 | leukemia-associated phosphoprotein p18 (| 3.3 | 931 | 279 | 5.6 |
| | 116625 | F01601 | Hs.241567 | RNA binding motif, single stranded inter | 3.6 | 36 | 1 | 1.9 |
| | 116674 | AI768015 | Hs.92127 | ESTs | 4.5 | 96 | 22 | 6.9 |
| 5 | 116680 | AW902848 | Hs.273829 | ESTs | 4.2 | 42 | 1 | 2.7 |
| | 116710 | F10577 | Hs.306088 | v-crk avian sarcoma virus CT10 oncogene | 7.1 | 71 | 9 | 6.9 |
| | 116724 | AA741307 | Hs.65641 | hypothetical protein FLJ20073 | 4.3 | 190 | 44 | 5.4 |
| | 116786 | H25836 | Hs.301527 | ESTs, Moderately similar to unknown [H.s | 22.8 | 228 | 9 | 12.4 |
| | 116787 | AW362955 | Hs.15641 | Homo sapiens cDNA FLJ14415 fis, clone HE | 4.9 | 108 | 22 | 9 |
| 10 | 116790 | AW161357 | Hs.101174 | microtubule-associated protein tau | 4.6 | 163 | 35 | 7.3 |
| | 116844 | H64938 | Hs.337434 | ESTs, Weakly similar to A46010 X-linked | 6.9 | 69 | 10 | 2.4 |
| | 117027 | AW085208 | Hs.130093 | ESTs | 4.8 | 48 | 1 | 2.5 |
| | 117067 | H91164 | Hs.335797 | ESTs | 3.3 | 33 | 1 | 2.3 |
| | 117129 | H95785 | Hs.167652 | ESTs, Highly similar to 1819485A CENP-E | 3.1 | 38 | 13 | 1.7 |
| 15 | 117147 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 4.8 | 48 | 1 | 0.9 |
| | 117170 | N25929 | Hs.42500 | ADP-ribosylation factor-like 5 | 3.1 | 295 | 96 | 27.9 |
| | 117209 | W03011 | Hs.306881 | MSTP043 protein | 3.6 | 41 | 12 | 2.8 |
| | 117280 | M18217 | Hs.172129 | Homo sapiens cDNA: FLJ21409 fis, clone C | 3.9 | 322 | 83 | 4.4 |
| | 117367 | AI041793 | Hs.42502 | ESTs | 3.5 | 72 | 21 | 1.3 |
| 20 | 117412 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 17.4 | 174 | 9 | 6.9 |
| | 117475 | N30205 | Hs.93740 | ESTs, Weakly similar to I38022 hypotheti | 3.2 | 35 | 11 | 0.7 |
| | 117634 | AW341639 | Hs.13323 | hypothetical protein FLJ22059 | 5 | 50 | 1 | 4.7 |
| | 117667 | U59305 | Hs.44708 | Ser-Thr protein kinase related to the my | 4.5 | 211 | 47 | 5 |
| | 117852 | AW877787 | Hs.136102 | KIAA0853 protein | 4.6 | 46 | 1 | 3.8 |
| 25 | 117873 | N49967 | Hs.46624 | HSPC043 protein | 3.1 | 31 | 1 | 2.7 |
| | 117924 | AI521436 | Hs.38891 | ESTs | 4.9 | 49 | 1 | 4.4 |
| | 118138 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 5 | 50 | 2 | 3.1 |
| | 118449 | AI813865 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.6 | 89 | 25 | 0.9 |
| | 118467 | AF091434 | Hs.43080 | platelet derived growth factor C | 3.2 | 378 | 117 | 2.8 |
| 30 | 118472 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 14.5 | 145 | 1 | 2.4 |
| | 118475 | N66845 | Hs.43228 | gb:za46c11.s1 Soares fetal liver spleen | 3.1 | 199 | 64 | 1 |
| | 118509 | N22617 | Hs.43228 | Homo sapiens cDNA FLJ11835 fis, clone HE | 6 | 60 | 5 | 3.7 |
| | 118528 | AI949952 | Hs.49397 | ESTs | 3.3 | 81 | 25 | 1.5 |
| | 118828 | N79496 | Hs.50824 | EST, Moderately similar to I54374 gene N | 3.4 | 740 | 217 | 2.8 |
| 35 | 118836 | AW134482 | Hs.173001 | hypothetical protein FLJ13964 | 4.3 | 162 | 38 | 12.1 |
| | 118854 | T58283 | Hs.10450 | Homo sapiens cDNA: FLJ22063 fis, clone H | 3.4 | 118 | 35 | 2.3 |
| | 118873 | AI824009 | Hs.44577 | ESTs | 3.5 | 35 | 1 | 2.9 |
| | 118888 | AI191811 | Hs.54629 | ESTs | 8.4 | 84 | 10 | 0.8 |
| | 118901 | AW292577 | Hs.94445 | ESTs | 7.3 | 73 | 3 | 5.4 |
| 40 | 118981 | N29309 | Hs.39288 | ESTs | 5 | 50 | 5 | 4.7 |
| | 118991 | NM_016657 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 3.7 | 37 | 6 | 0.5 |
| | 119023 | N98488 | Hs.90790 | gb:zb82h01.s1 Soares_senescent_fibroblas | 3.3 | 36 | 11 | 0.6 |
| | 119088 | R39261 | Hs.117183 | Homo sapiens cDNA: FLJ22930 fis, clone K | 3.3 | 167 | 51 | 2.6 |
| | 119126 | R45175 | Hs.92482 | ESTs | 5.3 | 53 | 6 | 2.3 |
| 45 | 119128 | H09334 | Hs.65328 | ESTs | 3.7 | 37 | 4 | 3 |
| | 119271 | AI061118 | Hs.155478 | Fanconi anemia, complementation group F | 8.2 | 82 | 1 | 6.4 |
| | 119298 | NM_001241 | Hs.57787 | cyclin T2 | 4 | 40 | 4 | 1.2 |
| | 119307 | BE048061 | Hs.37054 | ephrin-A3 | 3.3 | 571 | 171 | 2 |
| | 119367 | T78324 | Hs.250895 | ribosomal protein L34 | 3.4 | 34 | 3 | 2.4 |
| 50 | 119427 | AW474547 | Hs.53565 | Homo sapiens PIG-M mRNA for mannosyltran | 4.6 | 60 | 13 | 4.8 |
| | 119580 | AL079310 | Hs.92260 | high-mobility group protein 2-like 1 | 8.1 | 94 | 12 | 6.5 |
| | 119586 | AF088033 | Hs.159225 | ESTs | 3.3 | 33 | 8 | 0.9 |
| | 119638 | NM_016122 | Hs.56148 | NY-REN-58 antigen | 3.3 | 33 | 10 | 0.5 |
| | 119676 | AA243837 | Hs.57787 | ESTs | 5.4 | 54 | 1 | 4.1 |
| 55 | 119717 | AA918317 | Hs.57987 | B-cell CLL/lymphoma 11B (zinc finger pro | 4.6 | 46 | 7 | 0.8 |
| | 119771 | AI905687 | Hs.2533 | EST | 3.5 | 2073 | 595 | 2.1 |
| | 119780 | NM_016625 | Hs.191381 | hypothetical protein | 4.4 | 44 | 1 | 3.1 |
| | 119786 | AL133396 | Hs.121281 | prion protein 2 (dublet) | 3.4 | 34 | 1 | 2.5 |
| | 119805 | AJ223810 | Hs.43213 | ESTs, Weakly similar to IEFS_HUMAN TRANS | 3.6 | 36 | 1 | 2.9 |
| 60 | 119859 | AW245741 | Hs.58461 | ESTs, Weakly similar to A35659 krueppel- | 5.2 | 52 | 6 | 1.8 |
| | 119899 | AI057404 | Hs.58698 | ESTs | 3.7 | 37 | 4 | 1.9 |
| | 119940 | AL050097 | Hs.272531 | DKFZP586B0319 protein | 6.9 | 162 | 24 | 2.6 |
| | 119943 | BE565849 | Hs.14158 | copine III | 3.7 | 590 | 159 | 3.8 |
| | 120132 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 6.9 | 319 | 47 | 2.1 |
| 65 | 120150 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 5.3 | 53 | 5 | 0.9 |
| | 120215 | AF109219 | Hs.108787 | phosphatidylinositol glycan, class N | 3.2 | 106 | 34 | 3.3 |
| | 120260 | AK000061 | Hs.101590 | hypothetical protein | 3.4 | 34 | 1 | 1.7 |

| | | | | | | | | |
|----|--------|----------|-----------|--|------|-----|-----|------|
| | 120296 | AW995911 | Hs.299883 | hypothetical protein FLJ23399 | 4.2 | 124 | 30 | 1.8 |
| | 120352 | R06859 | Hs.193172 | ESTs, Weakly similar to I38022 hypotheti | 7.5 | 112 | 15 | 2.5 |
| | 120378 | AA223249 | Hs.285728 | abl-Interactor 12 (SH3-containing protei | 3.3 | 33 | 10 | 2.8 |
| | 120418 | AW966893 | Hs.26613 | Homo sapiens mRNA; cDNA DKFZp586F1323 (f | 4.8 | 48 | 1 | 0.5 |
| 5 | 120473 | AA251973 | Hs.269988 | ESTs | 3.4 | 34 | 4 | 0.1 |
| | 120493 | AW968080 | Hs.152939 | Homo sapiens clone 24630 mRNA sequence | 3.9 | 161 | 42 | 2 |
| | 120524 | AA261852 | Hs.192905 | ESTs | 6.8 | 68 | 1 | 0.2 |
| | 120554 | AA284447 | Hs.271887 | ESTs | 3.2 | 32 | 5 | 0.6 |
| | 120562 | BE244580 | Hs.302267 | hypothetical protein FLJ10330 | 8.5 | 127 | 15 | 1.6 |
| 10 | 120571 | AB037744 | Hs.34892 | KIAA1323 protein | 3.7 | 37 | 1 | 0.5 |
| | 120572 | H39599 | Hs.294008 | ESTs | 3.6 | 36 | 8 | 0.2 |
| | 120588 | AA703226 | Hs.16193 | Homo sapiens mRNA; cDNA DKFZp586B211 (fr | 5.6 | 101 | 18 | 1.6 |
| | 120649 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 5.4 | 54 | 10 | 2.5 |
| | 120658 | AI952639 | Hs.98267 | ESTs | 3.2 | 32 | 8 | 3 |
| 15 | 120713 | AW449855 | Hs.96557 | Homo sapiens cDNA FLJ12727 fis, clone NT | 5.3 | 58 | 11 | 3.3 |
| | 120821 | Y19062 | Hs.96870 | stauferin (Drosophila, RNA-binding protein | 3.3 | 33 | 3 | 0.2 |
| | 120822 | AA347422 | Hs.238040 | EST, Weakly similar to B34087 hypothetic | 3.8 | 38 | 7 | 0.2 |
| | 120915 | AL135556 | Hs.97104 | ESTs | 3.5 | 37 | 11 | 0.1 |
| | 120922 | AA481003 | Hs.97128 | ESTs | 3.1 | 31 | 1 | 0.4 |
| 20 | 120977 | AA398155 | Hs.97600 | ESTs | 7.9 | 79 | 1 | 2.7 |
| | 120999 | AI972375 | Hs.29626 | hypothetical brain protein my038 | 5.1 | 51 | 1 | 2.4 |
| | 121125 | AL042981 | Hs.251278 | KIAA1201 protein | 3.7 | 37 | 10 | 1 |
| | 121176 | AL121523 | Hs.97774 | ESTs | 7 | 70 | 1 | 0.9 |
| | 121202 | AA970946 | Hs.97794 | ESTs | 3.9 | 39 | 1 | 0.2 |
| 25 | 121429 | AA406293 | Hs.41167 | ESTs | 3.4 | 34 | 1 | 0.8 |
| | 121448 | AF044197 | Hs.100431 | B-cell attracting chemokine 1 (CXCL13; | 3.5 | 35 | 1 | 2.6 |
| | 121463 | AK000282 | Hs.239681 | hypothetical protein FLJ20275 | 10.3 | 103 | 1 | 9.3 |
| | 121517 | AI002968 | Hs.235402 | ESTs, Weakly similar to T26525 hypotheti | 3.5 | 143 | 41 | 2.6 |
| | 121553 | AA412488 | Hs.48820 | TATA box binding protein (TBP)-associate | 4.6 | 46 | 3 | 0.8 |
| 30 | 121556 | AA412494 | Hs.98152 | EST | 4.2 | 77 | 19 | 1.4 |
| | 121581 | AA416568 | | gb:zu05c10.s1 Soares_testis_NHT Homo sap | 3.2 | 32 | 1 | 0.8 |
| | 121709 | AI338247 | Hs.98314 | Homo sapiens mRNA; cDNA DKFZp586L0120 (f | 3.4 | 34 | 10 | 0.7 |
| | 121723 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 2.9 | 214 | 74 | 3.7 |
| | 121831 | AA449644 | Hs.193063 | Homo sapiens cDNA FLJ14201 fis, clone NT | 3.9 | 39 | 1 | 0.2 |
| 35 | 121853 | AA425887 | Hs.98502 | hypothetical protein FLJ14303 | 4.4 | 48 | 11 | 0.9 |
| | 121873 | AV650929 | Hs.145696 | splicing factor (CC1.3) | 3.6 | 150 | 42 | 3.2 |
| | 121913 | AI249368 | Hs.98558 | ESTs; protease inhibitor 15 (PI15) | 2.7 | 864 | 321 | 0.6 |
| | 121916 | AW117207 | Hs.98523 | ESTs | 3.5 | 35 | 3 | 2.3 |
| | 122004 | AI810721 | Hs.95424 | ESTs | 4.9 | 49 | 7 | 3.7 |
| 40 | 122063 | AW794215 | Hs.301226 | KIAA1085 protein | 3.2 | 88 | 28 | 1.2 |
| | 122223 | AF169797 | Hs.27413 | adaptor protein containing pH domain, PT | 12.6 | 126 | 7 | 7.5 |
| | 122235 | AA436475 | Hs.112227 | membrane-associated nucleic acid binding | 4.1 | 43 | 11 | 1.6 |
| | 122273 | AI298368 | Hs.150926 | fucose-1-phosphate guanylyltransferase | 3.1 | 31 | 1 | 1 |
| | 122383 | AA446189 | Hs.99051 | ESTs | 3.3 | 53 | 16 | 4 |
| 45 | 122507 | BE567620 | Hs.99210 | ESTs | 3.2 | 291 | 91 | 4 |
| | 122524 | AA449453 | Hs.192915 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.1 | 31 | 6 | 0.8 |
| | 122636 | AW651706 | Hs.99519 | hypothetical protein FLJ14007 | 3.5 | 35 | 1 | 3 |
| | 122637 | AA454149 | Hs.99357 | EST | 3.2 | 32 | 10 | 3.1 |
| | 122798 | AW366286 | Hs.145696 | splicing factor (CC1.3) | 3.2 | 36 | 11 | 2.5 |
| 50 | 122861 | AA335721 | Hs.119394 | ESTs | 5.6 | 108 | 20 | 1.8 |
| | 122873 | AA749382 | Hs.118797 | ubiquitin-conjugating enzyme E2D 3 (homo | 3.6 | 36 | 1 | 3.4 |
| | 122946 | AI718702 | Hs.308026 | major histocompatibility complex, class | 3.7 | 162 | 44 | 12.4 |
| | 122963 | AA478446 | Hs.69559 | KIAA1096 protein | 7.2 | 72 | 1 | 5.7 |
| | 122974 | AA447871 | Hs.194215 | ESTs, Weakly similar to I38022 hypotheti | 4.7 | 59 | 13 | 4.7 |
| 55 | 123016 | AW338067 | Hs.323231 | Homo sapiens cDNA FLJ11946 fis, clone HE | 3.3 | 207 | 63 | 3.5 |
| | 123090 | AL135185 | Hs.48778 | niban protein | 3.8 | 207 | 55 | 5.5 |
| | 123137 | AI073913 | Hs.100686 | ESTs, Weakly similar to JE0350 Anterior | 9.9 | 351 | 36 | 13.9 |
| | 123255 | AA830335 | Hs.105273 | ESTs | 4.1 | 72 | 18 | 1.5 |
| | 123284 | AA488988 | Hs.293796 | ESTs | 3.7 | 41 | 11 | 1.6 |
| 60 | 123442 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 6.7 | 67 | 2 | 2.1 |
| | 123449 | AL049325 | Hs.112493 | Homo sapiens mRNA; cDNA DKFZp564D036 (fr | 3.4 | 34 | 1 | 2.6 |
| | 123475 | BE439553 | Hs.250528 | Homo sapiens, clone IMAGE-4098694, mRNA, | 9.7 | 102 | 11 | 6 |
| | 123494 | AW179019 | Hs.112110 | mitochondrial ribosomal protein L42 | 4.2 | 42 | 7 | 2.9 |
| | 123503 | AW975051 | Hs.293156 | ESTs, Weakly similar to I78885 serine/th | 3.9 | 39 | 1 | 3.2 |
| 65 | 123516 | AB037860 | Hs.173933 | nuclear factor I/A | 4.3 | 43 | 1 | 3.5 |
| | 123518 | AL035414 | Hs.21068 | hypothetical protein | 5.8 | 58 | 1 | 4.9 |
| | 123523 | AA608588 | | gb:ae54e06.s1 Stratagene lung carcinoma | 3.1 | 927 | 295 | 2.1 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|-----|-----|------|
| | 123527 | AF150208 | Hs.108327 | damage-specific DNA binding protein 1 (1 | 5 | 121 | 25 | 5.9 |
| | 123570 | AA608955 | Hs.109653 | ESTs | 6.8 | 68 | 10 | 6.1 |
| | 123619 | AA602964 | | gb:nc097c02.s1 NCJ_CGAP_Pr2 Homo sapiens | 8.5 | 85 | 1 | 4.3 |
| 5 | 123673 | BE550112 | Hs.158549 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 3.9 | 39 | 5 | 3.7 |
| | 123709 | AA706910 | Hs.112742 | ESTs | 3.9 | 60 | 16 | 4.8 |
| | 123926 | AA425769 | Hs.227933 | Alg5, S. cerevisiae, homolog of | 3.4 | 80 | 24 | 3.8 |
| | 123960 | AW082862 | Hs.287733 | hypothetical protein FLJ23189 | 4.5 | 45 | 2 | 3.6 |
| | 124006 | AI147155 | Hs.270016 | ESTs | 5.8 | 321 | 55 | 17 |
| 10 | 124059 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 10.4 | 880 | 85 | 5.3 |
| | 124287 | H88296 | Hs.5123 | inorganic pyrophosphatase | 3.1 | 41 | 14 | 2.7 |
| | 124292 | H11341 | Hs.13366 | Homo sapiens cDNA: FLJ23567 fis, clone L | 3.2 | 32 | 1 | 1.5 |
| | 124308 | AA249027 | Hs.241507 | ribosomal protein S6 | 10.5 | 105 | 1 | 9.9 |
| | 124315 | NM_005402 | Hs.288757 | v-ral simian leukemia viral oncogene hom | 12.8 | 141 | 11 | 12.2 |
| 15 | 124461 | AF283776 | Hs.80285 | Homo sapiens mRNA; cDNA DKFZp586C1723 (f | 3.1 | 31 | 1 | 1.8 |
| | 124483 | AI821780 | Hs.179864 | ESTs | 3.3 | 33 | 1 | 1.7 |
| | 124677 | R01073 | | gb:ye84c03.s1 Soares fetal liver spleen | 4.2 | 42 | 7 | 3 |
| | 124777 | R41933 | Hs.140237 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.4 | 210 | 63 | 3.3 |
| | 124940 | AF068846 | Hs.103804 | heterogeneous nuclear ribonucleoprotein | 6.5 | 162 | 25 | 14.7 |
| | 125079 | T90298 | Hs.271396 | ESTs | 3.1 | 31 | 6 | 2.4 |
| 20 | 125091 | T91518 | | gb:ye20f05.s1 Stratagene lung (937210) H | 3.4 | 985 | 286 | 2.8 |
| | 125103 | AA570056 | Hs.122730 | ESTs, Moderately similar to KIAA1215 pro | 3.6 | 224 | 63 | 4 |
| | 125144 | AB037742 | Hs.24336 | KIAA1321 protein | 6.3 | 63 | 6 | 5 |
| | 125150 | W38240 | | Empirically selected from AFFX single pr | 3.6 | 38 | 11 | 2.6 |
| | 125156 | W93048 | Hs.250723 | hypothetical protein MGC2747 | 3.1 | 31 | 1 | 2.8 |
| 25 | 125226 | AA782536 | Hs.122647 | N-myristoyltransferase 2 | 3.2 | 37 | 12 | 3.6 |
| | 125279 | AW401809 | Hs.4779 | KIAA1150 protein | 13.1 | 131 | 1 | 5.1 |
| | 125299 | T32982 | Hs.102720 | ESTs | 7.7 | 81 | 11 | 7.6 |
| | 125303 | AA173319 | Hs.288193 | hypothetical protein MGC12217 | 14.3 | 143 | 9 | 13.1 |
| 30 | 125377 | W72949 | Hs.77495 | UBX domain-containing 1 | 3.3 | 34 | 11 | 3.2 |
| | 125390 | AL038165 | Hs.75187 | translocase of outer mitochondrial membr | 8.2 | 124 | 15 | 11.5 |
| | 125471 | AA421691 | Hs.152601 | UDP-glucose ceramide glucosyltransferase | 3.7 | 224 | 61 | 21 |
| | 125617 | AA287921 | Hs.164950 | ESTs | 6.7 | 67 | 1 | 6 |
| | 125621 | T62641 | Hs.278544 | acetyl-Coenzyme A acetyltransferase 2 (a | 5.5 | 55 | 10 | 4.2 |
| 35 | 125628 | AA418069 | Hs.241493 | natural killer-tumor recognition sequenc | 5.5 | 63 | 12 | 1 |
| | 125660 | AW292171 | Hs.23978 | scaffold attachment factor B | 4.3 | 68 | 16 | 2.8 |
| | 125698 | AF078847 | Hs.191356 | general transcription factor IIH, polype | 4.8 | 48 | 5 | 4.1 |
| | 125745 | AI858032 | Hs.75722 | ribophorin II | 6.8 | 223 | 33 | 2.8 |
| | 125770 | AA143045 | Hs.81665 | v-kit Hardy-Zuckerman 4 feline sarcoma v | 8.3 | 87 | 11 | 0.4 |
| 40 | 125827 | NM_003403 | Hs.97496 | YY1 transcription factor | 11.3 | 124 | 11 | 9.7 |
| | 125852 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 30.6 | 306 | 4 | 26.5 |
| | 126349 | T30968 | Hs.13531 | hypothetical protein FLJ10971 | 4.9 | 68 | 14 | 1.4 |
| | 126384 | AW090198 | Hs.4779 | KIAA1150 protein | 6.4 | 74 | 12 | 6.6 |
| | 126590 | W78968 | Hs.181307 | H3 histone, family 3A | 5 | 264 | 53 | 3.4 |
| 45 | 126645 | AA316181 | Hs.61635 | slx transmembrane epithelial antigen of | 3.8 | 38 | 1 | 2.7 |
| | 126663 | AW518478 | Hs.181297 | ESTs | 3.6 | 36 | 6 | 2.9 |
| | 126695 | AA643322 | Hs.172028 | a disintegrin and metalloproteinase doma | 3.1 | 31 | 1 | 2.5 |
| | 126764 | AA036755 | Hs.102178 | syntaxin 16 | 4.4 | 76 | 18 | 1 |
| | 126801 | AW663887 | Hs.7337 | hypothetical protein FLJ10936 | 3.8 | 38 | 1 | 3 |
| 50 | 126813 | AW163483 | Hs.48320 | double ring-finger protein, Dofin | 6.7 | 155 | 23 | 1.4 |
| | 126838 | AL043489 | Hs.279609 | mitochondrial carrier homolog 2 | 8.8 | 110 | 13 | 10.5 |
| | 126855 | AA129640 | Hs.128065 | ESTs | 3.6 | 36 | 10 | 1.9 |
| | 126971 | T26989 | Hs.283664 | aspartate beta-hydroxylase | 5.5 | 79 | 15 | 4.4 |
| | 127167 | AA625690 | Hs.190272 | ESTs | 3.1 | 33 | 11 | 2.3 |
| 55 | 127251 | AA936428 | Hs.128638 | ESTs | 3.5 | 35 | 1 | 3.1 |
| | 127349 | AA412108 | Hs.269350 | ESTs | 4.8 | 106 | 22 | 1 |
| | 127439 | D60237 | Hs.14368 | SH3 domain binding glutamic acid-rich pr | 7.5 | 75 | 1 | 6.5 |
| | 127537 | AI926047 | Hs.162859 | ESTs | 3.8 | 38 | 7 | 3.4 |
| | 127542 | AA703684 | Hs.245474 | ESTs, Moderately similar to ALU5_HUMAN A | 3.3 | 33 | 9 | 0.9 |
| 60 | 127677 | AF175265 | Hs.264190 | vacuolar protein sorting 35 (yeast homol | 4.3 | 152 | 35 | 12.5 |
| | 127774 | AA313639 | Hs.119488 | cystein-rich hydrophobic domain 2 | 5.4 | 73 | 14 | 6.8 |
| | 127999 | AW978827 | Hs.69851 | nucleolar protein family A, member 1 (H/ | 5.2 | 81 | 16 | 1.1 |
| | 128218 | AA186733 | Hs.292154 | stromal cell protein | 3.9 | 220 | 57 | 2.5 |
| | 128305 | AI954968 | Hs.279009 | matrix Gla protein | 9.4 | 94 | 3 | 5.3 |
| 65 | 128470 | AL049974 | Hs.100261 | Homo sapiens mRNA; cDNA DKFZp564B222 (fr | 4.6 | 46 | 8 | 3.9 |
| | 128482 | AI694143 | Hs.296251 | programmed cell death 4 | 7.2 | 72 | 1 | 5.8 |
| | 128501 | AL133572 | Hs.199009 | protein containing CXXC domain 2 | 3.8 | 38 | 1 | 0.9 |
| | 128517 | AW994403 | Hs.100861 | hypothetical protein FLJ14600 | 5.6 | 73 | 13 | 6.1 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| 5 | 128530 | AI932995 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 4.2 | 104 | 25 | 7.8 |
| | 128579 | N25956 | Hs.101810 | Homo sapiens cDNA FLJ14232 fis, clone NT | 3.1 | 172 | 55 | 3.1 |
| | 128595 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | 3.3 | 105 | 32 | 3 |
| | 128610 | N48373 | Hs.10247 | activated leucocyte cell adhesion molecu | 7.3 | 106 | 15 | 5 |
| | 128653 | D87432 | Hs.10315 | solute carrier family 7 (cationic amino | 3.1 | 31 | 1 | 2.2 |
| 10 | 128742 | AA307211 | Hs.251531 | proteasome (prosome, macropain) subunit, | 3.6 | 130 | 36 | 3.5 |
| | 128773 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 3.9 | 43 | 11 | 1.8 |
| | 128790 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 17.4 | 409 | 24 | 7.8 |
| | 128793 | AB011125 | Hs.105749 | KIAA0553 protein | 3.1 | 34 | 11 | 2.7 |
| | 128794 | NM_014720 | Hs.105751 | Ste20-related serine/threonine kinase | 3.6 | 36 | 5 | 1.5 |
| 15 | 128835 | AK001731 | Hs.106390 | Homo sapiens mRNA; cDNA DKFZp586H0924 (f3.3) | 11.3 | 288 | 87 | 7.9 |
| | 128906 | R57988 | Hs.10706 | epithelial protein lost in neoplasm beta | 11.3 | 113 | 8 | 2.5 |
| | 128925 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 7.1 | 392 | 56 | 3.6 |
| | 128949 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 4.6 | 132 | 29 | 9.7 |
| | 129017 | AA115333 | Hs.107968 | ESTs | 8.2 | 82 | 1 | 7.4 |
| 20 | 129075 | BE250162 | Hs.83765 | dihydrofolate reductase | 5 | 50 | 1 | 3.3 |
| | 129095 | L12350 | Hs.108623 | thrombospondin 2 | 3.2 | 814 | 257 | 2.4 |
| | 129151 | N23018 | Hs.171391 | C-terminal binding protein 2 | 4.4 | 44 | 1 | 3.8 |
| | 129168 | AI132988 | Hs.109052 | chromosome 14 open reading frame 2 | 14.2 | 142 | 6 | 9.4 |
| | 129229 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 7.1 | 71 | 1 | 6.2 |
| 25 | 129243 | BE169531 | Hs.109727 | TAK1-binding protein 2; KIAA0733 protein | 5 | 64 | 13 | 6.3 |
| | 129259 | AF220050 | Hs.181385 | uncharacterized hematopoietic stem/proge | 5.2 | 75 | 15 | 6.4 |
| | 129278 | NM_015344 | Hs.11000 | leptin receptor overlapping transcript-I | 3.7 | 39 | 11 | 3.2 |
| | 129337 | NM_014918 | Hs.110488 | KIAA0990 protein | 9.5 | 95 | 1 | 8.5 |
| | 129351 | AL049538 | Hs.62349 | ras association (RalGDS/AF-6) domain con | 7.6 | 92 | 12 | 1.4 |
| 30 | 129366 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 7.1 | 150 | 21 | 14.5 |
| | 129393 | BE219987 | Hs.166982 | phosphatidylinositol glycan, class F | 3.9 | 54 | 14 | 5.1 |
| | 129457 | X61959 | Hs.207776 | asparitylglucosaminidase | 3.6 | 36 | 1 | 2.7 |
| | 129486 | NM_005754 | Hs.220689 | Ras-GTPase-activating protein SH3-domain | 4 | 40 | 4 | 3.2 |
| | 129586 | AW964541 | Hs.11500 | hypothetical protein FLJ21127 | 4.6 | 199 | 44 | 2.3 |
| 35 | 129598 | N30436 | Hs.11556 | Homo sapiens cDNA FLJ12566 fis, clone NT | 4.2 | 42 | 1 | 3.8 |
| | 129691 | M26939 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 6.4 | 1111 | 175 | 5 |
| | 129698 | BE242144 | Hs.12013 | ATP-binding cassette, sub-family E (OABP | 4.8 | 48 | 8 | 3.8 |
| | 129721 | NM_001415 | Hs.211539 | eukaryotic translation initiation factor | 5.8 | 171 | 30 | 2.9 |
| | 129740 | BE165866 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 4.5 | 45 | 1 | 2.4 |
| 40 | 129755 | R42216 | Hs.12342 | Homo sapiens clone 24538 mRNA sequence | 5.3 | 53 | 9 | 3.6 |
| | 129801 | R39246 | Hs.239666 | Homo sapiens cDNA FLJ13495 fis, clone PL | 3.1 | 31 | 2 | 2.5 |
| | 129821 | AB028945 | Hs.12696 | cortactin SH3 domain-binding protein | 11.4 | 114 | 1 | 10 |
| | 129869 | AI222069 | Hs.13015 | hypothetical protein similar to mouse Dn | 4.7 | 556 | 119 | 4.5 |
| | 129865 | T71333 | Hs.13854 | ESTs | 3.1 | 31 | 3 | 3 |
| 45 | 129977 | NM_000399 | Hs.1395 | early growth response 2 (Krox-20) Drosop | 3.2 | 32 | 1 | 0.2 |
| | 130036 | BE061916 | Hs.125849 | chromosome 8 open reading frame 2 | 6.7 | 67 | 1 | 5.7 |
| | 130057 | AF027153 | Hs.324787 | solute carrier family 5 (inositol transp | 1 | 1 | 1 | 1 |
| | 130095 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 14.6 | 219 | 15 | 7.6 |
| | 130115 | T47294 | Hs.149923 | X-box binding protein 1 | 3.1 | 1336 | 434 | 1.4 |
| 50 | 130170 | AW977534 | Hs.151469 | calcium/calmodulin-dependent serine prot | 5.3 | 53 | 9 | 3.2 |
| | 130173 | U38847 | Hs.151518 | TAR (HIV) RNA-binding protein 1 | 4.2 | 46 | 11 | 1.1 |
| | 130343 | AB040914 | Hs.278628 | KIAA1481 protein | 13.2 | 331 | 25 | 12.4 |
| | 130356 | AF127577 | Hs.155017 | nuclear receptor interacting protein 1 | 3.3 | 354 | 108 | 4 |
| | 130367 | AL135301 | Hs.8768 | hypothetical protein FLJ10849 | 8.1 | 81 | 9 | 5.5 |
| 55 | 130385 | AW067800 | Hs.155223 | stanniocalcin 2 | 72.2 | 722 | 1 | 1.9 |
| | 130407 | BE385099 | Hs.334727 | hypothetical protein MGC3017 | 6.5 | 65 | 4 | 5.3 |
| | 130417 | AW163518 | Hs.155485 | huntingtin interacting protein 2 | 3.5 | 79 | 23 | 2.5 |
| | 130441 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 6.1 | 61 | 1 | 5.7 |
| | 130455 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 10.8 | 706 | 66 | 9.2 |
| 60 | 130466 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 3.9 | 39 | 1 | 1.9 |
| | 130526 | AW876523 | Hs.15929 | hypothetical protein FLJ12910 | 3.9 | 39 | 1 | 2.6 |
| | 130567 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 4.4 | 44 | 1 | 4.1 |
| | 130604 | AA383256 | Hs.1657 | estrogen receptor 1 | 32.2 | 322 | 1 | 4.7 |
| | 130614 | AI354355 | Hs.16697 | down-regulator of transcription 1, TBP-b | 5.2 | 251 | 48 | 21 |
| 65 | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 10 | 100 | 1 | 7.6 |
| | 130619 | AI963376 | Hs.12532 | chromosome 1 open reading frame 21 | 3.9 | 39 | 1 | 3.4 |
| | 130625 | AF176012 | Hs.260720 | J domain containing protein 1 | 10.5 | 105 | 1 | 9 |
| | 130677 | AL161961 | Hs.17767 | KIAA1554 protein | 6.8 | 129 | 19 | 12.1 |
| | 130681 | R62676 | Hs.17820 | Rho-associated, coiled-coil containing p | 4.1 | 41 | 1 | 3.6 |
| 65 | 130693 | R68537 | Hs.17962 | ESTs | 9.2 | 234 | 26 | 16.8 |
| | 130712 | AJ271881 | Hs.279762 | bromodomain-containing 7 | 17.5 | 175 | 2 | 12.8 |

| | | | | | | | | |
|----|--------|-----------|-----------|---|------|------|-----|------|
| 5 | 130723 | BE247676 | Hs.18442 | E-1 enzyme | 8.1 | 81 | 3 | 2.8 |
| | 130751 | AF052105 | Hs.18879 | chromosome 12 open reading frame | 4.9 | 49 | 1 | 4.3 |
| | 130780 | AA197226 | Hs.19347 | hypothetical protein MGC11321 | 3.6 | 100 | 28 | 6.6 |
| | 130863 | Y10805 | Hs.20521 | HMT1 (hnRNP methyltransferase, S. cerevi | 3.4 | 525 | 154 | 5.3 |
| | 130871 | AF080158 | Hs.226573 | inhibitor of kappa light polypeptide gen | 10.5 | 121 | 12 | 1.6 |
| | 130888 | AL044315 | Hs.173094 | Homo sapiens mRNA for KIAA1750 protein, | 6 | 202 | 34 | 3.7 |
| | 130974 | NM_003528 | Hs.2178 | H2B histone family, member Q | 7.1 | 100 | 14 | 7.5 |
| | 130979 | NM_012446 | Hs.169833 | single-stranded-DNA-binding protein | 3.2 | 87 | 27 | 1.7 |
| 10 | 130987 | BE613269 | Hs.21893 | hypothetical protein DKFZp761N0624 | 3.5 | 124 | 35 | 6.5 |
| | 130993 | T97401 | Hs.21929 | ESTs | 4.5 | 45 | 1 | 2.5 |
| | 131076 | AA749230 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosam | 3.2 | 210 | 66 | 3.8 |
| | 131085 | BE207357 | Hs.3454 | KIAA1821 protein | 3.8 | 42 | 11 | 0.6 |
| | 131126 | NM_016156 | Hs.181326 | KIAA1073 protein | 6.7 | 67 | 6 | 1.9 |
| | 131129 | BE541042 | Hs.23240 | Homo sapiens cDNA: FLJ21848 fis, clone H | 5.8 | 115 | 20 | 2.5 |
| 15 | 131148 | AW953575 | Hs.303125 | p53-induced protein PIGPC1 | 3.8 | 585 | 153 | 3.7 |
| | 131164 | AW013807 | Hs.182265 | keratin 19 | 5.2 | 1320 | 256 | 3.2 |
| | 131176 | AA465113 | Hs.23853 | ESTs, Weakly similar to A34615 profilagg | 3.8 | 38 | 1 | 3.3 |
| | 131200 | BE540516 | Hs.293732 | hypothetical protein MGC3195 | 4.8 | 48 | 1 | 4.1 |
| | 131216 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 6.1 | 343 | 56 | 16.4 |
| 20 | 131245 | AL080080 | Hs.24766 | thioredoxin domain-containing | 8 | 100 | 13 | 2.9 |
| | 131248 | AI038989 | Hs.332633 | Bardet-Biedl syndrome 2 | 4 | 95 | 24 | 1.1 |
| | 131273 | AW206008 | Hs.283378 | Homo sapiens cDNA: FLJ21778 fis, clone H | 4.6 | 239 | 53 | 3.5 |
| | 131319 | NM_003155 | Hs.25590 | stannocalcin 1 | 3.5 | 402 | 114 | 2.1 |
| | 131367 | AI750575 | Hs.173933 | nuclear factor I/A | 3.3 | 775 | 233 | 2.4 |
| 25 | 131375 | AW293165 | Hs.143134 | ESTs | 3.8 | 38 | 1 | 3 |
| | 131379 | AK001123 | Hs.26176 | hypothetical protein FLJ10261 | 3.9 | 116 | 30 | 0.5 |
| | 131388 | NM_014810 | Hs.92200 | KIAA0480 gene product | 7.6 | 76 | 1 | 5 |
| | 131475 | AA992841 | Hs.27263 | KIAA1458 protein | 5.1 | 113 | 22 | 6.1 |
| | 131492 | AI452601 | Hs.288869 | nuclear receptor subfamily 2, group F, m | 8.4 | 169 | 20 | 4.6 |
| 30 | 131501 | AV661958 | Hs.8207 | GK001 protein | 3.1 | 197 | 63 | 18.7 |
| | 131535 | N22120 | Hs.75277 | hypothetical protein FLJ13910 | 5.9 | 59 | 1 | 4.4 |
| | 131544 | AL355715 | Hs.28555 | programmed cell death 9 (PDCD9) | 5.1 | 51 | 1 | 3.9 |
| | 131546 | AA093668 | Hs.28578 | muscleblind (Drosophila)-like | 3.8 | 79 | 21 | 6.9 |
| | 131562 | NM_003512 | Hs.28777 | H2A histone family, member L | 4 | 350 | 88 | 3 |
| 35 | 131564 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 4.7 | 381 | 81 | 6.4 |
| | 131604 | AA306477 | Hs.29379 | hypothetical protein FLJ10687 | 4.6 | 46 | 7 | 3.8 |
| | 131684 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | 3.2 | 82 | 26 | 6.6 |
| | 131687 | BE297635 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 6.7 | 93 | 14 | 8.4 |
| | 131689 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 3.8 | 51 | 14 | 1.7 |
| 40 | 131693 | AW963776 | Hs.110796 | SAR1 protein | 7.2 | 72 | 4 | 5.7 |
| | 131739 | AF017986 | Hs.31386 | secreted frizzled-related protein 2 | 2.1 | 1561 | 757 | 1.7 |
| | 131742 | AA961420 | Hs.31433 | ESTs | 11.7 | 117 | 1 | 10.1 |
| | 131775 | AB014548 | Hs.31921 | KIAA0648 protein | 4.8 | 48 | 1 | 4.6 |
| | 131787 | D87077 | Hs.196275 | KIAA0240 protein | 3.2 | 207 | 64 | 5.5 |
| 45 | 131798 | X86098 | Hs.301449 | adenovirus 5 E1A binding protein | 3.4 | 115 | 34 | 9.1 |
| | 131836 | W00712 | Hs.32990 | DKFZP566F084 protein | 5.8 | 91 | 16 | 1.4 |
| | 131853 | AI681917 | Hs.3321 | ESTs, Highly similar to IRIX1_HUMAN IROQU | 4.9 | 632 | 129 | 1.7 |
| | 131877 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 6.8 | 68 | 1 | 5.6 |
| | 131881 | AW361018 | Hs.3383 | upstream regulatory element binding prot | 4 | 140 | 35 | 1.8 |
| 50 | 131885 | BE502341 | Hs.3402 | ESTs | 5.7 | 57 | 1 | 4.5 |
| | 131904 | AF078866 | Hs.284296 | Homo sapiens cDNA: FLJ22993 fis, clone K | 5.5 | 90 | 17 | 2.9 |
| | 131919 | T15803 | Hs.272458 | protein phosphatase 3 (formerly 2B), cat | 5.6 | 95 | 17 | 9.1 |
| | 131941 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 7.4 | 103 | 14 | 6.5 |
| | 131945 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.7 | 37 | 1 | 3.4 |
| 55 | 131949 | AK000010 | Hs.258798 | hypothetical protein FLJ20003 | 3.5 | 35 | 1 | 2.5 |
| | 131965 | W79283 | Hs.35962 | ESTs | 5.5 | 168 | 31 | 4.4 |
| | 131977 | U90441 | Hs.3622 | procollagen-proline, 2-oxoglutarate 4-di | 3.7 | 37 | 9 | 2.8 |
| | 131985 | AA503020 | Hs.36563 | hypothetical protein FLJ22418 | 40.2 | 402 | 1 | 4 |
| | 131993 | AI878910 | Hs.3688 | cisplatin resistance-associated overexpr | 7.3 | 73 | 1 | 1.2 |
| 60 | 132064 | AA121098 | Hs.3838 | serum-inducible kinase | 22.6 | 226 | 10 | 0.9 |
| | 132094 | NM_016045 | Hs.3945 | CGI-107 protein | 3.1 | 227 | 73 | 16.8 |
| | 132109 | AW190902 | Hs.40098 | cysteine knot superfamily 1, BMP antagon | 3.5 | 73 | 21 | 6.3 |
| | 132116 | AW960474 | Hs.40289 | ESTs | 3.6 | 141 | 39 | 12.6 |
| | 132143 | D52059 | Hs.7972 | KIAA0871 protein | 4.9 | 49 | 1 | 4.1 |
| 65 | 132160 | W26406 | Hs.295923 | seven in absentia (Drosophila) homolog 1 | 4.4 | 53 | 12 | 2.1 |
| | 132164 | AI752235 | Hs.41270 | procollagen-lysine, 2-oxoglutarate 5-dio | 5 | 225 | 45 | 9.1 |
| | 132180 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 10.7 | 433 | 41 | 7.2 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|-----|-----|------|
| | 132197 | AI699482 | Hs.42151 | ESTs | 3.4 | 58 | 17 | 4 |
| | 132256 | AI078645 | Hs.431 | murine leukemia viral (bmi-1) oncogene h | 4.2 | 42 | 1 | 2.2 |
| | 132298 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 3.4 | 34 | 2 | 3 |
| 5 | 132316 | U28831 | Hs.44566 | KIAA1641 protein | 18.6 | 186 | 10 | 1.5 |
| | 132325 | N37065 | Hs.44856 | hypothetical protein FLJ12116 | 5.5 | 323 | 59 | 10.5 |
| | 132358 | NM_003542 | Hs.46423 | H4 histone family, member G | 3.3 | 979 | 298 | 2.2 |
| | 132384 | AA312135 | Hs.46967 | HSPCO34 protein | 3.6 | 36 | 1 | 3.1 |
| | 132388 | W32624 | Hs.278626 | Arg/Ab-Interacting protein ArgBP2 | 5.9 | 186 | 32 | 3.7 |
| | 132393 | AL135094 | Hs.47334 | hypothetical protein FLJ14495 | 4.2 | 159 | 38 | 7.1 |
| 10 | 132407 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 4.6 | 46 | 1 | 4.3 |
| | 132425 | N87549 | Hs.125287 | zinc finger protein ZNF140-like protein | 3.6 | 146 | 41 | 1.1 |
| | 132440 | AB020699 | Hs.112751 | KIAA0892 protein | 3.3 | 33 | 4 | 2.9 |
| | 132465 | AW169847 | Hs.49169 | KIAA1634 protein | 8.3 | 145 | 18 | 3.7 |
| | 132522 | AB023164 | Hs.5070 | KIAA0947 protein | 4.6 | 46 | 1 | 4.4 |
| 15 | 132528 | T78736 | Hs.50758 | SMC4 (structural maintenance of chromoso | 9.3 | 93 | 1 | 8.4 |
| | 132530 | AA306105 | Hs.50785 | SEC22, vesicle trafficking protein (S. c | 4.9 | 49 | 1 | 4.4 |
| | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 11.8 | 201 | 17 | 19.1 |
| | 132572 | AI929659 | Hs.237825 | signal recognition particle 72kD | 3.8 | 38 | 1 | 3 |
| | 132592 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fls, clone H | 4.8 | 93 | 20 | 3.1 |
| 20 | 132602 | AW606927 | Hs.5306 | hypothetical protein DKFZp586F1122 simil | 6.1 | 61 | 2 | 5.9 |
| | 132616 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 3.4 | 193 | 58 | 12.3 |
| | 132617 | AF037335 | Hs.5338 | carbonic anhydrase XII | 14.2 | 390 | 28 | 22.5 |
| | 132618 | AL050025 | Hs.279916 | hypothetical protein FLJ20151 | 3.3 | 909 | 274 | 3.2 |
| | 132632 | AU076916 | Hs.5398 | guanine monophosphate synthetase | 5 | 50 | 1 | 4.1 |
| 25 | 132668 | AB018319 | Hs.5460 | KIAA0776 protein | 4.2 | 171 | 41 | 12.6 |
| | 132742 | AA025480 | Hs.292812 | ESTs, Weakly similar to T33468 hypotheti | 6.5 | 65 | 1 | 5.6 |
| | 132790 | AW242243 | Hs.168670 | peroxisomal farnesylated protein | 3.7 | 37 | 1 | 2.2 |
| | 132811 | U25435 | Hs.57419 | CCCTC-binding factor (zinc finger protei | 7 | 115 | 17 | 5.4 |
| | 132852 | AL120050 | Hs.58220 | Homo sapiens cDNA: FLJ23005 fls, clone L | 3.3 | 61 | 19 | 5.1 |
| 30 | 132856 | NM_001448 | Hs.58367 | glypican 4 | 4.8 | 48 | 1 | 3.6 |
| | 132880 | BE077155 | Hs.177537 | hypothetical protein DKFZp761B1514 | 12.6 | 126 | 8 | 9.9 |
| | 132902 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 11 | 187 | 17 | 10.4 |
| | 132906 | BE613337 | Hs.234896 | geminin | 3.3 | 106 | 33 | 2.6 |
| | 132914 | AL047045 | Hs.60293 | Homo sapiens clone 122482 unknown mRNA | 3.5 | 110 | 32 | 2.1 |
| 35 | 132968 | AF234532 | Hs.61638 | myosin X | 4.1 | 62 | 15 | 4.9 |
| | 132977 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 22.1 | 221 | 9 | 17.8 |
| | 132990 | X77343 | Hs.334334 | transcription factor AP-2 alpha (activat | 12.7 | 311 | 25 | 2.4 |
| | 132994 | AA112748 | Hs.279905 | clone HQ0310 PRO0310p1 | 3 | 380 | 127 | 5.5 |
| 40 | 133011 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 7.3 | 271 | 37 | 2.3 |
| | 133015 | AJ002744 | Hs.246315 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 4.6 | 427 | 93 | 10.4 |
| | 133070 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 3.6 | 36 | 1 | 3.1 |
| | 133091 | AK001628 | Hs.64691 | KIAA0483 protein | 5.2 | 117 | 23 | 5 |
| | 133192 | AA218564 | Hs.67052 | vacuolar protein sorting 26 (yeast homol | 3.1 | 359 | 118 | 2.5 |
| | 133197 | AI275243 | Hs.180201 | hypothetical protein FLJ20671 | 5.1 | 58 | 12 | 5.7 |
| 45 | 133199 | AF231981 | Hs.250175 | homolog of yeast long chain polyunsatura | 3 | 816 | 275 | 3.9 |
| | 133221 | W32474 | Hs.301746 | RAP2A, member of RAS oncogene family | 3.1 | 234 | 76 | 8.6 |
| | 133240 | AK001489 | Hs.242894 | ADP-ribosylation factor-like 1 | 8.1 | 81 | 1 | 4.6 |
| | 133271 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 12.4 | 124 | 6 | 10.8 |
| | 133291 | BE297855 | Hs.69855 | NRAS-related gene | 3.3 | 33 | 1 | 2.9 |
| 50 | 133294 | AJ001388 | Hs.69997 | zinc finger protein 238 | 7.9 | 234 | 30 | 18.9 |
| | 133350 | AI499220 | Hs.71573 | hypothetical protein FLJ10074 | 4.6 | 46 | 5 | 3.5 |
| | 133362 | AK001519 | Hs.7194 | CGI-74 protein | 5 | 110 | 22 | 9.7 |
| | 133370 | AF245505 | Hs.72157 | DKFZP564I1922 protein | 3.2 | 725 | 227 | 3.2 |
| | 133407 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 4.1 | 374 | 91 | 1.1 |
| 55 | 133422 | AB033061 | Hs.73287 | KIAA1235 protein | 4.3 | 43 | 1 | 3.9 |
| | 133435 | AI929357 | Hs.323966 | Homo sapiens clone H63 unknown mRNA | 5.5 | 186 | 34 | 16.5 |
| | 133479 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 3.5 | 35 | 7 | 2.1 |
| | 133493 | AW998046 | Hs.194369 | arginine-glutamic acid dipeptide (RE) re | 3.6 | 39 | 11 | 0.4 |
| | 133504 | NM_004415 | Hs.74316 | desmoplakin (DPI, DPII) | 4.1 | 640 | 158 | 3 |
| 60 | 133517 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 3.2 | 351 | 111 | 5.2 |
| | 133536 | W25797 | Hs.177486 | amyloid beta (A4) precursor protein (pro | 3.2 | 226 | 71 | 2.8 |
| | 133578 | AU077050 | Hs.75066 | translin | 3.4 | 178 | 53 | 8.8 |
| | 133633 | D21262 | Hs.75337 | nucleolar and coiled-body phosphoprotein | 4.7 | 47 | 1 | 4 |
| | 133640 | AW246428 | Hs.75355 | ubiquitin-conjugating enzyme E2N (homolo | 8.5 | 85 | 1 | 7.2 |
| 65 | 133669 | NM_006925 | Hs.166975 | splicing factor, arginine/serine-rich 5 | 3.6 | 36 | 1 | 0.4 |
| | 133681 | AI352558 | Hs.75544 | tyrosine 3-monooxygenase/tryptophan 5-mo | 3.4 | 234 | 68 | 10.7 |
| | 133746 | AW410035 | Hs.75862 | MAD (mothers against decapentaplegic, Dr | 9.3 | 93 | 1 | 7.8 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| | 133765 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 3.2 | 560 | 174 | 2.6 |
| | 133780 | AA557660 | Hs.76152 | decorin | 5.4 | 144 | 27 | 13.3 |
| | 133784 | BE622743 | Hs.301064 | arfaplin 1 | 4.7 | 47 | 1 | 4.1 |
| 5 | 133814 | NM_002462 | Hs.76391 | myxovirus (influenza) resistance 1, homo | 3.3 | 380 | 114 | 4.9 |
| | 133829 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 6.7 | 304 | 46 | 7.8 |
| | 133845 | AA147026 | Hs.76704 | ESTs | 6.2 | 600 | 97 | 4.1 |
| | 133913 | AU076964 | Hs.7753 | calumenin | 3.3 | 889 | 267 | 5 |
| | 133968 | AA355986 | Hs.232068 | transcription factor 8 (represses interl | 3.7 | 91 | 25 | 2.6 |
| 10 | 133990 | R48316 | Hs.7822 | Homo sapiens mRNA; cDNA DKFZp564C1216 (f | 3.4 | 91 | 27 | 8.5 |
| | 133999 | AA535244 | Hs.78305 | RAB2, member RAS oncogene family | 7.8 | 78 | 1 | 5.6 |
| | 134032 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 5.9 | 59 | 1 | 3.3 |
| | 134064 | AF091622 | Hs.78893 | KIAA0244 protein | 5.8 | 58 | 1 | 4.9 |
| | 134087 | U51166 | Hs.173824 | thymine-DNA glycosylase | 6.4 | 100 | 16 | 4.4 |
| | 134089 | R51273 | Hs.79029 | ESTs | 5.1 | 51 | 9 | 3.8 |
| 15 | 134095 | NM_004354 | Hs.79069 | cyclin G2 | 5 | 50 | 1 | 3.2 |
| | 134098 | BE513171 | Hs.79086 | mitochondrial ribosomal protein L3 | 4.8 | 246 | 51 | 3.9 |
| | 134110 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | 4.5 | 1472 | 330 | 2.1 |
| | 134125 | NM_014781 | Hs.50421 | KIAA0203 gene product | 4.6 | 69 | 15 | 5.8 |
| | 134246 | D28459 | Hs.80612 | ubiquitin-conjugating enzyme E2A (RAD6 h | 7 | 97 | 14 | 7.5 |
| 20 | 134257 | C05768 | Hs.8078 | Homo sapiens clone FBD3 Cri-du-chat crit | 3.4 | 34 | 5 | 2.6 |
| | 134272 | X76040 | Hs.278614 | protease, serine, 15 | 3.6 | 36 | 1 | 2.8 |
| | 134282 | R45621 | Hs.81057 | hypothetical protein MGC2718 | 6.7 | 67 | 9 | 5.7 |
| | 134288 | AI022650 | Hs.8117 | erbB2-interacting protein ERBIN | 4.5 | 137 | 31 | 12 |
| | 134321 | BE538082 | Hs.8172 | ESTs, Moderately similar to A46010 X-lin | 5.2 | 52 | 1 | 4.9 |
| 25 | 134326 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 8.6 | 568 | 66 | 22.4 |
| | 134328 | AW959281 | Hs.8184 | ESTs | 4.8 | 53 | 11 | 3.7 |
| | 134348 | AW291946 | Hs.82065 | interleukin 6 signal transducer (gp130, | 7.1 | 71 | 4 | 6.4 |
| | 134359 | NM_001982 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 3 | 68 | 23 | 2.8 |
| | 134367 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 4.4 | 44 | 1 | 4.1 |
| 30 | 134374 | N22687 | Hs.8236 | ESTs | 13.3 | 445 | 34 | 6 |
| | 134380 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 4.5 | 45 | 2 | 3.4 |
| | 134395 | AA456539 | Hs.8262 | lysosomal | 6 | 60 | 5 | 5.9 |
| | 134401 | AI916662 | Hs.211577 | kinectin 1 (kinesin receptor) | 4.1 | 301 | 73 | 6.1 |
| | 134405 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 4.6 | 1216 | 267 | 4.4 |
| 35 | 134415 | AI750762 | Hs.82911 | protein tyrosine phosphatase type IVA, m | 4.9 | 163 | 34 | 15.1 |
| | 134417 | NM_006416 | Hs.82921 | solute carrier family 35 (CMP-sialic aci | 4.9 | 49 | 3 | 3.8 |
| | 134419 | W95642 | Hs.82961 | trefoil factor 3 (intestinal) | 3.2 | 1872 | 592 | 3.3 |
| | 134421 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 6.3 | 1075 | 171 | 3.8 |
| | 134436 | U29344 | Hs.83190 | fatty acid synthase | 3.3 | 710 | 217 | 2 |
| 40 | 134485 | X82153 | Hs.83942 | cathepsin K (pseudosclerosis) | 34.3 | 411 | 12 | 5.1 |
| | 134487 | AF061739 | Hs.83954 | protein associated with PRK1 | 4.8 | 153 | 32 | 4.3 |
| | 134495 | D63477 | Hs.84087 | KIAA0143 protein | 3.1 | 147 | 48 | 12.7 |
| | 134520 | BE091005 | Hs.74861 | activated RNA polymerase II transcriptio | 3.3 | 33 | 1 | 2 |
| | 134542 | M14156 | Hs.85112 | insulin-like growth factor 1 (somatomedi | 4.2 | 42 | 5 | 2.6 |
| 45 | 134570 | U66615 | Hs.172280 | SWI/SNF related, matrix associated, acti | 3.9 | 39 | 1 | 2.5 |
| | 134590 | AW903849 | Hs.173840 | HUEL (C4orf1)-interacting protein | 3.7 | 41 | 11 | 0.6 |
| | 134604 | NM_002884 | Hs.865 | RAP1A, member of RAS oncogene family | 5.2 | 52 | 1 | 3 |
| | 134612 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 4.9 | 49 | 1 | 3.7 |
| | 134643 | AW299723 | Hs.87223 | bone morphogenetic protein receptor, typ | 5.2 | 52 | 5 | 3.5 |
| 50 | 134654 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 6.4 | 64 | 1 | 5.1 |
| | 134656 | AI750878 | Hs.87409 | thrombospondin 1 | 12.6 | 126 | 1 | 10.8 |
| | 134672 | AF271212 | Hs.322901 | disruptor of silencing 10 | 5.4 | 81 | 15 | 2.6 |
| | 134700 | AK000506 | Hs.8868 | golgi SNAP receptor complex member 1 | 3.4 | 179 | 52 | 1.5 |
| | 134711 | X04011 | Hs.88974 | cytochrome b-245, beta polypeptide (chro | 3.2 | 143 | 45 | 13.9 |
| 55 | 134722 | AF129536 | Hs.284226 | F-box only protein 6 | 7 | 70 | 6 | 6 |
| | 134856 | BE281128 | Hs.9030 | TONDU | 3.1 | 31 | 1 | 2.3 |
| | 134880 | AI879195 | Hs.90606 | 15 kDa selenoprotein | 5.7 | 57 | 1 | 5 |
| | 134917 | X87241 | Hs.166994 | FAT tumor suppressor (Drosophila) homolo | 3.2 | 153 | 48 | 4.7 |
| | 134921 | AL137491 | Hs.125511 | Homo sapiens mRNA; cDNA DKFZp434P1530 (f | 4 | 452 | 114 | 2 |
| 60 | 134982 | AK002085 | Hs.92308 | Homo sapiens cDNA FLJ11223 fis, clone PL | 5.1 | 150 | 30 | 7.2 |
| | 134989 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked mol | 8.2 | 114 | 14 | 9.9 |
| | 135029 | H58818 | Hs.187579 | hydroxysteroid (17-beta) dehydrogenase 7 | 11.5 | 115 | 1 | 10 |
| | 135035 | AL034344 | Hs.284186 | forkhead box C1 | 5.4 | 259 | 48 | 1.4 |
| | 135051 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.3 | 1296 | 394 | 2.2 |
| 65 | 135062 | AK000967 | Hs.93872 | KIAA1682 protein | 3.8 | 240 | 64 | 3.2 |
| | 135073 | W55956 | Hs.94030 | Homo sapiens mRNA; cDNA DKFZp586E1624 (f | 8.1 | 101 | 13 | 7.9 |
| | 135098 | AW274526 | Hs.277721 | ovarian carcinoma antigen CA125 | 3.3 | 33 | 1 | 2.6 |

| | | | | | | | | | |
|----|--------|-----------|-----------|---|------|------|-----|------|--|
| | 135117 | W52493 | Hs.94694 | Homo sapiens cDNA FLJ10561 fis, clone NT | 5.3 | 53 | 1 | 4.1 | |
| | 135144 | NM_016255 | Hs.95260 | Autosomal Highly Conserved Protein | 7.4 | 74 | 5 | 2.4 | |
| | 135154 | AK001835 | Hs.267812 | sorting nexin 4 | 6.6 | 69 | 11 | 6.3 | |
| 5 | 135155 | AI207958 | Hs.166556 | Homo sapiens, Similar to TEA domain fami | 6.1 | 61 | 1 | 5.1 | |
| | 135172 | AB028956 | Hs.12144 | KIAA1033 protein | 3.4 | 88 | 26 | 1.4 | |
| | 135242 | AI583187 | Hs.9700 | cyclin E1 | 3.1 | 31 | 1 | 2.3 | |
| | 135243 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 3.4 | 169 | 50 | 9.1 | |
| | 135269 | NM_003403 | Hs.97496 | YY1 transcription factor | 3.4 | 475 | 142 | 2.5 | |
| 10 | 135356 | BE312948 | Hs.18104 | hypothetical protein FLJ11274 | 3.1 | 31 | 10 | 1.7 | |
| | 135357 | AI565004 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 4.7 | 710 | 151 | 2.5 | |
| | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 20.6 | 206 | 4 | 19.1 | |
| | 135397 | L14922 | Hs.166563 | replication factor C (activator 1) 1 (14 | 3.2 | 32 | 1 | 2.4 | |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 3.2 | 117 | 37 | 9.4 | |
| 15 | | AI471525 | Hs.247486 | ESTs | 3.8 | 58 | 16 | 5.5 | |
| | | X70683 | Hs.93668 | ESTs | 1.8 | 1047 | 596 | 1.6 | |
| | | L14922 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein | 5 | 285 | 58 | 1.2 | |
| | | M23263 | Hs.904 | amylase-1;6-glucosidase; 4-alpha-glucanotransferase | 3.1 | 31 | 1 | 2.6 | |
| | | AI267886 | Hs.148027 | polymerase (RNA) II (DNA directed) polypeptide B | 7.8 | 137 | 18 | 11.9 | |
| | | AA044840 | Hs.241676 | stromal cell-derived factor 1 | 4.7 | 114 | 25 | 0.9 | |
| 20 | | N90960 | Hs.227459 | ESTs; Moderately similar to !!!! ALU SUBFAMILY | 4.7 | 151 | 32 | 9.3 | |
| | | AA873285 | Hs.137947 | ESTs | 4.7 | 47 | 3 | 4.4 | |
| | | T56679 | Hs.865 | RAP1A; member of RAS oncogene family | 4 | 40 | 1 | 3.4 | |
| | | AA305536 | | *EST176522 Colon carcinoma (Caco-2) cell line II | 3.6 | 121 | 34 | 11.8 | |
| | | AI369384 | | arylsulfatase D | 3.5 | 113 | 33 | 1.7 | |
| 25 | | AA219081 | Hs.242396 | ESTs; Moderately similar to !!!! ALU SUBFAMILY] | 3.4 | 107 | 32 | 9.9 | |

TABLE 10A

Table 10 A shows the accession numbers for those pkeys lacking unigeneID's for Table 10. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|-------------------------|-------------------------------------|
| 123619 | 371681_1 | AA602964 AA609200 |
| 104602 | 524482_2 | H47610 R86920 |
| 121581 | 283769_1 | AA416568 AA442889 AA417233 AA442223 |
| 123523 | genbank_AA608588 | AA608588 |
| 100821 | tigr_HT4306 | M26460 U09116 |
| 125091 | genbank_T91518 | T91518 |
| 125150 | NOT_FOUND_entrez_W38240 | W38240 |
| 118475 | genbank_N66845 | N66845 |
| 104787 | genbank_AA027317 | AA027317 |
| 106055 | genbank_AA417034 | AA417034 |
| 113702 | genbank_T97307 | T97307 |
| 101046 | entrez_K01160 | K01160 |
| 101447 | entrez_M21305 | M21305 |
| 101624 | entrez_M55998 | M55998 |
| 124677 | genbank_R01073 | R01073 |
| 110581 | genbank_H61560 | H61560 |
| 119023 | genbank_N98488 | N98488 |
| 110775 | genbank_N22414 | N22414 |
| 112092 | genbank_R44538 | R44538 |
| 112253 | genbank_R51818 | R51818 |
| 107014 | genbank_AA598820 | AA598820 |
| 114988 | genbank_AA251089 | AA251089 |

TABLE 11: Figure 11 from BRCA 001-3 PCT

5 **Table 11 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.**

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue
 R2: Ratio of 90th percentile tumor to normal body
 R3: Ratio of 75th percentile normal body to tumor
 R4: Ratio of tumor to normal breast tissue

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 | R3 | R4 |
|--------|-----------|-----------|--|------|------|-----|------|
| 100131 | D12485 | Hs.11951 | ectonucleotide pyrophosphatase/phosphodi | 13.2 | 244 | 19 | 9.9 |
| 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fasciclin | 15.7 | 1030 | 66 | 5 |
| 100522 | X51501 | Hs.99949 | prolactin-induced protein | 22.7 | 760 | 34 | 1.4 |
| 100666 | L05424 | Hs.169610 | CD44 antigen (homing function and Indian | 8.5 | 85 | 1 | 3.2 |
| 101104 | AW862258 | Hs.169266 | neuropeptide Y receptor Y1 | 15.3 | 153 | 1 | 14.1 |
| 101478 | NM_002890 | Hs.758 | RAS p21 protein activator (GTPase activa | 9.6 | 96 | 1 | 8.5 |
| 101724 | L11690 | Hs.620 | bullous pemphigoid antigen 1 (230/240kD) | 9.4 | 94 | 1 | 0.3 |
| 101754 | S70114 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-bi | 8.9 | 89 | 5 | 8 |
| 101888 | AL049610 | Hs.95243 | transcription elongation factor A (SII)- | 7.3 | 73 | 1 | 5.3 |
| 102165 | BE313280 | Hs.159627 | death associated protein 3 | 9.3 | 93 | 5 | 8 |
| 102304 | AF015224 | Hs.46452 | mammaglobin 1 | 8.5 | 2058 | 243 | 1.4 |
| 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 6.4 | 428 | 67 | 2.3 |
| 102457 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 20.2 | 202 | 5 | 1.3 |
| 102567 | U63830 | Hs.146847 | TRAF family member-associated NFKB activ | 8.2 | 82 | 1 | 6.8 |
| 102823 | D85390 | Hs.5057 | carboxypeptidase D | 5.6 | 56 | 1 | 5.3 |
| 103557 | AL133415 | Hs.297753 | vimentin | 7.5 | 136 | 18 | 3.4 |
| 103613 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 7.3 | 73 | 1 | 5.2 |
| 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal | 29 | 290 | 1 | 26.8 |
| 104667 | AI239923 | Hs.30098 | ESTs | 14.9 | 149 | 1 | 6.4 |
| 104804 | AI858702 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapien | 7.7 | 77 | 1 | 5.1 |
| 104807 | AI139058 | Hs.125790 | leucine-rich repeat-containing 2 | 7 | 70 | 1 | 6.5 |
| 104896 | AW015318 | Hs.23165 | ESTs | 7.4 | 74 | 1 | 6 |
| 104943 | AF072873 | Hs.114218 | frizzled (Drosophila) homolog 6 | 16.2 | 162 | 1 | 4.2 |
| 105038 | AW503733 | Hs.9414 | KIAA1488 protein | 5.5 | 55 | 1 | 5.2 |
| 105329 | AA234561 | Hs.22862 | ESTs | 2.8 | 131 | 47 | 3.9 |
| 105500 | AW602166 | Hs.222399 | CEGP1 protein | 25.4 | 508 | 20 | 3 |
| 105516 | AK001269 | Hs.30738 | hypothetical protein FLJ10407 | 8.3 | 83 | 3 | 1.8 |
| 105730 | AW377314 | Hs.5364 | DKFZP564I052 protein | 6.9 | 69 | 1 | 4.4 |
| 106012 | AI240665 | Hs.8895 | ESTs | 21.2 | 212 | 6 | 17.4 |
| 106095 | AF115402 | Hs.11713 | E74-like factor 5 (ets domain transcript | 26.3 | 356 | 14 | 1 |
| 106155 | AA425414 | Hs.33287 | nuclear factor I/B | 9.9 | 483 | 49 | 1.8 |
| 107102 | AB037765 | Hs.30652 | KIAA1344 protein | 6.3 | 63 | 1 | 5.4 |
| 107136 | AV661958 | Hs.8207 | GK001 protein | 2.5 | 392 | 155 | 4.3 |
| 107151 | AW378065 | Hs.8687 | ESTs | 15.6 | 156 | 7 | 10.8 |
| 107922 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 9 | 90 | 1 | 5.5 |
| 108339 | AW151340 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 18.7 | 187 | 1 | 17 |
| 109112 | AW419196 | Hs.257924 | hypothetical protein FLJ13782 | 4.1 | 334 | 82 | 3.4 |
| 109292 | AW975746 | Hs.188662 | KIAA1702 protein | 7.1 | 71 | 1 | 6.5 |
| 109415 | U80736 | Hs.110826 | trinucleotide repeat containing 9 | 12.3 | 123 | 1 | 11.3 |
| 109912 | AW390822 | Hs.301528 | L-tryptophan/alpha-aminoadipate aminotra | 14.2 | 142 | 1 | 9.5 |
| 110009 | BE075297 | Hs.6614 | ESTs, Weakly similar to A43932 mucin 2 p | 6.3 | 693 | 110 | 7.2 |
| 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 20.9 | 209 | 1 | 19.5 |
| 111164 | N46180 | Hs.122489 | Homo sapiens cDNA FLJ13289 fls, clone OV | 7.7 | 77 | 1 | 5 |

| | | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-----|------|
| | 111179 | AK000136 | Hs.10760 | asporin (LRR class 1) | 25.1 | 288 | 12 | 6.7 |
| | 111190 | AK002065 | Hs.151046 | hypothetical protein FLJ11193 | 6.3 | 63 | 1 | 5.8 |
| | 111223 | AA852773 | Hs.334838 | KIAA1866 protein | 3.6 | 402 | 112 | 4.9 |
| | 111357 | BE314949 | Hs.87128 | hypothetical protein FLJ23309 | 3.8 | 425 | 111 | 4 |
| 5 | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 5.7 | 567 | 100 | 6.7 |
| | 113047 | AI571940 | Hs.7549 | ESTs | 9.6 | 124 | 13 | 9 |
| | 113702 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen | 12.3 | 129 | 11 | 11.7 |
| | 114124 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 24.2 | 242 | 10 | 5.6 |
| | 114138 | AW384793 | Hs.15740 | Homo sapiens mRNA; cDNA DKFZp434E033 (fr | 6.7 | 67 | 1 | 6.3 |
| 10 | 114768 | AF212848 | Hs.182339 | ets homologous factor | 13.7 | 137 | 1 | 8.9 |
| | 114860 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 9.1 | 91 | 1 | 7.6 |
| | 114965 | AI733881 | Hs.72472 | BMP-R1B | 35.9 | 359 | 10 | 29.7 |
| | 114988 | AA251089 | | gb:zs04f05.s1 NCI_CGAP_GCB1 Homo sapiens | 11.5 | 115 | 1 | 6.9 |
| | 115206 | AW183695 | Hs.186572 | ESTs | 5.8 | 58 | 1 | 5 |
| 15 | 115719 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 7.6 | 144 | 19 | 13.9 |
| | 115844 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 6.2 | 62 | 1 | 5.4 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 1.8 | 1047 | 596 | 1.6 |
| | 116786 | H25836 | Hs.301527 | ESTs, Moderately similar to unknown [H.s | 22.8 | 228 | 9 | 12.4 |
| | 117280 | M18217 | Hs.172129 | Homo sapiens cDNA: FLJ21409 fis, clone C | 3.9 | 322 | 83 | 4.4 |
| 20 | 117412 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 17.4 | 174 | 9 | 6.9 |
| | 118472 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 14.5 | 145 | 1 | 2.4 |
| | 119271 | AI061118 | Hs.65328 | Fanconi anemia, complementation group F | 8.2 | 82 | 1 | 6.4 |
| | 119771 | AI905687 | Hs.2533 | EST | 3.5 | 2073 | 595 | 2.1 |
| | 120562 | BE244580 | Hs.302267 | hypothetical protein FLJ10330 | 8.5 | 127 | 15 | 1.6 |
| 25 | 121463 | AK000282 | Hs.239681 | hypothetical protein FLJ20275 | 10.3 | 103 | 1 | 9.3 |
| | 121723 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 2.9 | 214 | 74 | 3.7 |
| | 122963 | AA478446 | Hs.69559 | KIAA1096 protein | 7.2 | 72 | 1 | 5.7 |
| | 123137 | AI073913 | Hs.100686 | ESTs, Weakly similar to JE0350 Anterior | 9.9 | 351 | 36 | 13.9 |
| | 123619 | AA602964 | | gb:nc097c02.s1 NCI_CGAP_Pr2 Homo sapiens | 8.5 | 85 | 1 | 4.3 |
| 30 | 123709 | AA706910 | Hs.112742 | ESTs | 3.9 | 60 | 16 | 4.8 |
| | 124006 | AI147155 | Hs.270016 | ESTs | 5.8 | 321 | 55 | 17 |
| | 124059 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 10.4 | 880 | 85 | 5.3 |
| | 124308 | AA249027 | Hs.241507 | ribosomal protein S6 | 10.5 | 105 | 1 | 9.9 |
| | 125279 | AW401809 | Hs.4779 | KIAA1150 protein | 13.1 | 131 | 1 | 5.1 |
| 35 | 125617 | AA287921 | Hs.164950 | ESTs | 6.7 | 67 | 1 | 6 |
| | 127439 | D60237 | Hs.14368 | SH3 domain binding glutamic acid-rich pr | 30.6 | 306 | 4 | 26.5 |
| | 128305 | AI954968 | Hs.279009 | matrix Gla protein | 7.5 | 75 | 1 | 6.5 |
| | 128482 | AI694143 | Hs.296251 | programmed cell death 4 | 7.2 | 72 | 1 | 5.8 |
| | 128790 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 17.4 | 409 | 24 | 7.8 |
| 40 | 128925 | R67419 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 7.1 | 392 | 56 | 3.6 |
| | 129017 | AA115333 | Hs.107968 | ESTs | 8.2 | 82 | 1 | 7.4 |
| | 129229 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 7.1 | 71 | 1 | 6.2 |
| | 129337 | NM_014918 | Hs.110488 | KIAA0990 protein | 9.5 | 95 | 1 | 8.5 |
| | 129366 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 7.1 | 150 | 21 | 14.5 |
| 45 | 129821 | AB028945 | Hs.12696 | cortactin SH3 domain-binding protein | 11.4 | 114 | 1 | 10 |
| | 130036 | BE061916 | Hs.125849 | chromosome 8 open reading frame 2 | 6.7 | 67 | 1 | 5.7 |
| | 130057 | AF027153 | Hs.324787 | solute carrier family 5 (inositol transp | 1 | 1 | 1 | 1 |
| | 130095 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 14.6 | 219 | 15 | 7.6 |
| | 130343 | AB040914 | Hs.278628 | KIAA1481 protein | 13.2 | 331 | 25 | 12.4 |
| 50 | 130385 | AW067800 | Hs.155223 | stannocalcin 2 | 72.2 | 722 | 1 | 1.9 |
| | 130407 | BE385099 | Hs.334727 | hypothetical protein MGC3017 | 6.5 | 65 | 4 | 5.3 |
| | 130441 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 6.1 | 61 | 1 | 5.7 |
| | 130455 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 10.8 | 706 | 66 | 9.2 |
| | 130604 | AA383256 | Hs.1657 | estrogen receptor 1 | 32.2 | 322 | 1 | 4.7 |
| 55 | 130617 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 10 | 100 | 1 | 7.6 |
| | 130712 | AJ271881 | Hs.279762 | bromodomain-containing 7 | 17.5 | 175 | 2 | 12.8 |
| | 131148 | AW953575 | Hs.303125 | p53-induced protein PIGPC1 | 3.8 | 585 | 153 | 3.7 |
| | 131388 | NM_014810 | Hs.92200 | KIAA0480 gene product | 7.6 | 76 | 1 | 5 |
| | 131564 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 4.7 | 381 | 81 | 6.4 |
| 60 | 131742 | AA961420 | Hs.31433 | ESTs | 11.7 | 117 | 1 | 10.1 |
| | 131877 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 6.8 | 68 | 1 | 5.6 |
| | 131985 | AA503020 | Hs.36563 | hypothetical protein FLJ22418 | 40.2 | 402 | 1 | 4 |
| | 132316 | U28831 | Hs.44566 | KIAA1641 protein | 18.6 | 186 | 10 | 1.5 |
| | 132528 | T78736 | Hs.50758 | SMC4 (structural maintenance of chromoso | 9.3 | 93 | 1 | 8.4 |
| 65 | 132742 | AA025480 | Hs.292812 | ESTs, Weakly similar to T33468 hypotheti | 6.5 | 65 | 1 | 5.6 |
| | 132990 | X77343 | Hs.334334 | transcription factor AP-2 alpha (activat | 12.7 | 311 | 25 | 2.4 |
| | 133015 | AJ002744 | Hs.246315 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 4.6 | 427 | 93 | 10.4 |

| | | | | | | | | |
|----|--------|----------|-----------|--|------|------|-----|------|
| 5 | 133199 | AF231981 | Hs.250175 | homolog of yeast long chain polyunsatura | 3 | 816 | 275 | 3.9 |
| | 133240 | AK001489 | Hs.242894 | ADP-ribosylation factor-like 1 | 8.1 | 81 | 1 | 4.6 |
| | 133271 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 12.4 | 124 | 6 | 10.8 |
| | 133640 | AW246428 | Hs.75355 | ubiquitin-conjugating enzyme E2N (homolo | 8.5 | 85 | 1 | 7.2 |
| | 133746 | AW410035 | Hs.75862 | MAD (mothers against decapentaplegic, Dr | 9.3 | 93 | 1 | 7.8 |
| 10 | 133999 | AA535244 | Hs.78305 | RAB2, member RAS oncogene family | 7.8 | 78 | 1 | 5.6 |
| | 134110 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | 4.5 | 1472 | 330 | 2.1 |
| | 134485 | X82153 | Hs.83942 | cathepsin K (pseudosclerosis) | 34.3 | 411 | 12 | 5.1 |
| | 134654 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 6.4 | 64 | 1 | 5.1 |
| | 134880 | AI879195 | Hs.90606 | 15 kDa selenoprotein | 5.7 | 57 | 1 | 5 |
| | 135029 | H58818 | Hs.187579 | hydroxysteroid (17-beta) dehydrogenase 7 | 11.5 | 115 | 1 | 10 |
| | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 20.6 | 206 | 4 | 19.1 |
| | 128305 | AI954968 | Hs.279009 | matrix Gla protein | 9.4 | 94 | 3 | 5.3 |

TABLE 11A

Table 11A shows the accession numbers for those pkeys lacking unigeneID's for Table 11. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|------------------|-------------------|
| 123619 | 371681_1 | AA602964 AA609200 |
| 113702 | genbank_T97307 | T97307 |
| 114988 | genbank_AA251089 | AA251089 |

TABLE 12: Figure 12 from BRCA 001-3 PCT

5 **Table 12** depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

| | | | | | | | | |
|----|----------------|---|-----------|--|------|------|-----|-----|
| 10 | Pkey: | Unique Eos probaset identifier number | | | | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | | | | |
| | UnigenelD: | Unigene number | | | | | | |
| | Unigene Title: | Unigene gene title | | | | | | |
| 15 | R1: | Ratio of tumor to normal body tissue | | | | | | |
| | R2: | Ratio of 90 th percentile tumor to body | | | | | | |
| | R3: | Ratio of 75 th percentile body to tumor | | | | | | |
| | R4: | Ratio of tumor to normal breast tissue | | | | | | |
| 20 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 | R3 | R4 |
| | 100131 | D12485 | Hs.11951 | phosphodiesterase I (PC-1) | 13.2 | 244 | 19 | 9.9 |
| | 105500 | AW602166 | Hs.222399 | ESTs | 25.4 | 508 | 20 | 3 |
| | 112244 | AB029000 | Hs.70823 | KIAA1077 protein | 5.7 | 567 | 100 | 6.7 |
| | 114124 | W57554 | Hs.125019 | ESTs | 24.2 | 242 | 10 | 5.6 |
| | 119771 | AI905687 | Hs.2533 | ESTs | 3.5 | 2073 | 595 | 2.1 |
| | 121723 | AA243499 | Hs.104800 | ESTs | 2.9 | 214 | 74 | 3.7 |
| | 128790 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 17.4 | 409 | 24 | 7.8 |
| | 131148 | AW953575 | Hs.303125 | ESTs | 3.8 | 585 | 153 | 3.7 |
| | 131985 | AA503020 | Hs.36563 | ESTs | 40.2 | 402 | 1 | 4 |
| | 133199 | AF231981 | Hs.250175 | Homo sapiens clone 23904 mRNA sequence | 3 | 816 | 275 | 3.9 |

TABLE 13: Table 1 from BRCA 001-5 US

5 **Table 13 depicts a preferred group of genes upregulated in breast cancer cells.**

| | | | | | |
|----|----------------|---|------------|---|------|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal body tissue | | | |
| 15 | | | | | |
| | Pkey | ExAccn | Unigene ID | Unigene Title | R1 |
| | 100038 | M97935 | | control | 16.7 |
| | 100039 | M97935 | | control | 6.3 |
| 20 | 100040 | M97935 | | control | 8.3 |
| | 100041 | M97935 | | control | 14.8 |
| | 100082 | AB003103 | Hs.4295 | proteasome (prosome; macropain) 26S sub | 7.5 |
| | 100091 | AF000177 | Hs.111783 | Lsm1 protein | 4.9 |
| | 100100 | AF006084 | Hs.11538 | actin related protein 2/3 complex; subunit | 4.7 |
| 25 | 100103 | AF007875 | Hs.5085 | dolichyl-phosphate mannosyltransferase p | 13.4 |
| | 100114 | D00596 | Hs.82962 | thymidylate synthetase | 15.9 |
| | 100121 | D10495 | Hs.155342 | protein kinase C; delta | 4.6 |
| | 100123 | D10523 | Hs.168669 | oxoglutarate dehydrogenase (lipoamide) | 7.5 |
| | 100128 | D11094 | Hs.61153 | proteasome (prosome; macropain) 26S sub | 4.4 |
| 30 | 100131 | D12485 | Hs.11951 | phosphodiesterase 1/nucleotide pyrophosp | 8.7 |
| | 100137 | D13627 | Hs.15071 | chaperonin containing TCP1; subunit 8 (t | 9.5 |
| | 100144 | D13643 | Hs.75616 | Human mRNA for KIAA0018 gene; comp | 6 |
| | 100147 | D13666 | Hs.136348 | osteoblast specific factor 2 (fascin-like | 8.5 |
| | 100154 | D14657 | Hs.81892 | KIAA0101 gene product | 10.5 |
| 35 | 100164 | D14812 | Hs.173714 | MORF-related gene X | 4.6 |
| | 100169 | D14878 | Hs.82043 | D123 gene product | 7.9 |
| | 100190 | D21090 | Hs.178658 | RAD23 (S. cerevisiae) homolog B | 5.6 |
| | 100203 | D25538 | Hs.172199 | adenylate cyclase 7 | 9.9 |
| | 100209 | D26308 | Hs.76289 | biliverdin reductase B (flavin reductase (N | 4.9 |
| 40 | 100215 | D26598 | Hs.82793 | proteasome (prosome; macropain) subunit | 14.2 |
| | 100216 | D26599 | Hs.1390 | proteasome (prosome; macropain) subunit | 11.3 |
| | 100219 | D28137 | Hs.118110 | bone marrow stromal cell antigen 2 | 5.7 |
| | 100227 | D28915 | Hs.82316 | interferon-induced; hepatitis C-associated | 5.7 |
| | 100248 | D31888 | Hs.78398 | KIAA0071 protein | 7.4 |
| 45 | 100287 | D43950 | Hs.1600 | chaperonin containing TCP1; subunit 5 (e | 5.6 |
| | 100294 | D49396 | Hs.75454 | antioxidant protein 1 | 12.9 |
| | 100307 | D50525 | Hs.699 | hypothetical protein | 8.4 |
| | 100335 | D63391 | Hs.6793 | platelet-activating factor acetylhydrolase; | 6.8 |
| | 100340 | D63487 | Hs.82563 | KIAA0153 protein | 4.4 |
| 50 | 100355 | D78129 | Hs.71465 | Homo sapiens mRNA for squalene epoxid | 12.6 |
| | 100363 | D78514 | Hs.78563 | ubiquitin-conjugating enzyme E2G 1 (hom | 4.6 |
| | 100368 | D79987 | Hs.153479 | extra spindle poles; S. cerevisiae; homolo | 6.5 |
| | 100372 | D79997 | Hs.184339 | KIAA0175 gene product | 8.4 |
| | 100375 | D80004 | Hs.75909 | KIAA0182 protein | 4.5 |
| 55 | 100379 | D82060 | Hs.278721 | Ke4 gene; mouse; human homolog of | 8.1 |
| | 100387 | D83777 | Hs.75137 | KIAA0193 gene product | 10.7 |
| | 100393 | D84145 | Hs.39913 | novel RGD-containing protein | 7.2 |
| | 100398 | D84557 | Hs.155462 | minichromosome maintenance deficient (m | 7.2 |
| | 100405 | D86425 | Hs.82733 | ndogen 2 | 5.4 |
| 60 | 100406 | D86479 | Hs.118397 | AE-binding protein 1 | 4.3 |
| | 100409 | D86957 | Hs.80712 | KIAA0202 protein | 11.9 |
| | 100421 | D86985 | Hs.79276 | Human mRNA for KIAA0232 gene; comp | 9.7 |
| | 100446 | D87464 | Hs.10037 | KIAA0274 gene product | 6.4 |
| | 100447 | D87465 | Hs.74583 | KIAA0275 gene product | 10 |
| 65 | 100448 | D87469 | Hs.57652 | EGF-like-domain; multiple 2 | 6.2 |

| | | | | | |
|----|--------|---------|-----------|--|------|
| | 100467 | D89052 | Hs.7476 | ATPase; H ⁺ transporting; lysosomal (vacu | 7.5 |
| | 100468 | D89289 | Hs.118722 | fucosyltransferase 8 (alpha (1;6) fucosyltr | 5 |
| | 100486 | HT1112 | Hs.10842 | Ras-Like Protein Tc4 | 16.9 |
| | 100497 | HT1400 | Hs.79137 | Carboxyl Methyltransferase, Aspartate, A | 5.6 |
| 5 | 100618 | HT2710 | Hs.114599 | Collagen, Type VII, Alpha 1 | 7.5 |
| | 100661 | HT3018 | Hs.132748 | Ribosomal Protein L39 Homolog | 4.4 |
| | 100667 | HT3127 | Hs.169610 | Epican, Alt. Splice 11 | 4.6 |
| | 100668 | HT3938 | Hs.169610 | Epican, Alt. Splice 12 | 4.4 |
| | 100676 | HT3742 | Hs.287820 | Fibronectin, Alt. Splice 1 | 9 |
| 10 | 100775 | HT26388 | Hs.89603 | Mucin 1, Epithelial, Alt. Splice 9 | 4.7 |
| | 100783 | HT4018 | Hs.191356 | Basic Transcription Factor, 44 Kda Subun | 13.7 |
| | 100829 | HT4343 | Hs.278544 | Cytosolic Acetoacetyl-Coenzyme A Thio | 10.6 |
| | 100830 | HT4344 | Hs.4756 | Rad2 | 5.5 |
| | 100840 | HT4392 | Hs.183418 | Protein Kinase Pitsre, Alpha, Alt. Splice | 4.1 |
| 15 | 100850 | HT417 | Hs.297939 | Cathepsin B | 4 |
| | 100866 | HT4582 | Hs.75113 | Transcription Factor Iiia | 4.9 |
| | 100906 | HT5158 | Hs.5398 | Guanosine 5'-Monophosphate Synthase | 8.7 |
| | 100914 | HT511 | Hs.324178 | Ras Inhibitor Inf | 7.2 |
| | 100916 | HT544 | Hs.73946 | Endothelial Cell Growth Factor 1 | 5.9 |
| 20 | 100945 | HT884 | Hs.180686 | Oncogene E6-Ap, Papillomavirus | 4.6 |
| | 100975 | J02923 | Hs.76506 | lymphocyte cytosolic protein 1 (L-plastin | 30.1 |
| | 100988 | J03589 | Hs.76480 | ubiquitin-like 4 | 8.3 |
| | 100996 | J03909 | Hs.14623 | interferon; gamma-inducible protein 30 | 6.9 |
| | 100999 | J03934 | Hs.80706 | diaphorase (NADH/NADPH) (cytochrom | 4.3 |
| 25 | 101011 | J04430 | Hs.1211 | acid phosphatase 5; tartrate resistant | 5.9 |
| | 101017 | J04599 | Hs.821 | biglycan | 5.1 |
| | 101031 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B; | 37.2 |
| | 101038 | J05249 | Hs.79411 | replication protein A2 (32kD) | 6.1 |
| | 101054 | K02405 | Hs.73931 | Human MHC class II HLA-DQ-beta mRN | 4.3 |
| 30 | 101061 | K03515 | Hs.180532 | glucose phosphate isomerase | 4.3 |
| | 101091 | L06132 | Hs.149155 | voltage-dependent anion channel 1 | 7.4 |
| | 101097 | L06797 | Hs.89414 | chemokine (C-X-C motif); receptor 4 (fus | 4.6 |
| | 101104 | L07615 | Hs.169266 | Human neuropeptide Y receptor Y1 (NPY | 18.3 |
| | 101143 | L12723 | Hs.90093 | heat shock 70kD protein 4 | 17.4 |
| 35 | 101152 | L13800 | Hs.9884 | Homo sapiens liver expressed protein gen | 7.6 |
| | 101183 | L19779 | Hs.795 | H2A histone family; member O | 10.9 |
| | 101216 | L25876 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 7.4 |
| | 101233 | L29008 | Hs.878 | sorbitol dehydrogenase | 14.6 |
| | 101247 | L33801 | Hs.78802 | glycogen synthase kinase 3 beta | 7.5 |
| 40 | 101282 | L38810 | Hs.79387 | proteasome (prosome; macropain) 26S sub | 4.4 |
| | 101326 | L42572 | Hs.78504 | inner membrane protein; mitochondrial (m | 5.8 |
| | 101332 | L47276 | Hs.156346 | Homo sapiens (cell line HL-6) alpha topo | 18.9 |
| | 101348 | L77213 | Hs.30954 | phosphomevalonate kinase | 7.5 |
| | 101352 | L77701 | Hs.16297 | COX17 (yeast) homolog; cytochrome c ox | 9.3 |
| 45 | 101378 | M13755 | Hs.833 | interferon-stimulated protein; 15 kDa | 18.1 |
| | 101396 | M15796 | Hs.78996 | proliferating cell nuclear antigen | 8.6 |
| | 101404 | M16342 | Hs.182447 | heterogeneous nuclear ribonucleoprotein C | 4.5 |
| | 101439 | M20902 | Hs.268571 | apolipoprotein C-I | 6.1 |
| | 101464 | M22538 | Hs.51299 | NADH dehydrogenase (ubiquinone) flavo | 8.7 |
| 50 | 101469 | M22877 | Hs.169248 | Human somatic cytochrome c (HCS) gene | 4.2 |
| | 101472 | M22960 | Hs.118126 | protective protein for beta-galactosidase (| 6.5 |
| | 101478 | M23379 | Hs.758 | RAS p21 protein activator (GTPase activa | 14 |
| | 101484 | M24594 | Hs.20315 | interferon-induced protein 56 | 9.2 |
| | 101539 | M30818 | Hs.926 | myxovirus (influenza) resistance 2; homol | 5.1 |
| 55 | 101540 | M30938 | Hs.84981 | X-ray repair complementing defective rep | 4.7 |
| | 101544 | M31169 | | Human propionyl-CoA carboxylase beta-s | 5.5 |
| | 101552 | M31642 | Hs.82314 | hypoxanthine phosphoribosyltransferase 1 | 8.5 |
| | 101580 | M34677 | Hs.83363 | DNA segment on chromosome X (unique) | 4.5 |
| | 101600 | M37583 | Hs.119192 | H2A histone family; member Z | 5.7 |
| 60 | 101663 | M60750 | Hs.2178 | H2B histone family; member A | 5.8 |
| | 101664 | M60752 | Hs.121017 | H2A histone family; member A | 13.5 |
| | 101667 | M60858 | Hs.79110 | nucleolin | 4 |
| | 101684 | M63256 | Hs.75124 | cerebellar degeneration-related protein (62 | 7.6 |
| | 101702 | M64929 | Hs.179574 | protein phosphatase 2 (formerly 2A); regu | 4.2 |
| 65 | 101754 | M77142 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-b | 4.5 |
| | 101758 | M77836 | Hs.79217 | pyrroline-5-carboxylate reductase 1 | 5.7 |
| | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 21.7 |

| | | | | | |
|----|--------|--------|-----------|---|------|
| | 101770 | M81601 | Hs.78869 | transcription elongation factor A (SII); 1 | 4.6 |
| | 101791 | M83822 | Hs.62354 | cell division cycle 4-like | 9.7 |
| | 101803 | M86546 | Hs.155691 | pre-B-cell leukemia transcription factor 1 | 5.5 |
| 5 | 101809 | M86849 | Hs.323733 | Homo sapiens connexin 26 (GJB2) mRNA | 22.5 |
| | 101839 | M83036 | Hs.692 | membrane component; chromosomal 4; su | 4 |
| | 101851 | M94250 | Hs.82045 | midkine (neurite growth-promoting factor | 7.6 |
| | 101888 | M99701 | Hs.95243 | transcription elongation factor A (SII)-like | 11.4 |
| | 101973 | S82597 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:po | 4.6 |
| 10 | 101991 | U00968 | Hs.166 | Human SREBP-1 mRNA; complete cds | 4.1 |
| | 102009 | U02680 | Hs.82643 | protein tyrosine kinase 9 | 4.4 |
| | 102025 | U03911 | Hs.78934 | mutS (E. coli) homolog 2 (colon cancer; n | 4 |
| | 102047 | U07158 | Hs.83734 | syntaxin 4A (placental) | 6.1 |
| | 102051 | U07550 | Hs.1197 | heat shock 10kD protein 1 (chaperonin 10 | 4.4 |
| 15 | 102083 | U10323 | Hs.75117 | Interleukin enhancer binding factor 2; 45k | 10.4 |
| | 102095 | U11313 | Hs.75760 | sterol carrier protein 2 | 9.5 |
| | 102130 | U15009 | Hs.1575 | small nuclear ribonucleoprotein D3 polyp | 6.6 |
| | 102133 | U15173 | Hs.155596 | BCL2/adenovirus E1B 19kD-interacting p | 4.3 |
| | 102148 | U16954 | Hs.75823 | ALL1-fused gene from chromosome 1q | 6.9 |
| 20 | 102179 | U19713 | Hs.76364 | allograft inflammatory factor 1 | 4.8 |
| | 102180 | U19718 | Hs.83551 | microfibrillar-associated protein 2 | 7.2 |
| | 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin; b | 7.2 |
| | 102198 | U21090 | Hs.74598 | polymerase (DNA directed); delta 2; regu | 4.3 |
| | 102202 | U21931 | Hs.574 | fructose-bisphosphatase 1 | 4.5 |
| 25 | 102209 | U22970 | Hs.265827 | interferon; alpha-inducible protein (clone | 9.9 |
| | 102211 | U23070 | Hs.78776 | putative transmembrane protein | 4.9 |
| | 102220 | U24389 | Hs.65436 | lysyl oxidase-like 1 | 8.5 |
| | 102224 | U24704 | Hs.148495 | proteasome (prosome; macropain) 26S sub | 5.4 |
| | 102234 | U26312 | Hs.278554 | chromobox homolog 3 (Drosophila HP1 g | 7.7 |
| 30 | 102250 | U28014 | Hs.74122 | caspase 4; apoptosis-related cysteine prot | 5.4 |
| | 102260 | U28386 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1; impo | 6.3 |
| | 102261 | U28488 | Hs.155935 | complement component 3a receptor 1 | 5.7 |
| | 102273 | U30888 | Hs.75981 | ubiquitin specific protease 14 (tRNA-guan | 6.1 |
| | 102298 | U32849 | Hs.54483 | N-myc (and STAT) interactor | 4.1 |
| 35 | 102302 | U33052 | Hs.69171 | protein kinase C-like 2 | 4.3 |
| | 102305 | U33286 | Hs.90073 | chromosome segregation 1 (yeast homolo | 5.4 |
| | 102320 | U34683 | Hs.82327 | glutathione synthetase | 4.1 |
| | 102330 | U35451 | Hs.77254 | chromobox homolog 1 (Drosophila HP1 b | 4 |
| | 102348 | U37519 | Hs.87539 | aldehyde dehydrogenase 8 | 9.4 |
| 40 | 102361 | U39400 | Hs.75859 | chromosome 11 open reading frame 4 | 5.2 |
| | 102362 | U39412 | Hs.75932 | N-ethylmaleimide-sensitive factor attachm | 9.3 |
| | 102369 | U39840 | Hs.299867 | hepatocyte nuclear factor 3; alpha | 7.7 |
| | 102395 | U41767 | Hs.92208 | a disintegrin and metalloproteinase domai | 10.4 |
| | 102409 | U43286 | Hs.118725 | selenophosphate synthetase 2 | 6.2 |
| 45 | 102418 | U43923 | Hs.79058 | suppressor of Ty (S.cerevisiae) 4 homolog | 4.1 |
| | 102425 | U44772 | Hs.3873 | palmitoyl-protein thioesterase (ceroid-lipo | 4.8 |
| | 102457 | U48807 | Hs.2359 | dual specificity phosphatase 4 | 6.3 |
| | 102465 | U49352 | Hs.81548 | 2;4-dienoyl CoA reductase 1; mitochondri | 9.4 |
| | 102495 | U51240 | Hs.79356 | Lysosomal-associated multispanning mem | 6.5 |
| 50 | 102534 | U56833 | Hs.198307 | von Hippel-Lindau binding protein 1 | 8.6 |
| | 102546 | U57877 | Hs.3577 | succinate dehydrogenase complex; subuni | 4.3 |
| | 102549 | U58046 | Hs.198899 | eukaryotic translation initiation factor 3; s | 6.3 |
| | 102557 | U58766 | Hs.264428 | tissue specific transplantation antigen P35 | 5 |
| | 102562 | U59309 | Hs.75653 | fumarate hydratase | 6 |
| 55 | 102568 | U59877 | Hs.223025 | RAB31; member RAS oncogene family | 9.1 |
| | 102580 | U60808 | Hs.152981 | CDP-diacylglycerol synthase (phosphatid | 7.9 |
| | 102581 | U61145 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 7.6 |
| | 102590 | U62136 | Hs.79300 | Homo sapiens enterocyte differentiation a | 7 |
| | 102591 | U62325 | Hs.324125 | amyloid beta (A4) precursor protein-blndi | 4 |
| | 102592 | U62389 | Hs.11223 | Human putative cytosolic NADP-depende | 5 |
| 60 | 102617 | U65928 | Hs.198767 | Jun activation domain binding protein | 6.1 |
| | 102618 | U65932 | Hs.81071 | extracellular matrix protein 1 | 23.2 |
| | 102638 | U67319 | Hs.9216 | caspase 7; apoptosis-related cysteine prot | 8.9 |
| | 102663 | U70322 | Hs.168075 | karyopherin (importin) beta 2 | 7.1 |
| 65 | 102666 | U70660 | Hs.279910 | ATX1 (antioxidant protein 1; yeast) homo | 4.7 |
| | 102679 | U72661 | Hs.11342 | injurin 1; nerve injury-induced protein-1 | 4.7 |
| | 102687 | U73379 | Hs.93002 | ubiquitin carrier protein E2-C | 7.7 |
| | 102704 | U76638 | Hs.54089 | BRCA1 associated RING domain 1 | 5.6 |

| | | | | | |
|----|--------|--------|-----------|---|------|
| | 102705 | U77180 | Hs.50002 | small inducible cytokine subfamily A (Cy | 11.8 |
| | 102721 | U79241 | Hs.118666 | Human clone 23759 mRNA; partial cds | 15 |
| | 102729 | U79254 | Hs.181311 | asparaginyl-HRNA synthetase | 5 |
| | 102739 | U79282 | Hs.155572 | Human clone 23801 mRNA sequence | 6 |
| 5 | 102742 | U79293 | Hs.159264 | Human clone 23948 mRNA sequence | 13.1 |
| | 102761 | U82130 | Hs.118910 | tumor susceptibility gene 101 | 7 |
| | 102788 | U86602 | Hs.74407 | nucleolar protein p40 | 4.1 |
| | 102790 | U87269 | Hs.154196 | E4F transcription factor 1 | 7.1 |
| | 102801 | U89606 | Hs.38041 | pyridoxal (pyridoxine; vitamin B6) kinase | 4.7 |
| 10 | 102808 | U90426 | Hs.179606 | nuclear RNA helicase; DECD variant of D | 7.5 |
| | 102817 | U90904 | Hs.83724 | Human clone 23773 mRNA sequence | 15.2 |
| | 102823 | U90914 | Hs.5057 | carboxypeptidase D | 6.6 |
| | 102827 | U91327 | Hs.6456 | chaperonin containing TCP1; subunit 2 (b | 6 |
| | 102838 | U94592 | Hs.80658 | Human uncoupling protein homolog (UCP | 6.1 |
| 15 | 102841 | U95006 | Hs.37616 | Human D9 splice variant B mRNA; comp | 4.2 |
| | 102844 | U96113 | Hs.324275 | Homo sapiens Nedd-4-like ubiquitin-prot | 6.8 |
| | 102868 | X02419 | Hs.77274 | plasminogen activator; urokinase | 4 |
| | 102907 | X06985 | Hs.202833 | heme oxygenase (decycling) 1 | 22.7 |
| | 102919 | X12447 | | aldolase A; fructose-bisphosphate | 9.9 |
| 20 | 102929 | X13238 | Hs.74649 | cytochrome c oxidase subunit VIc | 5.4 |
| | 102973 | X16663 | Hs.14601 | hematopoietic cell-specific Lyn substrate | 4.8 |
| | 102983 | X17620 | Hs.118638 | non-metastatic cells 1; protein (NM23A) | 4.6 |
| | 102985 | X17644 | Hs.2707 | G1 to S phase transition 1 | 20.6 |
| | 103003 | X52003 | Hs.1406 | trefoil factor 1 (breast cancer; estrogen-ind | 10.7 |
| 25 | 103018 | X53296 | Hs.81134 | interleukin 1 receptor antagonist | 5.8 |
| | 103023 | X53793 | Hs.117950 | multifunctional polypeptide similar to SA | 4 |
| | 103036 | X54925 | Hs.83169 | matrix metalloproteinase 1 (interstitial col | 7.3 |
| | 103060 | X57766 | Hs.155324 | matrix metalloproteinase 11 (stromelysin | 17.8 |
| | 103073 | X59417 | Hs.74077 | proteasome (prosome; macropain) subunit | 5.6 |
| 30 | 103075 | X59543 | Hs.2934 | ribonucleotide reductase M1 polypeptide | 4.2 |
| | 103080 | X59798 | Hs.82932 | cyclin D1 (PRAD1; parathyroid adenomat | 6.7 |
| | 103094 | X60787 | Hs.296281 | interleukin enhancer binding factor 1 | 5.7 |
| | 103105 | X61970 | Hs.76913 | proteasome (prosome; macropain) subunit | 5.8 |
| | 103121 | X63679 | Hs.4147 | translocating chain-associating membrane | 4.2 |
| 35 | 103149 | X66363 | Hs.171834 | PCTAIRE protein kinase 1 | 12 |
| | 103180 | X69433 | Hs.5337 | isocitrate dehydrogenase 2 (NADP+); mit | 18.9 |
| | 103182 | X69819 | Hs.99995 | intercellular adhesion molecule 3 | 10.7 |
| | 103188 | X70040 | Hs.2942 | macrophage stimulating 1 receptor (c-met | 4.1 |
| | 103191 | X70218 | Hs.2903 | protein phosphatase 4 (formerly X); cataly | 10.7 |
| 40 | 103193 | X70476 | Hs.75724 | coatamer protein complex; subunit beta 2 | 8.2 |
| | 103194 | X70649 | Hs.78580 | DEAD/H (Asp-Glu-Ala-Asp/His) box pol | 13.7 |
| | 103195 | X70940 | Hs.2642 | eukaryotic translation elongation factor 1 | 13.4 |
| | 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 15.1 |
| | 103207 | X72790 | | Human endogenous retrovirus mRNA for | 5.3 |
| 45 | 103208 | X72841 | Hs.31314 | retinoblastoma-binding protein 7 | 12.3 |
| | 103216 | X74262 | Hs.16003 | retinoblastoma-binding protein 4 | 4.1 |
| | 103226 | X75042 | Hs.44313 | v-rel avian reticuloendotheliosis viral onco | 6.9 |
| | 103230 | X75861 | Hs.74637 | testis enhanced gene transcript | 7.9 |
| | 103262 | X78565 | Hs.289114 | hexabrachion (tenascin C; cytotoxicin) | 5 |
| 50 | 103278 | X79882 | Hs.80680 | lung resistance-related protein | 5.7 |
| | 103297 | X81788 | Hs.9078 | immature colon carcinoma transcript 1 | 4.6 |
| | 103302 | X82103 | Hs.3059 | coatamer protein complex; subunit beta | 4.5 |
| | 103316 | X83301 | Hs.324728 | SMA5 | 7.1 |
| | 103330 | X85373 | Hs.77496 | small nuclear ribonucleoprotein polypepti | 4 |
| 55 | 103349 | X89059 | | serine/threonine kinase 9 | 4.7 |
| | 103352 | X89398 | Hs.78853 | uracil-DNA glycosylase | 5.3 |
| | 103364 | X90872 | Hs.279929 | SULT1C sulfotransferase | 4 |
| | 103374 | X91788 | Hs.84974 | chloride channel; nucleotide-sensitive; 1A | 4.2 |
| | 103380 | X92396 | Hs.24167 | synaptobrevin-like 1 | 13.6 |
| 60 | 103395 | X94754 | Hs.279946 | methionine-tRNA synthetase | 14.2 |
| | 103402 | X95404 | Hs.180370 | cofilin 1 (non-muscle) | 4.6 |
| | 103410 | X96506 | Hs.295362 | DR1-associated protein 1 (negative cofact | 8.3 |
| | 103420 | X97065 | Hs.173497 | Sec23 (S. cerevisiae) homolog B | 4.9 |
| | 103421 | X97074 | Hs.119591 | adaptor-related protein complex 2; sigma | 5 |
| 65 | 103427 | X97303 | Hs.250655 | H.sapiens mRNA for Ptg-12 protein | 7 |
| | 103430 | X97544 | Hs.20716 | translocase of inner mitochondrial membr | 4.5 |
| | 103438 | X98263 | Hs.152720 | M-phase phosphoprotein 6 | 4.5 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 103464 | Y00285 | Hs.76473 | insulin-like growth factor 2 receptor | 4.2 |
| | 103470 | Y00796 | Hs.174103 | integrin; alpha L (antigen CD11A (p180); | 4.5 |
| | 103494 | Y08991 | Hs.83050 | phosphatidylinositol 3-kinase-associated p | 4.1 |
| | 103505 | Y09912 | Hs.33102 | transcription factor AP-2 beta (activating | 4.5 |
| 5 | 103547 | Z14982 | Hs.180062 | proteasome (prosome; macropain) subunit | 4.3 |
| | 103551 | Z15115 | Hs.75248 | topoisomerase (DNA) II beta (180kD) | 4 |
| | 103565 | Z22548 | Hs.146354 | thioredoxin-dependent peroxidase reductase | 7.6 |
| | 103587 | Z29083 | Hs.82128 | 5T4 oncofetal trophoblast glycoprotein | 14.6 |
| | 103621 | Z47727 | Hs.150675 | polymerase (RNA) II (DNA directed) pol | 6.3 |
| 10 | 103622 | Z48042 | Hs.278672 | membrane component; chromosome 11; s | 4.4 |
| | 103658 | Z74615 | Hs.172928 | collagen; type I; alpha 1 | 5.9 |
| | 103680 | Z93784 | | Homo sapiens DNA sequence from PAC | 4.4 |
| | 103772 | AA092473 | Hs.278554 | chromobox homolog 3 (Drosophila HP1 g | 4.9 |
| | 103774 | AA092898 | Hs.92918 | ESTs; Weakly similar to R07G3.8 [C.eleg | 6.1 |
| 15 | 103821 | AA157623 | Hs.198793 | KIAA0750 gene product | 23.3 |
| | 103835 | AA172215 | Hs.93748 | ESTs; Moderately similar to TRANSCRIP | 4 |
| | 103886 | AA236384 | Hs.105737 | ESTs; Weakly similar to gene 9306 protel | 4.9 |
| | 103890 | AA236843 | Hs.72085 | ESTs; Weakly similar to unknown [S.cere | 7.8 |
| | 103892 | AA243523 | Hs.239189 | ESTs | 4.8 |
| 20 | 104054 | AA393432 | Hs.7100 | hypothetical protein | 5.3 |
| | 104115 | AA428090 | Hs.26102 | ESTs | 28.7 |
| | 104136 | AA442669 | Hs.268371 | zv68f6.r1 Soares_total_fetus_Nb2HF8_9w | 5.7 |
| | 104147 | AA451992 | Hs.283037 | ESTs; Highly similar to HSPC039 protein | 6.9 |
| | 104173 | AA476564 | Hs.76561 | ESTs; Weakly similar to finger protein HZ | 5.2 |
| 25 | 104181 | AA479521 | Hs.283740 | ESTs | 7.8 |
| | 104183 | AA480838 | Hs.114309 | ESTs | 5.1 |
| | 104192 | AA486946 | Hs.21321 | Homo sapiens mRNA; cDNA DKFZp564 | 4.3 |
| | 104209 | AB000221 | Hs.16530 | small inducible cytokine subfamily A (Cy | 12.3 |
| | 104234 | AB002357 | Hs.168212 | kinesin family member 3B | 6.2 |
| 30 | 104271 | C01687 | Hs.7381 | ATP synthase; H+ transporting; mitochon | 4.2 |
| | 104278 | C02582 | Hs.109253 | ESTs; Highly similar to N-terminal acetyl | 4.5 |
| | 104307 | D52818 | Hs.111680 | endosulfine alpha | 4.7 |
| | 104309 | D55869 | Hs.284123 | Homo sapiens mRNA full length insert cD | 4.2 |
| | 104370 | H19378 | Hs.21851 | Homo sapiens mRNA; cDNA DKFZp586 | 6.4 |
| 35 | 104446 | L44497 | Hs.7351 | ESTs | 4.9 |
| | 104453 | M19169 | Hs.123114 | cystatin SN | 11.6 |
| | 104476 | N33807 | Hs.324275 | protease; serine; 15 | 5.6 |
| | 104558 | R56678 | Hs.88959 | Human DNA sequence from clone 967N2 | 6.3 |
| | 104592 | R81003 | Hs.325820 | serine protease; umbilical endothelium | 13.6 |
| 40 | 104634 | AA004274 | Hs.19151 | ESTs | 6.3 |
| | 104636 | AA004415 | Hs.106106 | ESTs | 10.1 |
| | 104658 | AA007145 | Hs.27268 | Homo sapiens mRNA; cDNA DKFZp564 | 4.3 |
| | 104667 | AA007234 | Hs.30098 | ESTs | 16.6 |
| | 104675 | AA009596 | Hs.301553 | ESTs; Moderately similar to IIII ALU SU | 4.6 |
| 45 | 104767 | AA025534 | Hs.8852 | ESTs | 4.8 |
| | 104785 | AA027163 | Hs.7942 | ESTs | 8.1 |
| | 104791 | AA029046 | Hs.301871 | ESTs; Moderately similar to cAMP induc | 10.9 |
| | 104804 | AA031357 | Hs.31803 | ESTs; Weakly similar to N-WASP [H.sap | 5.5 |
| | 104807 | AA032147 | Hs.23296 | ESTs | 10.4 |
| 50 | 104837 | AA039469 | Hs.21126 | ESTs; Weakly similar to KIAA0299 [H.s | 4.6 |
| | 104849 | AA040270 | Hs.241507 | Homo sapiens mRNA; cDNA DKFZp564 | 4.3 |
| | 104867 | AA045481 | Hs.225979 | Human gene from PACs 37M17 and 305B | 4.5 |
| | 104884 | AA053021 | Hs.14511 | SCO (cytochrome oxidase deficient; yeast | 4.7 |
| | 104906 | AA055809 | Hs.26802 | ESTs; Weakly similar to phosphoprotein [| 8.8 |
| 55 | 104919 | AA057193 | Hs.25252 | ESTs | 5.5 |
| | 104921 | AA057839 | Hs.1508 | ESTs | 4.2 |
| | 104926 | AA058846 | Hs.33363 | DKFZP434N093 protein | 7 |
| | 104938 | AA064627 | Hs.318725 | ESTs; Highly similar to CGI-72 protein [H | 7.1 |
| | 104943 | AA065217 | Hs.114218 | ESTs | 5.7 |
| 60 | 104957 | AA074919 | Hs.10026 | ESTs; Weakly similar to ORF YJL063c [S | 4.7 |
| | 104961 | AA076672 | Hs.33905 | ESTs | 5.5 |
| | 104968 | AA084602 | Hs.29669 | ESTs | 4.3 |
| | 104975 | AA086071 | Hs.50758 | chromosome-associated polypeptide C | 8.3 |
| | 104977 | AA088228 | Hs.18272 | ESTs | 6.2 |
| 65 | 104978 | AA088458 | Hs.19322 | ESTs | 6.7 |
| | 104987 | AA101723 | Hs.11861 | ESTs | 9.2 |
| | 105002 | AA113266 | Hs.182704 | ESTs; Moderately similar to alternatively | 6.9 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 105012 | AA116036 | Hs.9329 | chromosome 20 open reading frame 1 | 10.7 |
| | 105019 | AA121879 | Hs.9280 | proteasome (prosome; macropain) subunit | 5.7 |
| | 105029 | AA126855 | Hs.13268 | ESTs | 4.4 |
| 5 | 105033 | AA127964 | Hs.274329 | TP53 target gene 1 | 6.3 |
| | 105035 | AA128486 | Hs.8859 | ESTs | 6.5 |
| | 105039 | AA130349 | Hs.36475 | ESTs | 4 |
| | 105062 | AA134968 | Hs.36529 | ESTs | 4.3 |
| | 105076 | AA142858 | Hs.37810 | ESTs | 6.4 |
| | 105087 | AA147884 | Hs.9812 | ESTs | 9.2 |
| 10 | 105091 | AA148859 | Hs.179909 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.7 |
| | 105093 | AA149051 | Hs.32405 | ESTs | 6.3 |
| | 105107 | AA152302 | Hs.25035 | DKFZP566G223 protein | 6.2 |
| | 105127 | AA158132 | Hs.301957 | ESTs; Weakly similar to contains similar | 5.7 |
| 15 | 105132 | AA159501 | Hs.247280 | HBV associated factor | 4.2 |
| | 105143 | AA165333 | Hs.24808 | ESTs | 4.7 |
| | 105154 | AA171736 | Hs.35947 | methyl-CpG binding domain protein 4 | 9 |
| | 105162 | AA176690 | Hs.4084 | KIAA1025 protein | 9.1 |
| | 105186 | AA191512 | Hs.28005 | Homo sapiens mRNA; cDNA DKFZp564 | 19.3 |
| | 105209 | AA205072 | Hs.227743 | KIAA0980 protein | 7.4 |
| 20 | 105223 | AA211388 | Hs.7750 | ESTs | 5.1 |
| | 105252 | AA227428 | Hs.9728 | ESTs; Weakly similar to KIAA0512 prote | 11.1 |
| | 105253 | AA227448 | Hs.5003 | KIAA0456 protein | 6.4 |
| | 105261 | AA227871 | Hs.6361 | MEK partner 1 | 9.1 |
| | 105263 | AA227926 | Hs.6682 | ESTs | 6.7 |
| 25 | 105274 | AA228122 | Hs.281866 | ATPase; H+ transporting; lysosomal (vacu | 5.3 |
| | 105297 | AA233451 | Hs.183858 | transcriptional intermediary factor 1 | 8.7 |
| | 105309 | AA233790 | Hs.4104 | ESTs; Weakly similar to cDNA EST yk38 | 7.4 |
| | 105312 | AA233854 | Hs.23348 | S-phase kinase-associated protein 2 (p45) | 5.8 |
| 30 | 105342 | AA235286 | Hs.157078 | ESTs | 4.5 |
| | 105376 | AA236559 | Hs.8768 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.8 |
| | 105386 | AA236950 | Hs.8115 | ESTs | 5.5 |
| | 105397 | AA242868 | Hs.7395 | ESTs; Weakly similar to house-keeping p | 7.7 |
| | 105399 | AA243007 | Hs.16420 | ESTs; Highly similar to SH3 domain-bind | 5.6 |
| 35 | 105400 | AA243052 | Hs.65648 | RNA binding motif protein 8 | 5.8 |
| | 105404 | AA243303 | Hs.21187 | ESTs | 9.1 |
| | 105409 | AA243562 | Hs.301855 | ESTs | 4.4 |
| | 105436 | AA252172 | Hs.237856 | ESTs; Moderately similar to cAMP induc | 5.1 |
| | 105483 | AA255874 | Hs.23458 | ESTs | 4.9 |
| 40 | 105493 | AA256268 | Hs.10283 | ESTs | 6 |
| | 105495 | AA256317 | Hs.28785 | Homo sapiens mRNA; cDNA DKFZp586 | 5.2 |
| | 105496 | AA256323 | Hs.301997 | DKFZP434N126 protein | 8.7 |
| | 105500 | AA256485 | Hs.222399 | CGI-96 protein | 9.5 |
| | 105507 | AA256678 | Hs.226318 | ESTs; Moderately similar to CCR4-associ | 4.1 |
| 45 | 105538 | AA258860 | Hs.32597 | ring finger protein (C3H2C3 type) 6 | 4.1 |
| | 105544 | AA261954 | Hs.24678 | ESTs | 8 |
| | 105546 | AA262032 | Hs.268281 | ESTs; Weakly similar to 62D9.a [D.melan | 8.1 |
| | 105549 | AA262417 | Hs.5415 | ESTs | 4.6 |
| | 105551 | AA262477 | Hs.25292 | ribonuclease H1; large subunit | 9.1 |
| 50 | 105560 | AA262783 | Hs.306915 | ESTs | 4.5 |
| | 105565 | AA278302 | Hs.18349 | ESTs; Weakly similar to partial CDS [C.e | 4.2 |
| | 105566 | AA278323 | Hs.17481 | Homo sapiens clone 24606 mRNA sequen | 11.9 |
| | 105575 | AA278717 | Hs.12772 | ESTs | 5.9 |
| | 105584 | AA279012 | Hs.3454 | ESTs; Weakly similar to KIAA0665 prote | 4.4 |
| 55 | 105596 | AA279418 | Hs.18490 | ESTs | 4 |
| | 105604 | AA279787 | Hs.15467 | ESTs; Moderately similar to putative pho | 5.6 |
| | 105610 | AA279991 | Hs.99872 | ESTs; Weakly similar to trihorax homolo | 5.3 |
| | 105621 | AA280865 | Hs.6375 | Homo sapiens mRNA; cDNA DKFZp564 | 4.8 |
| | 105627 | AA281245 | Hs.23317 | ESTs | 7.5 |
| 60 | 105638 | AA281599 | Hs.247817 | Homo sapiens mRNA for for histone H2B | 5.9 |
| | 105645 | AA282138 | Hs.11325 | ESTs | 6.4 |
| | 105650 | AA282347 | Hs.25635 | ESTs; Highly similar to HSPC003 [H.sap | 11.3 |
| | 105666 | AA283930 | Hs.34906 | ESTs | 4.7 |
| | 105674 | AA284755 | Hs.279789 | CDW52 antigen (CAMPATH-1 antigen) | 8 |
| 65 | 105687 | AA286809 | Hs.28423 | ESTs | 7.1 |
| | 105700 | AA287643 | Hs.35254 | ESTs; Weakly similar to hypothetical pro | 4.9 |
| | 105705 | AA290767 | Hs.101282 | Homo sapiens mRNA; cDNA DKFZp434 | 8 |
| | 105709 | AA291268 | Hs.26761 | DKFZP586L0724 protein | 6.8 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 105731 | AA292711 | Hs.29131 | ESTs | 6.4 |
| | 105753 | AA299789 | Hs.110857 | ESTs | 7 |
| | 105774 | AA348014 | Hs.23412 | ESTs | 7.1 |
| 5 | 105784 | AA350771 | Hs.17850 | ESTs | 13.4 |
| | 105791 | AA358038 | Hs.14368 | SH3-binding domain glutamic acid-rich p | 4.3 |
| | 105807 | AA393803 | Hs.16869 | ESTs; Moderately similar to COLLAGEN | 5.3 |
| | 105808 | AA393808 | Hs.286131 | KIAA0438 gene product | 4.1 |
| | 105812 | AA394126 | Hs.20814 | ESTs; Highly similar to CGI-27 protein [H | 14.6 |
| | 105813 | AA394140 | Hs.18585 | ESTs | 4.9 |
| 10 | 105819 | AA397920 | Hs.28783 | Homo sapiens mRNA; cDNA DKFZp564 | 4.9 |
| | 105870 | AA399623 | Hs.101067 | ESTs | 4.8 |
| | 105874 | AA400074 | Hs.171118 | ESTs | 4 |
| | 105896 | AA400999 | Hs.7838 | Human ring zinc-finger protein (ZNF127- | 4.8 |
| | 105934 | AA404248 | Hs.16577 | ESTs | 5.2 |
| 15 | 105935 | AA404277 | Hs.263727 | ESTs; Weakly similar to bisphosphate 3'- | 4 |
| | 105966 | AA406105 | Hs.5344 | adaptor-related protein complex 1; gamma | 8.3 |
| | 105974 | AA406321 | Hs.6224 | KIAA0895 protein | 4.6 |
| | 105990 | AA410336 | Hs.29403 | ESTs; Weakly similar to PROBABLE AT | 4.5 |
| | 105995 | AA410510 | Hs.5345 | ESTs | 4.9 |
| 20 | 106000 | AA410972 | Hs.20726 | ESTs | 5.8 |
| | 106007 | AA411462 | Hs.11042 | ESTs; Weakly similar to vcl 1 [H.sapiens | 6.9 |
| | 106016 | AA411819 | Hs.8164 | KIAA0898 protein | 5 |
| | 106034 | AA412473 | Hs.14928 | ESTs | 6.6 |
| | 106042 | AA412700 | Hs.169895 | ubiquitin-conjugating enzyme E2L 6 | 4.6 |
| 25 | 106057 | AA417067 | Hs.289074 | ESTs | 4.5 |
| | 106065 | AA417558 | Hs.25206 | ESTs | 12.3 |
| | 106070 | AA417761 | Hs.5957 | Homo sapiens clone 24416 mRNA sequen | 5 |
| | 106103 | AA421104 | Hs.12094 | ESTs | 15.4 |
| | 106126 | AA424006 | Hs.22972 | ESTs; Moderately similar to H5AR [M.m | 6.4 |
| 30 | 106154 | AA425304 | Hs.6994 | ESTs | 5.1 |
| | 106157 | AA425367 | Hs.34892 | ESTs | 11.1 |
| | 106166 | AA425872 | Hs.19561 | NADH dehydrogenase (ubiquinone) 1 alp | 19.3 |
| | 106204 | AA428024 | Hs.21479 | ESTs | 4.7 |
| | 106210 | AA428239 | Hs.10338 | ESTs | 5.7 |
| 35 | 106220 | AA428582 | Hs.32196 | ESTs; Moderately similar to metargidin p | 7.7 |
| | 106236 | AA429951 | Hs.21104 | ESTs | 8 |
| | 106240 | AA430074 | Hs.18552 | ESTs; Weakly similar to Ylr218cp [S.cere | 4.4 |
| | 106263 | AA431462 | Hs.28329 | ESTs | 4.9 |
| | 106288 | AA435536 | Hs.24336 | ESTs | 8.8 |
| 40 | 106293 | AA435591 | Hs.301444 | signal sequence receptor; gamma (transloc | 8.7 |
| | 106310 | AA436244 | Hs.17240 | ESTs | 4.5 |
| | 106317 | AA436568 | Hs.108124 | ESTs | 4 |
| | 106328 | AA436705 | Hs.28020 | KIAA0766 gene product | 4.4 |
| | 106341 | AA441798 | Hs.5243 | ESTs; Moderately similar to pIL2 hypoth | 23.7 |
| 45 | 106348 | AA442253 | Hs.10702 | ESTs | 4.7 |
| | 106350 | AA442763 | Hs.194698 | cyclin B2 | 6.1 |
| | 106371 | AA443923 | Hs.170310 | ESTs | 6.8 |
| | 106389 | AA446949 | Hs.6236 | ESTs | 4.7 |
| | 106394 | AA447223 | Hs.25320 | Homo sapiens clone 25142 mRNA sequen | 4.4 |
| 50 | 106426 | AA448282 | Hs.16206 | ESTs; Weakly similar to F55C12.5 [C.ele | 4.5 |
| | 106459 | AA449741 | Hs.4029 | glioma-amplified sequence-41 | 4.8 |
| | 106462 | AA449912 | Hs.30532 | ESTs; Highly similar to CGI-77 protein [H | 5.2 |
| | 106468 | AA450047 | Hs.14770 | ESTs | 6.8 |
| | 106479 | AA450351 | Hs.75251 | ESTs | 12.4 |
| 55 | 106494 | AA452108 | Hs.18387 | transcription factor AP-2 alpha (activating | 4.5 |
| | 106503 | AA452411 | Hs.29679 | ESTs; Highly similar to mediator [H.sapie | 5.1 |
| | 106507 | AA452584 | Hs.267819 | protein phosphatase 1; regulatory (inhibito | 4.9 |
| | 106533 | AA453786 | Hs.145998 | ESTs | 8.3 |
| | 106568 | AA455970 | Hs.28285 | patched related protein translocated in ren | 7.6 |
| 60 | 106586 | AA456598 | Hs.57787 | ESTs | 8.2 |
| | 106589 | AA456646 | Hs.28661 | ESTs | 4.8 |
| | 106606 | AA457730 | Hs.283437 | Homo sapiens clone 23851 mRNA sequen | 4.4 |
| | 106611 | AA458904 | Hs.26267 | ESTs; Weakly similar to torsinA [H.sapie | 7 |
| | 106614 | AA458934 | Hs.256150 | ESTs | 4.5 |
| 65 | 106628 | AA459657 | Hs.12311 | Homo sapiens clone 23570 mRNA sequen | 6.5 |
| | 106637 | AA459961 | Hs.250824 | ESTs | 5.5 |
| | 106644 | AA460239 | Hs.12680 | ESTs | 4.4 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 106664 | AA460969 | Hs.7510 | mitogen-activated protein kinase kinase ki | 8.4 |
| | 106698 | AA463745 | Hs.29403 | ESTs; Weakly similar to PROBABLE AT | 5.3 |
| | 106719 | AA465171 | Hs.236844 | ESTs | 5.6 |
| | 106726 | AA465339 | Hs.3886 | ESTs | 10.1 |
| 5 | 106747 | AA476473 | Hs.171957 | triple functional domain (PTPRF interacti | 10.4 |
| | 106759 | AA477263 | Hs.25584 | ESTs | 4.2 |
| | 106765 | AA477717 | Hs.306117 | interleukin 13 receptor; alpha 1 | 6.9 |
| | 106784 | AA478558 | Hs.227913 | API5-like 1 | 5.1 |
| | 106831 | AA482014 | Hs.29463 | centrin; EF-hand protein; 3 (CDC31 yeast | 5.1 |
| 10 | 106836 | AA482112 | Hs.238707 | ESTs | 4.8 |
| | 106840 | AA482548 | Hs.5534 | ESTs | 10.3 |
| | 106856 | AA486183 | Hs.285123 | ESTs; Weakly similar to similar to oxyste | 6.2 |
| | 106865 | AA487228 | Hs.19479 | ESTs | 4.5 |
| | 106878 | AA488872 | Hs.12314 | Homo sapiens mRNA; cDNA DKFZp586 | 7.9 |
| 15 | 106888 | AA489101 | Hs.24734 | oxysterol binding protein | 6.4 |
| | 106895 | AA489665 | Hs.25245 | ESTs | 4.6 |
| | 106909 | AA490323 | Hs.250747 | SUMO-1 activating enzyme subunit 1 | 4.2 |
| | 106919 | AA490885 | Hs.21766 | ESTs | 12.3 |
| | 106920 | AA490899 | Hs.296323 | ESTs | 6.2 |
| 20 | 106941 | AA496204 | Hs.237971 | ESTs | 4 |
| | 106942 | AA496347 | Hs.31314 | retinoblastoma-binding protein 7 | 4.8 |
| | 106948 | AA496788 | Hs.21077 | KIAA0532 protein | 4 |
| | 106968 | AA504631 | Hs.26813 | ESTs; Weakly similar to hypothetical 43.2 | 4.4 |
| | 106973 | AA505141 | Hs.11923 | Human DNA sequence from clone 167A1 | 5.4 |
| 25 | 106980 | AA521121 | Hs.8858 | bromodomain adjacent to zinc finger dom | 4.1 |
| | 106981 | AA521157 | Hs.74101 | ESTs | 5.7 |
| | 106998 | AA598461 | Hs.195464 | insulin-like growth factor binding protein | 18.7 |
| | 107008 | AA598710 | Hs.23740 | ESTs | 6.2 |
| | 107028 | AA599214 | Hs.24143 | ESTs | 4.1 |
| 30 | 107032 | AA599472 | Hs.247309 | succinate-CoA ligase; GDP-forming; beta | 5.3 |
| | 107052 | AA600134 | Hs.12482 | glyceronephosphate O-acyltransferase | 4.8 |
| | 107053 | AA600147 | Hs.5741 | ESTs; Weakly similar to NADH-cytochro | 5.8 |
| | 107056 | AA600310 | Hs.18720 | programmed cell death 8 (apoptosis-induc | 4.9 |
| | 107080 | AA609210 | Hs.19221 | ESTs | 8.4 |
| 35 | 107102 | AA609723 | Hs.30652 | ESTs | 8 |
| | 107109 | AA609943 | Hs.32793 | ESTs | 9.5 |
| | 107129 | AA620553 | Hs.4756 | flap structure-specific endonuclease 1 | 4.9 |
| | 107132 | AA620598 | Hs.9052 | ESTs | 5.3 |
| | 107136 | AA620795 | Hs.8207 | ESTs | 4 |
| 40 | 107140 | AA620889 | Hs.170088 | ESTs | 6.7 |
| | 107151 | AA621169 | Hs.8687 | ESTs | 19 |
| | 107159 | AA621340 | Hs.10600 | ESTs; Weakly similar to ORF YKR081c [| 8.1 |
| | 107174 | AA621714 | Hs.25338 | ESTs | 8.5 |
| 45 | 107217 | D51095 | Hs.35861 | DKFZP586E1621 protein | 7.2 |
| | 107252 | D59971 | Hs.25925 | ESTs | 7.9 |
| | 107295 | T34527 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine;po | 5.6 |
| | 107299 | T40327 | Hs.30661 | lung resistance-related protein | 8.4 |
| | 107324 | T81665 | Hs.278422 | DKFZP586G1122 protein | 7.5 |
| | 107372 | U85625 | Hs.8297 | ribonuclease 6 precursor | 4.7 |
| 50 | 107373 | U85773 | Hs.154695 | phosphomannomutase 2 | 4.8 |
| | 107481 | W58247 | Hs.279766 | Homo sapiens kinesin superfamily motor | 6.3 |
| | 107531 | Y13936 | Hs.17883 | protein phosphatase 1G (formerly 2C); ma | 8.3 |
| | 107859 | AA024835 | Hs.47584 | potassium voltage-gated channel; delayed | 7.3 |
| | 107890 | AA026030 | Hs.61311 | ESTs; Weakly similar to CALPAIN 2; LA | 7.3 |
| 55 | 107908 | AA026894 | Hs.42826 | ESTs | 4.9 |
| | 108039 | AA041341 | Hs.46670 | ESTs | 5.4 |
| | 108040 | AA041551 | Hs.159971 | ESTs | 8.4 |
| | 108102 | AA046424 | Hs.49433 | ESTs; Weakly similar to HYPOTHETICA | 6.6 |
| | 108217 | AA058686 | Hs.62588 | ESTs | 7.7 |
| 60 | 108255 | AA063157 | Hs.172608 | ESTs | 4 |
| | 108358 | AA071514 | Hs.1634 | ESTs | 4 |
| | 108609 | AA100694 | Hs.69499 | Human DNA sequence from BAC 15E1 o | 5.5 |
| | 108647 | AA112396 | Hs.44276 | ESTs; Moderately similar to HOMEBO | 14.3 |
| | 108676 | AA115562 | Hs.274417 | Homo sapiens mRNA; cDNA DKFZp564 | 5.2 |
| 65 | 108687 | AA120785 | Hs.54347 | ESTs | 5.6 |
| | 108695 | AA121315 | Hs.70823 | KIAA1077 protein | 10.5 |
| | 108733 | AA126422 | | zn84f1.s1 Stratagene lung carcinoma 9372 | 4.4 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 108774 | AA128125 | Hs.71040 | ESTs; Moderately similar to CELL GROW | 4.6 |
| | 108828 | AA131584 | Hs.273344 | DKFZP564O0463 protein | 5.5 |
| | 108872 | AA134063 | Hs.111680 | ESTs | 7.2 |
| 5 | 108884 | AA134958 | Hs.293591 | ESTs | 11.3 |
| | 108893 | AA135894 | Hs.194691 | retinoic acid induced 3 | 8.9 |
| | 109008 | AA156360 | Hs.87128 | ESTs | 14.7 |
| | 109010 | AA156460 | Hs.44229 | dual specificity phosphatase 12 | 4.9 |
| | 109011 | AA156542 | Hs.72127 | ESTs | 4.6 |
| 10 | 109042 | AA159525 | Hs.71779 | Homo sapiens DNA from chromosome 19 | 7.2 |
| | 109086 | AA166695 | Hs.270737 | tumor necrosis factor (ligand) superfamily | 4 |
| | 109090 | AA167006 | Hs.70499 | ESTs | 5.9 |
| | 109101 | AA167708 | Hs.52184 | ESTs | 4.2 |
| | 109112 | AA169379 | Hs.257924 | ESTs | 4 |
| 15 | 109160 | AA179387 | Hs.301997 | DKFZP434N126 protein | 4 |
| | 109166 | AA179845 | Hs.73625 | RAB6 interacting; kinesin-like (rakinesin | 13.6 |
| | 109178 | AA181600 | Hs.283707 | ESTs | 11.8 |
| | 109179 | AA181902 | Hs.192789 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.4 |
| | 109261 | AA195255 | Hs.61779 | ESTs | 6.7 |
| 20 | 109270 | AA195515 | Hs.3585 | ESTs; Weakly similar to alternatively spliced | 4.9 |
| | 109277 | AA196332 | Hs.86043 | ESTs | 5.4 |
| | 109313 | AA206800 | Hs.86276 | ESTs; Moderately similar to zinc finger p | 5.5 |
| | 109415 | AA227219 | Hs.110826 | trinucleotide repeat containing 9 | 20.1 |
| | 109454 | AA232255 | Hs.295232 | ESTs | 4.7 |
| | 109467 | AA232904 | Hs.63187 | ESTs | 6.8 |
| 25 | 109481 | AA233342 | Hs.289069 | ESTs; Weakly similar to WD40 protein C | 10.6 |
| | 109508 | AA233892 | Hs.55902 | ESTs; Weakly similar to !!!! ALU SUBFA | 8 |
| | 109514 | AA234087 | Hs.262346 | ESTs; Weakly similar to ORF2: function | 8.2 |
| | 109572 | F02027 | Hs.171937 | ESTs | 4.8 |
| 30 | 109632 | F04165 | Hs.235873 | ESTs; Weakly similar to K11C4.2 [C.eleg | 5.2 |
| | 109644 | F04477 | Hs.291531 | ESTs; Moderately similar to GLYCERAL | 6.6 |
| | 109703 | F09684 | Hs.24792 | ESTs; Weakly similar to ORF YOR283w | 7.1 |
| | 109726 | F10009 | Hs.9196 | ESTs | 5 |
| | 109747 | F10161 | Hs.22969 | ESTs | 4.7 |
| 35 | 109799 | F10770 | Hs.180378 | Homo sapiens clone 669 unknown mRNA | 4.5 |
| | 109814 | F10979 | Hs.153106 | Homo sapiens clone 23728 mRNA sequen | 8.7 |
| | 110189 | H20543 | Hs.6278 | DKFZP586B1621 protein | 16.6 |
| | 110240 | H25577 | Hs.176588 | ESTs; Weakly similar to CYTOCHROME | 6.2 |
| | 110280 | H29285 | Hs.32468 | ESTs | 4.5 |
| 40 | 110520 | H56965 | Hs.4082 | yr09f06.s1 Soares fetal liver spleen 1NFL | 5.7 |
| | 110561 | H59617 | Hs.5199 | ESTs; Weakly similar to UBIQUITIN-CO | 19.5 |
| | 110707 | H95079 | Hs.15617 | ESTs; Weakly similar to !!!! ALU SUBFA | 6.2 |
| | 110734 | H98714 | Hs.24131 | ESTs | 30.2 |
| | 110770 | N22262 | Hs.131705 | ESTs | 5.8 |
| 45 | 110780 | N23174 | Hs.22891 | solute carrier family 7 (cationic amino aci | 8.2 |
| | 110787 | N24716 | Hs.12244 | ESTs; Weakly similar to C44B9.1 [C.eleg | 6.7 |
| | 110794 | N25262 | Hs.27931 | ESTs | 5.9 |
| | 110799 | N26101 | Hs.323401 | Human ring zinc-finger protein (ZNF127- | 4 |
| | 110818 | N29454 | Hs.27552 | ESTs; Weakly similar to putative p150 [H | 4.3 |
| | 110839 | N30856 | Hs.30246 | solute carrier family 19 (thiamine transpo | 12.8 |
| 50 | 110844 | N31952 | Hs.167531 | Homo sapiens mRNA full length insert cD | 10.1 |
| | 110854 | N32919 | Hs.27931 | ESTs | 4.7 |
| | 110856 | N33063 | | ESTs; Weakly similar to S164 [H.sapiens | 4.2 |
| | 110860 | N33438 | Hs.170065 | ESTs | 12.5 |
| 55 | 110897 | N39148 | Hs.6880 | DKFZP434D156 protein | 4 |
| | 110915 | N46252 | Hs.29724 | ESTs | 23.2 |
| | 110935 | N48787 | Hs.305979 | protease inhibitor 1 (anti-elastase); alpha- | 4.8 |
| | 110970 | N51374 | Hs.96870 | Homo sapiens mRNA full length insert cD | 5.4 |
| | 111006 | N53375 | Hs.166146 | Homer; neuronal immediate early gene; 3 | 4.7 |
| | 111008 | N53388 | Hs.7222 | ESTs | 13.3 |
| 60 | 111018 | N54067 | Hs.3628 | mitogen-activated protein kinase kinase ki | 5.7 |
| | 111084 | N59543 | Hs.15456 | PDZ domain containing 1 | 8.3 |
| | 111100 | N62522 | Hs.20450 | ESTs | 14.3 |
| | 111125 | N63823 | Hs.269115 | ESTs | 7.9 |
| | 111132 | N64378 | Hs.83293 | ESTs; Highly similar to unknown function | 4.4 |
| 65 | 111139 | N64683 | Hs.290943 | ESTs | 6 |
| | 111164 | N66857 | Hs.14808 | ESTs; Weakly similar to !!!! ALU CLASS | 4.1 |
| | 111172 | N67102 | Hs.21851 | Homo sapiens mRNA; cDNA DKFZp586 | 5.5 |

| | | | | | |
|----|--------|--------|-----------|---|------|
| | 111178 | N67227 | Hs.24633 | ESTs | 5.7 |
| | 111179 | N67239 | Hs.10760 | ESTs | 37 |
| | 111181 | N67278 | Hs.171802 | ESTs; Weakly similar to hypothetical pro | 5.6 |
| | 111184 | N67437 | Hs.243901 | Homo sapiens mRNA; cDNA DKFZp564 | 8.7 |
| 5 | 111221 | N68869 | Hs.15119 | ESTs | 7.3 |
| | 111223 | N68921 | Hs.297939 | ESTs; Weakly similar to neogenin [H.sap | 9 |
| | 111229 | N69113 | Hs.110855 | ESTs | 8.9 |
| | 111241 | N69514 | Hs.288880 | ESTs; Weakly similar to CGI-82 protein [| 6.9 |
| | 111268 | N70481 | Hs.26118 | Homo sapiens clone 24766 mRNA sequen | 4.5 |
| 10 | 111295 | N73275 | Hs.21275 | ESTs; Weakly similar to ubiquitin-conjug | 5.6 |
| | 111299 | N73808 | Hs.24936 | ESTs | 8.5 |
| | 111336 | N79565 | Hs.29894 | ESTs | 6.7 |
| | 111357 | N91023 | Hs.87128 | ESTs | 15 |
| | 111370 | N92915 | Hs.94631 | brefeldin A-inhibited guanine nucleotide-e | 5.2 |
| 15 | 111806 | R33468 | Hs.279008 | ESTs | 10 |
| | 111825 | R35885 | Hs.286148 | stromal antigen 1 | 4.5 |
| | 111836 | R36228 | Hs.25119 | ESTs | 7.2 |
| | 111890 | R38678 | Hs.12365 | ESTs | 17.3 |
| | 111923 | R39995 | Hs.25925 | Homo sapiens clone 23860 mRNA sequen | 7.3 |
| 20 | 111942 | R40576 | Hs.21590 | ESTs | 9.2 |
| | 111987 | R42036 | Hs.6763 | KIAA0942 protein | 10.6 |
| | 112101 | R44793 | Hs.296341 | adenylyl cyclase-associated protein 2 | 5.3 |
| | 112134 | R46025 | Hs.7413 | ESTs | 17.4 |
| | 112197 | R49482 | Hs.5637 | ESTs | 4.4 |
| 25 | 112244 | R51309 | Hs.70823 | KIAA1077 protein | 11 |
| | 112253 | R51818 | Hs.26244 | Homo sapiens mRNA; cDNA DKFZp566 | 9.3 |
| | 112305 | R54822 | Hs.124186 | ESTs | 4.4 |
| | 112449 | R63802 | Hs.285885 | ring finger protein 2 | 6.3 |
| | 112483 | R66534 | Hs.11861 | ESTs | 4.9 |
| 30 | 112519 | R68631 | Hs.23643 | ESTs | 14.3 |
| | 112610 | R79392 | Hs.91065 | ESTs | 5.2 |
| | 112693 | R88741 | Hs.8207 | ESTs; Moderately similar to proliferation | 4.6 |
| | 112751 | R93507 | Hs.157160 | ESTs | 5.6 |
| 35 | 112801 | R97486 | Hs.4747 | protein kinase; DNA-activated; catalytic p | 8.7 |
| | 112869 | T03313 | Hs.12285 | dyskeratosis congenita 1; dyskerin | 5.9 |
| | 112871 | T03352 | Hs.3530 | ESTs | 5.8 |
| | 112908 | T10065 | Hs.102548 | TLS-associated serine-arginine protein | 4.1 |
| | 112966 | T17119 | Hs.83883 | glucocorticoid receptor DNA binding fact | 5.7 |
| | 112971 | T17185 | Hs.7155 | ESTs | 6.4 |
| 40 | 112995 | T23528 | Hs.7549 | ESTs; Weakly similar to TYKJ protein [M | 9.1 |
| | 113047 | T25867 | Hs.6986 | ESTs | 5.4 |
| | 113075 | T34660 | Hs.159153 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.7 |
| | 113117 | T47819 | Hs.241471 | ESTs | 5.8 |
| 45 | 113206 | T58044 | Hs.287420 | ESTs; Moderately similar to !!!! ALU SU | 6.4 |
| | 113248 | T63857 | Hs.11774 | yc16e1.s1 Stratagene lung (#93721) Homo | 4.6 |
| | 113260 | T64896 | Hs.11135 | ESTs | 6.9 |
| | 113277 | T65797 | Hs.191445 | protein (peptidyl-prolyl cis/trans isomerases | 5.6 |
| | 113278 | T65802 | Hs.5297 | yc11h10.s1 Stratagene lung (#937210) Ho | 4.5 |
| | 113440 | T86121 | Hs.23920 | ESTs | 4.1 |
| 50 | 113523 | T90037 | Hs.12921 | ESTs | 6.4 |
| | 113604 | T92735 | Hs.3496 | ESTs | 6.4 |
| | 113702 | T97307 | Hs.30504 | ESTs; Moderately similar to !!!! ALU SU | 8.7 |
| | 113783 | W19222 | Hs.8109 | ESTs; Weakly similar to !!!! ALU SUBFA | 9.5 |
| | 113794 | W37382 | Hs.177534 | ESTs | 5.2 |
| 55 | 113808 | W44735 | Hs.11090 | ESTs | 11.9 |
| | 113811 | W44928 | Hs.9286 | ESTs | 16.7 |
| | 113822 | W47350 | Hs.6994 | ESTs | 4 |
| | 113823 | W47388 | Hs.17466 | retinoic acid receptor responder (tazaroten | 4.8 |
| | 113836 | W56792 | Hs.55099 | rab6 GTPase activating protein (GAP and | 4 |
| 60 | 113857 | W65477 | Hs.12040 | ESTs; Weakly similar to KIAA0881 prote | 4.1 |
| | 113886 | W72471 | Hs.5297 | Homo sapiens mRNA; cDNA DKFZp564 | 4.3 |
| | 113895 | W73738 | Hs.23920 | ESTs | 4.6 |
| | 113923 | W80763 | Hs.12921 | ESTs | 7.1 |
| | 113931 | W81205 | Hs.3849 | ESTs; Weakly similar to FK506-binding p | 6.8 |
| 65 | 113950 | W85765 | Hs.3496 | ESTs | 6.1 |
| | 113970 | W86748 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434 | 14 |
| | 114051 | W94942 | Hs.8109 | ESTs | 15 |
| | | | Hs.177534 | dual specificity phosphatase 10 | 5.4 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 114057 | W96222 | Hs.34192 | ESTs | 4.8 |
| | 114086 | Z38266 | Hs.288649 | Homo sapiens PAC clone DJ0777023 fro | 5.1 |
| | 114098 | Z38347 | Hs.118338 | ESTs; Weakly similar to similar to S. cere | 6.2 |
| 5 | 114109 | Z38435 | Hs.184108 | ribosomal protein L21 | 4.6 |
| | 114124 | Z38595 | Hs.125019 | ESTs; Highly similar to KIAA0886 prote | 22 |
| | 114138 | Z38763 | Hs.15740 | amyloid beta (A4) precursor protein-bindi | 8.8 |
| | 114149 | Z38814 | Hs.27196 | ESTs | 4 |
| | 114162 | Z38909 | Hs.22265 | ESTs | 7.2 |
| | 114177 | Z39062 | Hs.23740 | ESTs | 5.3 |
| 10 | 114196 | Z39211 | Hs.150926 | fructose-1-phosphate guanytyltransferase | 4.4 |
| | 114208 | Z39301 | Hs.7859 | ESTs | 5.1 |
| | 114250 | Z39897 | Hs.13297 | ESTs | 7.2 |
| | 114251 | Z39898 | Hs.21948 | ESTs | 14.7 |
| | 114292 | Z40715 | Hs.184641 | delta-6 fatty acid desaturase | 19.4 |
| 15 | 114297 | Z40758 | Hs.173091 | DKFZP434K151 protein | 8.9 |
| | 114334 | Z41342 | Hs.22941 | ESTs | 13.7 |
| | 114460 | AA024604 | Hs.26102 | ESTs | 10.1 |
| | 114471 | AA028074 | Hs.104613 | ESTs | 5.7 |
| | 114480 | AA032243 | Hs.151678 | UDP-N-acetyl-alpha-D-galactosamine:po | 7.3 |
| 20 | 114518 | AA046407 | Hs.106469 | suppressor of var1 (S.cerevisiae) 3-like 1 | 4.3 |
| | 114542 | AA055768 | Hs.293380 | ESTs | 11.7 |
| | 114549 | AA056484 | Hs.292833 | ESTs | 7.3 |
| | 114652 | AA101416 | Hs.107149 | ESTs; Weakly similar to PTB-ASSOCIAT | 6.1 |
| | 114673 | AA113303 | Hs.95583 | transmembrane 4 superfamily member (te | 4.3 |
| 25 | 114698 | AA126951 | Hs.110857 | ESTs; Highly similar to putative DNA-dir | 7.1 |
| | 114767 | AA148885 | Hs.154443 | minichromosome maintenance deficient (S | 5.3 |
| | 114799 | AA159323 | Hs.109929 | ESTs | 4.2 |
| | 114804 | AA160363 | Hs.269956 | ESTs | 4.8 |
| | 114811 | AA161161 | Hs.95907 | multiple inositol polyphosphate phosphata | 7.1 |
| 30 | 114821 | AA165313 | Hs.55468 | ESTs | 4.4 |
| | 114852 | AA235035 | Hs.38260 | ESTs; Moderately similar to ubiquitin spe | 5 |
| | 114901 | AA236276 | Hs.196437 | ESTs; Weakly similar to R26660_1; parti | 16.9 |
| | 114902 | AA236359 | Hs.39504 | ESTs | 5.1 |
| | 114940 | AA243012 | Hs.75928 | ESTs | 8.5 |
| 35 | 114965 | AA250737 | Hs.72472 | ESTs | 35.1 |
| | 115047 | AA252627 | Hs.82916 | homeo box B5 | 5.7 |
| | 115054 | AA252863 | Hs.87729 | ESTs | 6.2 |
| | 115061 | AA253217 | Hs.41271 | ESTs | 13 |
| | 115082 | AA255557 | Hs.198269 | NADH dehydrogenase (ubiquinone) 1 alp | 28.2 |
| 40 | 115116 | AA256486 | Hs.62275 | ESTs | 8.8 |
| | 115140 | AA258030 | Hs.279938 | ESTs; Weakly similar to supported by GE | 4.1 |
| | 115205 | AA262470 | Hs.284216 | ESTs | 8.3 |
| | 115206 | AA262491 | Hs.186572 | ESTs | 5.1 |
| | 115239 | AA278650 | Hs.73291 | ESTs; Weakly similar to similar to the bet | 4.6 |
| 45 | 115242 | AA278755 | Hs.283732 | ESTs | 8.3 |
| | 115249 | AA278961 | Hs.71124 | ESTs | 10.1 |
| | 115259 | AA279071 | Hs.13453 | splicing factor 3b; subunit 1; 155kD | 9.5 |
| | 115285 | AA279799 | Hs.293736 | ESTs | 5.8 |
| | 115291 | AA279943 | Hs.122579 | ESTs | 5.1 |
| 50 | 115357 | AA281793 | Hs.72988 | ESTs | 5 |
| | 115377 | AA282247 | Hs.193063 | ESTs | 6.1 |
| | 115400 | AA283198 | Hs.89113 | ESTs | 4.9 |
| | 115439 | AA284561 | Hs.193090 | ESTs | 5.8 |
| | 115471 | AA287138 | Hs.59346 | ESTs; Weakly similar to ASPARTYL-TR | 11.7 |
| 55 | 115506 | AA292537 | Hs.45207 | Human DNA sequence from clone 620E1 | 6.8 |
| | 115522 | AA331393 | Hs.47378 | ESTs | 5.8 |
| | 115572 | AA398392 | Hs.59594 | ESTs; Weakly similar to F33G12.3 gene p | 9.7 |
| | 115587 | AA399264 | Hs.283037 | ESTs; Highly similar to HSPC039 protein | 8.7 |
| | 115600 | AA400247 | Hs.42173 | ESTs | 4 |
| 60 | 115612 | AA400948 | Hs.71243 | ESTs; Weakly similar to zinc finger prote | 8.4 |
| | 115646 | AA404352 | Hs.305971 | ESTs | 5.3 |
| | 115652 | AA405098 | Hs.38178 | ESTs | 16.1 |
| | 115657 | AA405620 | Hs.55158 | ESTs; Weakly similar to weak similarity t | 4.7 |
| | 115658 | AA405625 | Hs.183056 | Human DNA sequence from clone 34B21 | 5.1 |
| 65 | 115675 | AA406546 | Hs.82065 | Homo sapiens mRNA; cDNA DKFZp564 | 20.5 |
| | 115721 | AA417102 | Hs.90960 | ESTs | 4.8 |
| | 115763 | AA421560 | | ESTs | 7 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 115764 | AA421562 | Hs.91011 | anterior gradient 2 (Xenopus laevis) homo | 41.6 |
| | 115835 | AA428576 | Hs.41371 | ESTs | 4.2 |
| | 115844 | AA430124 | Hs.7773 | ESTs | 11.9 |
| 5 | 115875 | AA433943 | Hs.43946 | ESTs; Weakly similar to Weak similarity | 33.5 |
| | 115888 | AA435839 | Hs.76591 | KIAA0887 protein | 7.2 |
| | 115922 | AA441911 | Hs.71869 | ESTs; Weakly similar to KIAA0926 prote | 5.1 |
| | 115941 | AA443602 | Hs.46679 | ESTs | 4.8 |
| | 115947 | AA443793 | Hs.94761 | ESTs | 8.3 |
| 10 | 115948 | AA443798 | Hs.43445 | poly(A)-specific ribonuclease (deadenylat | 13.5 |
| | 115951 | AA443918 | Hs.301048 | cofilin 1 (non-muscle) | 7.5 |
| | 115967 | AA446887 | Hs.42911 | ESTs | 8.8 |
| | 115984 | AA447687 | Hs.91109 | ESTs | 13.1 |
| | 116009 | AA449448 | Hs.44238 | ESTs | 5.5 |
| 15 | 116024 | AA451748 | Hs.83883 | Human DNA sequence from clone 718J7 | 7.5 |
| | 116028 | AA452112 | Hs.42644 | thioredoxin-like | 12.7 |
| | 116050 | AA453656 | Hs.88417 | ESTs | 7.2 |
| | 116097 | AA456099 | Hs.176376 | ESTs | 11.8 |
| | 116108 | AA457566 | Hs.28777 | ESTs | 4.5 |
| | 116121 | AA459254 | Hs.48855 | ESTs | 4.5 |
| 20 | 116127 | AA459703 | Hs.279884 | v-myc avian myelocytomatosis viral onco | 4.3 |
| | 116129 | AA459956 | Hs.49163 | ESTs; Highly similar to putative ribonucle | 7.6 |
| | 116142 | AA460649 | Hs.39457 | ESTs | 4.8 |
| | 116204 | AA465701 | Hs.108646 | ESTs | 6.8 |
| 25 | 116221 | AA478397 | Hs.50180 | ESTs | 4.9 |
| | 116222 | AA478415 | Hs.89986 | ESTs | 4 |
| | 116238 | AA479362 | Hs.47144 | DKFZP586N0819 protein | 4.6 |
| | 116246 | AA479961 | Hs.250646 | ESTs; Highly similar to ubiquitin-conjuga | 4 |
| | 116249 | AA480886 | Hs.86693 | ESTs | 18.5 |
| | 116250 | AA480975 | Hs.44829 | ESTs | 10.8 |
| 30 | 116254 | AA481146 | Hs.41086 | ESTs; Weakly similar to OXYSTEROL-B | 9.1 |
| | 116256 | AA481256 | Hs.88201 | ESTs; Weakly similar to lysophospholipa | 8.4 |
| | 116264 | AA482594 | Hs.272239 | Homo sapiens mRNA; cDNA DKFZp586 | 7.2 |
| | 116265 | AA482595 | Hs.55189 | ESTs; Weakly similar to F25B5.3 [C.eleg | 11.1 |
| | 116282 | AA486550 | Hs.204501 | ESTs; Weakly similar to Wiskott-Aldrich | 6.2 |
| 35 | 116298 | AA489046 | Hs.94109 | ESTs | 4.9 |
| | 116300 | AA489194 | Hs.159471 | ESTs; Weakly similar to snRNP protein B | 4.6 |
| | 116327 | AA490959 | Hs.28005 | Homo sapiens mRNA; cDNA DKFZp564 | 5.8 |
| | 116334 | AA491457 | Hs.48948 | ESTs | 4.3 |
| | 116337 | AA496127 | Hs.44070 | ESTs | 8.4 |
| 40 | 116351 | AA504116 | Hs.82501 | Homo sapiens mRNA; cDNA DKFZp434 | 5.3 |
| | 116357 | AA504806 | Hs.90797 | Homo sapiens clone 23620 mRNA sequen | 5.2 |
| | 116415 | AA609204 | Hs.27973 | KIAA0874 protein | 6.6 |
| | 116443 | AA620313 | Hs.190488 | ESTs; Weakly similar to KERATIN; TYP | 4.5 |
| 45 | 116470 | C13992 | Hs.83484 | ESTs | 4.5 |
| | 116480 | C14088 | | glyceraldehyde-3-phosphate dehydrogena | 5.6 |
| | 116578 | D51272 | Hs.75337 | nucleolar phosphoprotein p130 | 4.1 |
| | 116579 | D51276 | Hs.81915 | leukemia-associated phosphoprotein p18 | 5.8 |
| | 116626 | F02028 | Hs.81907 | ESTs | 4.9 |
| | 116647 | F03069 | Hs.15395 | ESTs; Weakly similar to ARGINYL-TRN | 6.1 |
| 50 | 116674 | F04816 | Hs.92127 | ESTs | 10.6 |
| | 116680 | F08813 | Hs.273829 | LINE retrotransposable element 1 | 4.2 |
| | 116700 | F09983 | Hs.317589 | ESTs | 13 |
| | 116724 | F13665 | Hs.65641 | ESTs | 8.5 |
| | 116726 | F13681 | Hs.53913 | ESTs | 5.6 |
| 55 | 116732 | F13779 | Hs.165909 | ESTs | 11.6 |
| | 116734 | F13789 | Hs.93796 | DKFZP586D2223 protein | 5.4 |
| | 116760 | H11054 | Hs.155342 | protein Kinase C; delta | 4.3 |
| | 116780 | H22566 | Hs.30098 | ESTs | 5.7 |
| | 116786 | H25836 | Hs.301527 | tumor necrosis factor (ligand) superfamily | 8.8 |
| 60 | 116787 | H28581 | Hs.15641 | ESTs | 8.6 |
| | 116790 | H29532 | Hs.101174 | microtubule-associated protein tau | 22.2 |
| | 116803 | H47357 | Hs.109701 | ESTs; Moderately similar to weak similar | 6.7 |
| | 116877 | H68116 | Hs.168732 | ESTs | 6.5 |
| 65 | 116921 | H72948 | Hs.821 | biglycan | 20.7 |
| | 117216 | N20083 | Hs.42792 | ESTs | 4.4 |
| | 117232 | N20579 | Hs.61153 | ESTs | 7.4 |
| | 117284 | N22162 | Hs.183779 | ESTs; Weakly similar to cDNA EST yk33 | 4.1 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 117344 | N24046 | Hs.210706 | ESTs | 7.4 |
| | 117367 | N24954 | Hs.42502 | ESTs | 10.5 |
| | 117392 | N26175 | Hs.93405 | ESTs | 5.8 |
| | 117394 | N26257 | Hs.39871 | KIAA0727 protein | 8.4 |
| 5 | 117412 | N26722 | Hs.42645 | ESTs | 18.1 |
| | 117498 | N31726 | Hs.44268 | ESTs; Highly similar to myelin gene expr | 5.8 |
| | 117557 | N33920 | Hs.44532 | diubiquitin | 12.3 |
| | 117634 | N36421 | Hs.13323 | ESTs; Weakly similar to SODIUM- AND | 4.4 |
| | 117639 | N36923 | Hs.44833 | ESTs | 6 |
| 10 | 117754 | N47469 | Hs.59757 | ESTs | 7.6 |
| | 117852 | N49408 | Hs.136102 | KIAA0853 protein | 5.9 |
| | 117879 | N50050 | Hs.303025 | ESTs; Weakly similar to keratin; 67K typ | 7.9 |
| | 117924 | N51056 | Hs.38891 | ESTs | 7.9 |
| | 117950 | N51394 | Hs.75478 | KIAA0956 protein | 5 |
| 15 | 117992 | N52000 | Hs.172089 | Homo sapiens mRNA; cDNA DKFZp586 | 7 |
| | 118138 | N57773 | Hs.93560 | ESTs; Weakly similar to trg [R.norvegicu | 4.8 |
| | 118215 | N62195 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A | 13.4 |
| | 118229 | N62339 | Hs.166254 | heat shock 90kD protein 1; alpha | 5.4 |
| | 118265 | N62827 | Hs.48645 | EST | 4.2 |
| 20 | 118336 | N63604 | Hs.47166 | ESTs | 7.2 |
| | 118363 | N64168 | Hs.48938 | ESTs | 6 |
| | 118429 | N66158 | Hs.74649 | ESTs | 4.1 |
| | 118470 | N66769 | Hs.291033 | ESTs | 5.4 |
| | 118472 | N66818 | Hs.42179 | ESTs | 10.8 |
| 25 | 118475 | N66845 | | ESTs; Weakly similar to !!!! ALU CLASS | 4.5 |
| | 118493 | N67149 | Hs.50115 | ESTs | 5.3 |
| | 118528 | N67889 | Hs.49397 | ESTs | 10.4 |
| | 118542 | N68010 | Hs.49427 | ESTs | 7.9 |
| | 118600 | N69222 | | ESTs | 9.2 |
| 30 | 118695 | N71781 | Hs.50081 | Homo sapiens mRNA full length insert cD | 9.8 |
| | 118698 | N72113 | Hs.50187 | ESTs | 4.3 |
| | 118901 | N90719 | Hs.94445 | ESTs | 8.1 |
| | 118952 | N92966 | | ESTs; Highly similar to CGI-90 protein [H | 12.5 |
| | 118976 | N93629 | Hs.93391 | ESTs | 5 |
| 35 | 118986 | N94362 | Hs.125830 | ESTs | 7.3 |
| | 118989 | N94439 | Hs.45105 | ESTs | 8.2 |
| | 119027 | N99256 | Hs.114611 | ESTs | 5 |
| | 119042 | R05316 | Hs.5472 | ESTs | 4 |
| | 119075 | R36451 | Hs.287820 | fibronectin 1 | 6 |
| 40 | 119260 | T15916 | Hs.102950 | ESTs; Highly similar to coat protein gamm | 4.1 |
| | 119271 | T16387 | Hs.65328 | ESTs | 12.1 |
| | 119298 | T23820 | Hs.155478 | cyclin T2 | 5.6 |
| | 119302 | T25725 | | ESTs | 14.3 |
| | 119341 | T62571 | Hs.146388 | microtubule-associated protein 7 | 4 |
| 45 | 119495 | W35390 | Hs.55533 | ESTs | 5.3 |
| | 119580 | W42451 | Hs.92260 | high-mobility group protein 2-like 1 | 5.6 |
| | 119602 | W46286 | Hs.233694 | ESTs; Weakly similar to ZK1058.5 [C.ele | 6.5 |
| | 119620 | W47620 | Hs.56009 | 2'-5'oligoadenylate synthetase 3 | 8.1 |
| | 119676 | W60473 | Hs.57787 | ESTs | 5.5 |
| 50 | 119717 | W69134 | Hs.57987 | ESTs | 4.6 |
| | 119729 | W69747 | Hs.94806 | KIAA1062 protein | 4 |
| | 119805 | W73788 | Hs.43213 | ESTs | 4 |
| | 119859 | W80702 | Hs.58461 | ESTs | 4.8 |
| | 119867 | W80852 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic re | 4.2 |
| 55 | 119873 | W81129 | Hs.44865 | Homo sapiens mRNA; cDNA DKFZp586 | 4.8 |
| | 119899 | W84767 | Hs.58698 | ESTs | 5.9 |
| | 119940 | W86779 | Hs.272531 | DKFZP586B0319 protein | 9 |
| | 119943 | W86835 | Hs.14158 | copine III | 4.8 |
| | 119970 | W87812 | Hs.93581 | Homo sapiens mRNA; cDNA DKFZp586 | 4 |
| 60 | 120131 | Z38656 | Hs.75887 | coatomer protein complex; subunit alpha | 4.2 |
| | 120150 | Z39549 | Hs.153746 | ESTs | 11 |
| | 120206 | Z40805 | Hs.91668 | ESTs | 8.2 |
| | 120241 | Z41815 | Hs.65946 | ESTs | 15.6 |
| | 120255 | AA169752 | Hs.5672 | ESTs; Weakly similar to Similarity to Yea | 4.2 |
| 65 | 120314 | AA194166 | Hs.221040 | KIAA1038 protein | 6.8 |
| | 120325 | AA195651 | Hs.104106 | ESTs | 15.2 |
| | 120352 | AA211400 | Hs.193172 | ESTs | 6.8 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 120428 | AA236822 | Hs.173694 | KIAA1097 protein | 5.6 |
| | 120524 | AA261852 | Hs.192905 | ESTs | 5.6 |
| | 120528 | AA262107 | Hs.104413 | ESTs | 4.5 |
| | 120571 | AA280738 | Hs.34892 | ESTs | 4.9 |
| 5 | 120649 | AA287115 | Hs.192843 | ESTs | 4.5 |
| | 120655 | AA287347 | Hs.238205 | ESTs | 6.7 |
| | 120668 | AA287833 | Hs.292913 | ESTs | 8.3 |
| | 120712 | AA292654 | Hs.102506 | eukaryotic translation initiation factor 2 al | 4.6 |
| | 120713 | AA292655 | Hs.96557 | ESTs | 10.6 |
| 10 | 120724 | AA293470 | Hs.100747 | ESTs | 5.4 |
| | 120873 | AA358015 | | EST | 7.1 |
| | 120885 | AA365515 | Hs.301872 | ESTs; Moderately similar to IIII ALU SU | 4.6 |
| | 120919 | AA381125 | Hs.301444 | ESTs | 8.2 |
| | 120948 | AA397822 | Hs.104650 | ESTs; Highly similar to similar to mago n | 8.6 |
| 15 | 120969 | AA398116 | Hs.129206 | casein kinase 1; gamma 3 | 10.5 |
| | 120977 | AA398155 | Hs.97600 | ESTs | 10.9 |
| | 121103 | AA398936 | Hs.97697 | EST | 7.4 |
| | 121291 | AA401753 | Hs.8186 | lung cancer candidate | 5.3 |
| | 121320 | AA403008 | Hs.301927 | T-cell receptor; alpha (V;D;J;C) | 13.5 |
| 20 | 121463 | AA411745 | Hs.239681 | ESTs; Weakly similar to KIAA0554 prote | 8.9 |
| | 121596 | AA416740 | Hs.174104 | ESTs | 22.6 |
| | 121723 | AA419622 | Hs.104800 | ESTs; Weakly similar to Mouse 19.5 mRN | 8 |
| | 121748 | AA421171 | Hs.234545 | ESTs | 5.6 |
| | 122125 | AA434411 | Hs.98806 | ESTs | 5.3 |
| 25 | 122522 | AA449444 | Hs.98969 | ESTs | 4 |
| | 122655 | AA454756 | Hs.97837 | ESTs | 4 |
| | 122704 | AA456326 | Hs.99445 | ESTs | 6.2 |
| | 122782 | AA459894 | Hs.99472 | ESTs | 5.3 |
| | 122856 | AA463740 | Hs.75367 | Src-like-adaptor | 13.1 |
| 30 | 122882 | AA465381 | Hs.108812 | ESTs; Weakly similar to B0041.5 [C.eleg | 5.5 |
| | 122928 | AA476578 | Hs.101840 | ESTs | 6.3 |
| | 122974 | AA478625 | Hs.194215 | ESTs | 6 |
| | 122997 | AA479295 | Hs.106290 | Kelch motif containing protein | 12.5 |
| | 123016 | AA480103 | Hs.323231 | ESTs; Weakly similar to alternatively spli | 4.4 |
| 35 | 123107 | AA486071 | Hs.104207 | ESTs | 8.3 |
| | 123111 | AA486273 | Hs.191721 | ESTs | 4.2 |
| | 123114 | AA486407 | Hs.129928 | ESTs; Moderately similar to KIAA0454 p | 5.2 |
| | 123136 | AA487449 | Hs.194024 | ESTs | 4.2 |
| | 123137 | AA487468 | Hs.100686 | ESTs; Weakly similar to secreted cement | 14.6 |
| 40 | 123169 | AA488892 | | ESTs; Weakly similar to Gag-Pol polyp | 4.5 |
| | 123176 | AA489020 | Hs.69233 | ESTs | 5.2 |
| | 123338 | AA504249 | Hs.187585 | ESTs | 4 |
| | 123436 | AA598714 | Hs.223014 | protease; serine; 15 | 7.3 |
| | 123442 | AA598803 | Hs.111496 | ESTs | 5.9 |
| 45 | 123449 | AA598899 | Hs.112493 | Homo sapiens mRNA; cDNA DKFZp564 | 4.1 |
| | 123494 | AA599786 | Hs.112110 | ESTs | 4 |
| | 123503 | AA600121 | Hs.293156 | ESTs | 12.8 |
| | 123533 | AA608751 | | ESTs; Weakly similar to IIII ALU SUBFA | 7.9 |
| | 123619 | AA609200 | | ESTs | 23.1 |
| 50 | 123673 | AA609471 | Hs.158549 | ESTs | 6.6 |
| | 123729 | AA609778 | Hs.278672 | membrane component; chromosome 11; s | 4.7 |
| | 123819 | AA620636 | Hs.112264 | ESTs | 4 |
| | 123960 | AA621785 | Hs.287733 | methylmalonate-semialdehyde dehydroge | 7.6 |
| | 124000 | D57317 | Hs.74861 | activated RNA polymerase II transcription | 4.4 |
| 55 | 124006 | D60302 | Hs.270016 | ESTs | 20.6 |
| | 124012 | D80240 | Hs.241471 | HUM5G11A Human fetal brain (TFujiwa | 6.7 |
| | 124021 | F02859 | Hs.13974 | ESTs | 4.7 |
| | 124049 | F10523 | Hs.74519 | primase; polypeptide 2A (58kD) | 4.7 |
| | 124059 | F13673 | Hs.283713 | ESTs | 7.7 |
| 60 | 124243 | H66710 | Hs.133525 | ESTs | 5.5 |
| | 124308 | H93575 | Hs.241507 | Homo sapiens mRNA; cDNA DKFZp564 | 11.4 |
| | 124314 | H94877 | Hs.215766 | GTP-binding protein | 13.7 |
| | 124315 | H94892 | Hs.288757 | v-ral simian leukemia viral oncogene hom | 14 |
| | 124350 | N21359 | Hs.101282 | Homo sapiens mRNA; cDNA DKFZp434 | 8.6 |
| 65 | 124352 | N21626 | Hs.102406 | ESTs | 7.2 |
| | 124357 | N22401 | | yw37g07.s1 Morton Fetal Cochlea Homo | 5.2 |
| | 124390 | N29325 | Hs.7535 | ESTs; Highly similar to COBW-like place | 7.9 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 124438 | N40188 | Hs.11090 | ESTs | 9.5 |
| | 124447 | N48000 | | Homo sapiens mRNA; cDNA DKFZp586 | 4.8 |
| | 124457 | N50114 | Hs.266175 | ESTs | 6.1 |
| 5 | 124539 | N63172 | Hs.146409 | cell division cycle 42 (GTP-binding prote | 5.6 |
| | 124626 | N74604 | Hs.11090 | ESTs | 12.8 |
| | 124632 | N79515 | Hs.306117 | interleukin 13 receptor; alpha 1 | 6.4 |
| | 124644 | N91279 | Hs.109654 | ESTs; Moderately similar to outer membr | 8.3 |
| | 124676 | R01037 | Hs.181013 | phosphoglycerate mutase 1 (brain) | 12.3 |
| | 124677 | R01073 | | ESTs; Weakly similar to !!!! ALU CLASS | 5.4 |
| 10 | 124724 | R12405 | Hs.112423 | Homo sapiens mRNA; cDNA DKFZp586 | 6.6 |
| | 124773 | R40923 | Hs.106604 | ESTs | 4.9 |
| | 124777 | R41933 | | ESTs | 7.2 |
| | 124792 | R44357 | Hs.48712 | ESTs; Weakly similar to cDNA EST EMB | 8.6 |
| | 124857 | R63652 | Hs.137190 | ESTs | 4.9 |
| 15 | 124911 | R88992 | Hs.180612 | ESTs | 4.7 |
| | 124955 | T10598 | Hs.324841 | ESTs; Weakly similar to !!!! ALU SUBFA | 4.4 |
| | 124958 | T11134 | Hs.431 | murine leukemia viral (bmi-1) oncogene h | 12.6 |
| | 125038 | T78089 | Hs.270134 | ESTs | 4.1 |
| | 125092 | T92544 | Hs.137548 | CD84 antigen (leukocyte antigen) | 14.8 |
| 20 | 125132 | W15495 | Hs.129781 | chromosome 21 open reading frame 5 | 6.7 |
| | 125144 | W37999 | Hs.24336 | ESTs | 4.8 |
| | 125154 | W38419 | | ESTs | 5.3 |
| | 125243 | W86423 | Hs.105413 | ESTs | 6.6 |
| | 125279 | W93640 | Hs.4779 | ESTs; Moderately similar to similar to AD | 5.8 |
| 25 | 125299 | Z39436 | Hs.102720 | ESTs | 12.2 |
| | 125303 | Z39821 | Hs.288193 | ESTs | 10.2 |
| | 125304 | Z39833 | Hs.124940 | GTP-binding protein | 6.8 |
| | 125474 | AA151216 | Hs.75103 | tyrosine 3-monooxygenase/tryptophan 5-m | 8 |
| | 125509 | AA044232 | Hs.288967 | ESTs | 5.4 |
| 30 | 125580 | AA126504 | Hs.267812 | sorting nexin 4 | 4.1 |
| | 125582 | AA507383 | Hs.74649 | cytochrome c oxidase subunit VIc | 11.5 |
| | 125670 | AI432621 | Hs.82685 | CD47 antigen (Rh-related antigen; integr | 4 |
| | 125698 | AA748483 | Hs.191356 | general transcription factor IIH; polypepti | 9.4 |
| | 125745 | AI283493 | Hs.75722 | ribophorin II | 6.2 |
| 35 | 125852 | H09290 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564 | 25.9 |
| | 125972 | AA434562 | Hs.35406 | ESTs | 4.1 |
| | 126160 | N90960 | Hs.265398 | ESTs; Weakly similar to transformation-r | 16.4 |
| | 126257 | N99638 | Hs.124084 | tumor necrosis factor receptor superfamily | 9.5 |
| | 126337 | AI066486 | Hs.40500 | similar to S. cerevisiae RER1 | 5.6 |
| 40 | 126405 | U46278 | Hs.122489 | ESTs | 7.5 |
| | 126537 | W40262 | Hs.146310 | ESTs; Weakly similar to putative p150 [H | 4.1 |
| | 126590 | W78968 | Hs.181307 | H3 histone; family 3A | 4.5 |
| | 126712 | AA205862 | Hs.7942 | ESTs | 5.2 |
| | 126721 | T72569 | Hs.125359 | Thy-1 cell surface antigen | 4.4 |
| 45 | 126764 | AI334393 | Hs.102178 | ESTs | 4.6 |
| | 126804 | AI203334 | Hs.160628 | ESTs | 11.7 |
| | 126819 | AA305536 | Hs.279607 | ESTs | 4 |
| | 126877 | AI052047 | Hs.26102 | ESTs | 7 |
| | 126991 | R31652 | Hs.821 | biglycan | 5.6 |
| 50 | 127479 | AA513722 | Hs.179729 | collagen; type X; alpha 1 (Schmid metaph | 14.3 |
| | 127514 | AA826926 | Hs.204214 | ESTs | 4.5 |
| | 127663 | W07286 | Hs.10340 | ESTs; Weakly similar to weak similarity I | 5.1 |
| | 127677 | AA916752 | Hs.264190 | ESTs; Highly similar to MEM3 [M.muscu | 17.3 |
| | 127814 | AA761755 | Hs.136713 | ESTs; Weakly similar to V4-1 [H.sapiens | 4.1 |
| 55 | 127997 | AI281549 | Hs.311054 | ESTs | 5.5 |
| | 128092 | AA904617 | Hs.166229 | ESTs | 5.8 |
| | 128218 | H02682 | Hs.292154 | ESTs; Moderately similar to recombination | 5.8 |
| | 128466 | D59653 | Hs.241471 | EST | 7.4 |
| | 128482 | U83908 | Hs.296251 | programmed cell death 4 | 5.8 |
| 60 | 128517 | AA280617 | Hs.100861 | ESTs; Weakly similar to p60 katanin [H.s | 8.3 |
| | 128530 | AA504343 | Hs.183475 | Homo sapiens clone 25061 mRNA sequen | 6.6 |
| | 128559 | AA226801 | Hs.101448 | metastasis associated 1 | 5.2 |
| | 128574 | AA412048 | Hs.38260 | keratin 8 | 5.1 |
| | 128595 | U31875 | Hs.152677 | short-chain alcohol dehydrogenase family | 27.1 |
| 65 | 128610 | L38608 | Hs.10247 | activated leucocyte cell adhesion molecule | 13.2 |
| | 128629 | AA399187 | Hs.102708 | DKFZP434A043 protein | 6.7 |
| | 128649 | AA142853 | Hs.103106 | Homo sapiens mRNA for G7b protein (G | 4.5 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 128651 | AA446990 | Hs.103135 | ESTs | 6.1 |
| | 128653 | R48943 | Hs.10315 | solute carrier family 7 (cationic amino aci | 4.4 |
| | 128656 | AA458542 | Hs.10326 | coatamer protein complex; subunit epsilon | 14.3 |
| 5 | 128717 | T30617 | Hs.104222 | Homo sapiens mRNA; cDNA DKFZp566 | 24.5 |
| | 128727 | M64174 | Hs.50651 | Janus kinase 1 (a protein tyrosine kinase) | 7.3 |
| | 128764 | N49308 | Hs.104938 | ESTs; Weakly similar to alpha 1(XVIII) c | 9.2 |
| | 128781 | X85372 | Hs.105465 | small nuclear ribonucleoprotein polypepti | 5.4 |
| | 128793 | W93562 | Hs.105749 | KIAA0553 protein | 4.6 |
| | 128835 | W15528 | Hs.106390 | Homo sapiens mRNA; cDNA DKFZp586 | 4 |
| 10 | 128845 | AA455658 | Hs.10649 | basement membrane-induced gene | 6.9 |
| | 128871 | AA400271 | Hs.106778 | Homo sapiens mRNA for putative Ca2+-t | 4.5 |
| | 128922 | AA252023 | Hs.9589 | ESTs; Weakly similar to HRIHFB2157 [H | 6.4 |
| | 128925 | D61676 | Hs.21851 | Homo sapiens mRNA; cDNA DKFZp586 | 6.4 |
| | 128938 | AA410325 | Hs.107260 | ESTs | 7 |
| 15 | 128946 | N29353 | Hs.107318 | kynurenine 3-monooxygenase (kynurenin | 5.2 |
| | 128948 | AA485655 | Hs.223025 | proteasome (prosome; macropain) subunit | 13.1 |
| | 128955 | F10290 | Hs.185807 | Homo sapiens clone 24758 mRNA sequen | 5.8 |
| | 129005 | AA460049 | Hs.13323 | ESTs; Weakly similar to SODIUM- AND | 12.6 |
| | 129009 | AA131421 | Hs.75607 | ESTs | 9.8 |
| 20 | 129017 | H13108 | Hs.107968 | ESTs | 13.9 |
| | 129057 | X62466 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 10.7 |
| | 129075 | AA129465 | Hs.83765 | ESTs | 4.7 |
| | 129095 | L12350 | Hs.108623 | thrombospondin 2 | 4.4 |
| 25 | 129124 | AA234530 | Hs.108802 | N-ethylmaleimide-sensitive factor | 20.7 |
| | 129160 | AA131252 | Hs.109007 | ESTs | 5.9 |
| | 129164 | AA282183 | Hs.109045 | ESTs | 5.8 |
| | 129180 | R40556 | Hs.318401 | ESTs; Highly similar to HSPC039 protein | 7.6 |
| | 129224 | X89109 | Hs.109606 | coronin; actin-binding protein; 1A | 12 |
| 30 | 129229 | AA211941 | Hs.109643 | polyadenylate binding protein-interacting | 7.9 |
| | 129240 | W24360 | Hs.237868 | interleukin 7 receptor | 5.3 |
| | 129241 | AA435665 | Hs.109706 | ESTs; Moderately similar to HN1 [M.mus | 8.4 |
| | 129243 | H88033 | Hs.109727 | KIAA0733 protein | 7.8 |
| | 129247 | AA151574 | Hs.109733 | pilin-like transcription factor | 6.4 |
| 35 | 129259 | AA090695 | Hs.181385 | ESTs | 6.2 |
| | 129270 | Z35227 | Hs.109918 | ras homolog gene family; member H | 5.4 |
| | 129281 | AA026318 | Hs.289101 | glucose regulated protein; 58kD | 4.4 |
| | 129300 | C20976 | Hs.110165 | ESTs; Highly similar to ribosomal protein | 5.7 |
| | 129318 | N93155 | Hs.285976 | calmodulin 1 (phosphorylase kinase; delta | 7.7 |
| | 129319 | AA037467 | Hs.30340 | ESTs | 6 |
| 40 | 129351 | AA167268 | Hs.62349 | Human ras inhibitor mRNA; 3' end | 9.3 |
| | 129366 | H18027 | Hs.184697 | plexin C1 | 18.2 |
| | 129383 | W92984 | Hs.288224 | ESTs | 5.9 |
| | 129388 | AA151621 | Hs.110964 | ESTs | 4.1 |
| 45 | 129391 | T80814 | Hs.11101 | discs; large (Drosophila) homolog 3 (neur | 10.9 |
| | 129404 | AA172056 | Hs.317584 | ESTs | 5.3 |
| | 129406 | N23707 | Hs.111138 | KIAA0712 gene product | 4 |
| | 129426 | AA412087 | Hs.111323 | EST; Highly similar to protein inhibitor o | 8 |
| | 129453 | AA421213 | Hs.111632 | Lsm3 protein | 5.5 |
| 50 | 129513 | C00225 | Hs.306163 | ESTs; Weakly similar to fos39554_1 [H.s | 5.5 |
| | 129519 | AA298786 | Hs.112242 | ESTs | 6.8 |
| | 129606 | R21443 | Hs.166254 | heat shock 90kD protein 1; alpha | 5 |
| | 129622 | AA278243 | Hs.323949 | ESTs | 6.8 |
| | 129626 | AA447410 | Hs.111334 | ESTs; Weakly similar to !!! ALU SUBFA | 5.1 |
| 55 | 129627 | AA258308 | Hs.71968 | Homo sapiens mRNA; cDNA DKFZp564 | 5.3 |
| | 129628 | U26727 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (mel | 8.2 |
| | 129642 | R50008 | Hs.11806 | 7-dehydrocholesterol reductase | 4.3 |
| | 129663 | AA442768 | Hs.11866 | translocase of inner mitochondrial membr | 4.4 |
| | 129665 | M88458 | Hs.118778 | KDEL (Lys-Asp-Glu-Leu) endoplasmic re | 4 |
| | 129691 | X06700 | Hs.119571 | collagen; type III; alpha 1 (Ehlers-Danlos | 6 |
| 60 | 129783 | AA454618 | Hs.12479 | associated molecule with the SH3 domain | 6.4 |
| | 129800 | AA252436 | Hs.12540 | lysophospholipase I | 7.7 |
| | 129836 | AA452161 | Hs.206521 | YME1 (S.cerevisiae)-like 1 | 5 |
| | 129850 | N20593 | Hs.288932 | GDP dissociation inhibitor 2 | 6.9 |
| | 129869 | AA102520 | Hs.13015 | ESTs; Weakly similar to heat shock prote | 5 |
| 65 | 129896 | AA043021 | Hs.13225 | UDP-Gal:betaGlcNAc beta 1,4- galactosy | 6.6 |
| | 129982 | M87789 | | immunoglobulin gamma 3 (Gm marker) | 4 |
| | 129985 | AA450045 | Hs.140452 | cargo selection protein (mannose 6 phosp | 5.8 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 130029 | AA236412 | Hs.236510 | ESTs; Moderately similar to PFT27 [M.m | 5.6 |
| | 130033 | M90696 | Hs.181301 | cathepsin S | 5.4 |
| | 130036 | AA195260 | Hs.125849 | ESTs; Moderately similar to IIII ALU SU | 7.4 |
| 5 | 130069 | AA055896 | Hs.146428 | collagen; type V; alpha 1 | 7.6 |
| | 130077 | T24055 | Hs.91379 | ribosomal protein L26 | 4 |
| | 130080 | X14850 | Hs.147097 | H2A histone family; member X | 12.1 |
| | 130096 | AA223874 | Hs.197955 | KIAA0704 protein | 5 |
| | 130114 | AA234717 | Hs.14992 | ESTs | 7.8 |
| | 130125 | M36803 | Hs.1504 | hemopexin | 7.2 |
| 10 | 130135 | M61764 | Hs.21635 | tubulin; gamma 1 | 5.6 |
| | 130170 | AA610070 | Hs.151469 | calcium/calmodulin-dependent serine pro | 7.5 |
| | 130189 | D43947 | Hs.151761 | KIAA0100 gene product | 6.4 |
| | 130208 | AA620556 | Hs.15250 | peroxisomal D3;D2-enoyl-CoA isomerase | 6.4 |
| | 130211 | D50840 | Hs.23703 | UDP-glucose ceramide glucosyltransferase | 4.5 |
| 15 | 130235 | X14046 | Hs.153053 | CD37 antigen | 9.1 |
| | 130276 | S75295 | Hs.169149 | karyopherin alpha 1 (importin alpha 5) | 8.6 |
| | 130280 | L13738 | Hs.153937 | activated p21cdc42Hs kinase | 5 |
| | 130313 | AA620323 | Hs.154320 | ubiquitin-activating enzyme E1C (homolo | 6.1 |
| | 130314 | D86967 | Hs.154332 | KIAA0212 gene product | 10 |
| 20 | 130328 | AA135673 | Hs.154668 | KIAA0391 gene product | 6.1 |
| | 130356 | X84373 | Hs.155017 | nuclear receptor interacting protein 1 | 10.6 |
| | 130367 | Z38501 | Hs.8768 | ESTs; Weakly similar to IIII ALU SUBFA | 8.3 |
| | 130378 | T47333 | Hs.155188 | TATA box binding protein (TBP)-associa | 7.1 |
| | 130384 | X66364 | Hs.166071 | cyclin-dependent kinase 5 | 5.6 |
| 25 | 130393 | D13630 | Hs.155291 | KIAA0005 gene product | 4.1 |
| | 130399 | AA449417 | Hs.155356 | Homo sapiens mRNA for putative glucosy | 4.6 |
| | 130407 | N29888 | Hs.155410 | ESTs | 7 |
| | 130414 | M21121 | Hs.241392 | small inducible cytokine A5 (RANTES) | 4.1 |
| | 130417 | U58522 | Hs.155485 | huntingtin-interacting protein 2 | 7.9 |
| 30 | 130421 | D21260 | Hs.178710 | clathrin; heavy polypeptide-like 2 | 4 |
| | 130441 | U35835 | Hs.155637 | protein kinase; DNA-activated; catalytic p | 6.8 |
| | 130455 | X17059 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acetyl | 26.4 |
| | 130498 | L38951 | Hs.180446 | karyopherin (importin) beta 1 | 4.8 |
| | 130499 | AA416723 | Hs.158286 | Homo sapiens mRNA for KIAA0446 prot | 6.1 |
| 35 | 130511 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pseud | 8.3 |
| | 130553 | AA430032 | Hs.252587 | pituitary tumor-transforming 1 | 7.5 |
| | 130558 | H96654 | Hs.15984 | ESTs; Weakly similar to gene pp21 protei | 5.6 |
| | 130568 | AA232535 | Hs.16085 | ESTs; Highly similar to CGI-13 protein [H | 4 |
| | 130583 | W24957 | Hs.293907 | ESTs; Moderately similar to similar to C.e | 13.3 |
| 40 | 130585 | H66211 | Hs.16331 | ESTs | 10.1 |
| | 130604 | X03635 | Hs.1657 | estrogen receptor 1 | 39.9 |
| | 130614 | AA132007 | Hs.16697 | ESTs | 5.1 |
| | 130619 | AA477739 | Hs.12532 | ESTs | 5.9 |
| | 130622 | AA235247 | Hs.16846 | ESTs; Weakly similar to cytochrome P45 | 4.1 |
| 45 | 130625 | F03969 | Hs.260720 | matrix metalloproteinase 2 (gelatinase A; | 8.3 |
| | 130627 | L23808 | Hs.1695 | matrix metalloproteinase 12 (macrophage | 10.3 |
| | 130629 | M60346 | Hs.1697 | ATPase; H+ transporting; lysosomal (vacu | 7 |
| | 130635 | M87503 | Hs.1706 | interferon-stimulated transcription factor | 5.5 |
| | 130639 | D59711 | Hs.17132 | ESTs | 7.2 |
| 50 | 130677 | H17861 | Hs.17767 | ESTs | 13.5 |
| | 130681 | D82808 | Hs.17820 | Rho-associated; coiled-coil containing pro | 6 |
| | 130693 | AA487202 | Hs.17962 | ESTs | 6.1 |
| | 130703 | N63295 | Hs.18103 | ESTs | 4.3 |
| | 130706 | AA488843 | Hs.201673 | cornichon-like | 4 |
| 55 | 130712 | AA292066 | Hs.279762 | adenylate cyclase 7 | 5.1 |
| | 130714 | X92896 | Hs.18212 | DNA segment on chromosome X (unique) | 8.4 |
| | 130715 | T98227 | Hs.171952 | occludin | 5.7 |
| | 130744 | AA203527 | Hs.18747 | POP7 (processing of precursor; S. cerevis | 6.2 |
| | 130747 | AA471293 | Hs.6879 | ESTs | 8.2 |
| 60 | 130751 | AA435633 | Hs.18879 | Homo sapiens clone 23965 mRNA sequen | 8.3 |
| | 130796 | R39390 | Hs.19525 | ESTs | 4.5 |
| | 130800 | AA223386 | Hs.19574 | ESTs; Weakly similar to katanin p80 subu | 7.7 |
| | 130855 | AA425439 | Hs.143323 | putative DNA/chromatin binding motif | 4.3 |
| | 130859 | AA287327 | Hs.20478 | ceroid-lipofuscinosis; neuronal 2; late infa | 9.8 |
| 65 | 130866 | M58028 | Hs.2055 | ubiquitin-activating enzyme E1 (A1S9T a | 4.3 |
| | 130880 | D14678 | Hs.20830 | kinesin-like 2 | 4.5 |
| | 130891 | D31891 | Hs.20991 | SET domain; bifurcated; 1 | 4 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 130905 | AA056489 | Hs.129998 | ESTs | 8.7 |
| | 130913 | W03592 | Hs.21198 | translocase of outer mitochondrial membr | 20.9 |
| | 130919 | AA291710 | Hs.21276 | collagen; type IV; alpha 3 (Goodpasture a | 9 |
| | 130921 | AA074596 | Hs.194688 | bromodomain adjacent to zinc finger dom | 5.3 |
| 5 | 130944 | M97935 | Hs.21486 | signal transducer and activator of transcrip | 18.8 |
| | 130974 | X57985 | Hs.2178 | H2B histone family; member Q | 13.4 |
| | 130987 | R45698 | Hs.21893 | ESTs; Weakly similar to cAMP inducible | 8.5 |
| | 130999 | N48963 | Hs.21992 | KIAA0689 protein | 7.2 |
| 10 | 131010 | AA435748 | Hs.169341 | ESTs; Weakly similar to phosphatidic acid | 5.2 |
| | 131046 | X02530 | Hs.2248 | small inducible cytokine subfamily B (Cy | 10.1 |
| | 131091 | T35341 | Hs.22880 | ESTs; Highly similar to dipeptidyl peptid | 6.3 |
| | 131153 | H11760 | Hs.23606 | ESTs | 7.3 |
| | 131185 | M25753 | Hs.23960 | cyclin B1 | 6.2 |
| 15 | 131200 | AA609427 | Hs.293732 | ESTs; Moderately similar to !!!! ALU SU | 4.3 |
| | 131206 | AA044078 | Hs.24210 | ESTs | 5.5 |
| | 131210 | AA430047 | Hs.95549 | ESTs | 7.1 |
| | 131227 | AA429472 | Hs.236522 | DKFZP434P106 protein | 5.6 |
| | 131244 | D38076 | Hs.24763 | RAN binding protein 1 | 5.5 |
| | 131245 | AA620599 | Hs.24766 | DKFZP564E1962 protein | 6.7 |
| 20 | 131257 | AA256042 | Hs.24908 | ESTs | 5.8 |
| | 131319 | U25997 | Hs.25590 | stanniocalcin | 8.9 |
| | 131339 | AA463450 | Hs.25812 | Nijmegen breakage syndrome 1 (nibrin) | 6.5 |
| | 131388 | R34531 | Hs.92200 | KIAA0480 gene product | 9.2 |
| 25 | 131410 | H84658 | Hs.279836 | ESTs | 12.1 |
| | 131472 | AA608962 | Hs.27258 | calcyclin binding protein | 18.1 |
| | 131475 | Z39053 | Hs.27263 | ESTs | 7.5 |
| | 131501 | AA121127 | Hs.8207 | H3 histone; family 3A | 5.5 |
| | 131514 | X02152 | Hs.2795 | lactate dehydrogenase A | 5.1 |
| 30 | 131524 | N39152 | Hs.301804 | ESTs | 4.3 |
| | 131528 | D60856 | Hs.28309 | UDP-glucose dehydrogenase | 8.4 |
| | 131544 | N33236 | Hs.28555 | ESTs; Weakly similar to B0511.8 [C.eleg | 5.6 |
| | 131557 | D30946 | Hs.28707 | signal sequence receptor; gamma (transloc | 8.7 |
| | 131562 | U90551 | Hs.28777 | H2A histone family; member L | 18.8 |
| 35 | 131564 | AA491465 | Hs.28792 | ESTs | 11.8 |
| | 131586 | AA235385 | Hs.26966 | ESTs; Moderately similar to alternatively | 4.7 |
| | 131587 | M15182 | Hs.183868 | glucuronidase; beta | 5.2 |
| | 131589 | U52100 | Hs.29191 | epithelial membrane protein 2 | 4.4 |
| | 131615 | D14533 | Hs.192803 | xeroderma pigmentosum; complementatio | 4.6 |
| 40 | 131664 | AA136126 | Hs.30327 | mitogen-activated protein kinase-activated | 4.3 |
| | 131679 | AA136660 | Hs.30579 | ESTs | 9.4 |
| | 131684 | U26174 | Hs.3066 | granzyme K (serine protease; granzyme 3 | 9.7 |
| | 131687 | L11066 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 6.2 |
| | 131689 | AA599653 | Hs.30696 | transcription factor-like 5 (basic helix-loop | 8.3 |
| 45 | 131693 | W60913 | Hs.110796 | ESTs; Weakly similar to cDNA EST yk45 | 9 |
| | 131710 | AA233225 | Hs.30985 | MRS1 protein | 5.2 |
| | 131716 | D49738 | Hs.31053 | cytoskeleton-associated protein 1 | 6.6 |
| | 131742 | D31352 | Hs.31433 | ESTs | 11 |
| | 131762 | H46831 | Hs.107767 | ESTs; Moderately similar to CaM-KII inh | 4.9 |
| 50 | 131781 | AA460450 | Hs.31989 | DKFZP586G1722 protein | 9.2 |
| | 131795 | N32724 | Hs.32317 | Sox-like transcriptional factor | 4.5 |
| | 131809 | L76517 | Hs.3260 | presenilin 1 (Alzheimer disease 3) | 5.4 |
| | 131814 | AA437226 | Hs.157 | interleukin 10 receptor; alpha | 4 |
| | 131838 | AA091932 | Hs.180628 | dynamin-like protein | 6.7 |
| 55 | 131877 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 5 |
| | 131885 | AA044095 | Hs.3402 | ESTs | 11.1 |
| | 131891 | AA158258 | Hs.30376 | heterogeneous nuclear protein similar to r | 5.6 |
| | 131925 | AA248470 | Hs.183180 | ESTs; Weakly similar to RING finger pro | 4.5 |
| | 131930 | AA205460 | Hs.69476 | ESTs | 14.3 |
| 60 | 131941 | D62657 | Hs.35086 | ubiquitin-specific protease 1 | 6.2 |
| | 131965 | W90146 | Hs.35962 | ESTs | 6.3 |
| | 131970 | D86960 | Hs.3610 | KIAA0205 gene product | 4.2 |
| | 131971 | R70167 | Hs.154938 | ESTs | 4.3 |
| | 131974 | AA410424 | Hs.268122 | Homo sapiens mRNA; cDNA DKFZp586 | 4.6 |
| 65 | 131977 | F09788 | Hs.3622 | procollagen-proline; 2-oxoglutarate 4-diox | 6.4 |
| | 131994 | AA479515 | Hs.279882 | Human DNA sequence from clone 703H1 | 12 |
| | 131997 | D82399 | Hs.136644 | Homo sapiens clone 23714 mRNA sequen | 10 |
| | 132017 | W67251 | Hs.267659 | Homo sapiens vav 3 oncogene (VAV3) m | 4.7 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| | 132021 | T68246 | Hs.306079 | chaperonin containing TCP1; subunit 5 (e | 5.2 |
| | 132065 | D82226 | Hs.211594 | proteasome (prosome; macropain) 26S sub | 8.5 |
| | 132085 | D44466 | Hs.3887 | proteasome (prosome; macropain) 26S sub | 13.5 |
| 5 | 132089 | AA131971 | Hs.39122 | ESTs | 4.8 |
| | 132109 | AA599801 | Hs.40098 | ESTs | 6.2 |
| | 132143 | AA257056 | Hs.7972 | KIAA0871 protein | 14.6 |
| | 132149 | T10822 | Hs.324743 | ESTs | 5.3 |
| | 132153 | N90141 | Hs.41066 | ESTs; Moderately similar to ELONGATI | 9.2 |
| 10 | 132160 | AA281770 | Hs.295923 | seven in absentia (Drosophila) homolog 1 | 5.5 |
| | 132164 | U84573 | Hs.41270 | procollagen-lysine; 2-oxoglutarate 5-dioxy | 8.1 |
| | 132180 | AA405569 | Hs.418 | fibroblast activation protein; alpha; seprax | 15.4 |
| | 132183 | L19183 | Hs.199695 | hypothetical protein | 12.2 |
| | 132225 | AA128980 | | ESTs | 5.6 |
| 15 | 132227 | AA412620 | Hs.4248 | ESTs | 6.7 |
| | 132235 | F09058 | Hs.42656 | ESTs | 6.2 |
| | 132256 | AA608856 | Hs.431 | murine leukemia viral (bmi-1) oncogene h | 6 |
| | 132298 | N41849 | Hs.7120 | Homo sapiens cytokine receptor related p | 5.6 |
| | 132314 | AA285290 | Hs.44499 | small EDRK-rich factor 2 | 6.8 |
| 20 | 132325 | N37065 | Hs.44856 | ESTs | 4.7 |
| | 132384 | AA479933 | Hs.46967 | Human DNA sequence from clone 167A1 | 4.2 |
| | 132387 | R70914 | Hs.281434 | heat shock 70kD protein 1 | 9.1 |
| | 132393 | W85888 | Hs.47334 | ESTs; Moderately similar to !!!! ALU SU | 4 |
| | 132406 | F09979 | Hs.4774 | ESTs | 15 |
| 25 | 132407 | AA431459 | Hs.47783 | ESTs | 8 |
| | 132413 | AA132969 | Hs.260116 | KIAA1104 protein | 4 |
| | 132446 | AA426218 | Hs.48764 | ESTs | 5.3 |
| | 132465 | AA047896 | Hs.49169 | ESTs | 15.4 |
| | 132482 | AA429478 | Hs.238126 | ESTs; Highly similar to CGI-49 protein [H | 9 |
| 30 | 132492 | T03749 | Hs.4990 | KIAA1089 protein | 8.5 |
| | 132528 | AA283006 | Hs.50758 | chromosome-associated polypeptide C | 4.3 |
| | 132540 | AA488987 | Hs.5097 | synaptogyrin 2 | 9.8 |
| | 132543 | AA417152 | Hs.5101 | protein regulator of cytokinesis 1 | 10.1 |
| | 132580 | L37042 | Hs.283738 | casein kinase 1; alpha 1 | 5.9 |
| 35 | 132586 | AA412452 | Hs.52515 | DKFZP434N024 protein | 4.2 |
| | 132608 | AA199588 | Hs.5321 | ARP3 (actin-related protein 3; yeast) hom | 4.2 |
| | 132616 | AA386264 | Hs.283558 | isocitrate dehydrogenase 2 (NADP+); mit | 5.2 |
| | 132617 | AA171913 | Hs.5338 | carbonic anhydrase XII | 10.1 |
| | 132618 | AA253330 | Hs.279916 | adaptor-related protein complex 1; gamma | 4.8 |
| 40 | 132640 | U33821 | Hs.5437 | Tax1 (human T-cell leukemia virus type I | 5.7 |
| | 132668 | AA453614 | Hs.5460 | KIAA0776 protein | 4.4 |
| | 132694 | M60830 | Hs.5509 | ecotropic viral integration site 2B | 15.6 |
| | 132700 | N47109 | Hs.5521 | ESTs | 7 |
| | 132724 | AA417962 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 5.6 |
| 45 | 132738 | W42674 | Hs.264636 | ESTs; Moderately similar to neuronal thre | 4.9 |
| | 132742 | AA490862 | Hs.292812 | ESTs; Weakly similar to C43H8.1 [C.eleg | 7.9 |
| | 132744 | X54326 | Hs.55921 | glutamyl-prolyl-IRNA synthetase | 4.1 |
| | 132795 | H99152 | Hs.57079 | ESTs | 8 |
| | 132807 | AA331777 | Hs.57301 | mutL (E. coli) homolog 1 (colon cancer; n | 8 |
| 50 | 132811 | U25435 | Hs.57419 | transcriptional repressor | 4 |
| | 132817 | AB004884 | Hs.57553 | tousled-like kinase 2 | 6.5 |
| | 132840 | N23817 | Hs.5807 | Homo sapiens clone 23675 mRNA sequen | 5.6 |
| | 132845 | D62588 | Hs.5813 | ESTs | 12.4 |
| | 132847 | T48195 | Hs.58189 | eukaryotic translation initiation factor 3; s | 7 |
| 55 | 132856 | W79865 | Hs.58367 | glypican 4 | 6.2 |
| | 132869 | N26855 | Hs.203961 | ESTs | 6.5 |
| | 132874 | AA425776 | Hs.58609 | ESTs | 5.6 |
| | 132880 | AA444369 | Hs.177537 | ESTs | 7.2 |
| | 132894 | D82422 | Hs.5944 | ESTs | 7.5 |
| 60 | 132900 | N56451 | Hs.5978 | LIM domain only 7 | 4.4 |
| | 132903 | AA235404 | Hs.5985 | Homo sapiens clone 25186 mRNA sequen | 9.1 |
| | 132904 | X83618 | Hs.59889 | 3-hydroxy-3-methylglutaryl-Coenzyme A | 10.7 |
| | 132906 | AA142857 | Hs.234896 | ESTs; Highly similar to geminin [H.sapie | 10.2 |
| | 132914 | AA496037 | Hs.60293 | ESTs | 4.7 |
| 65 | 132918 | AA252605 | Hs.6051 | KIAA0616 protein | 7.1 |
| | 132936 | AB002305 | Hs.6111 | KIAA0307 gene product | 8.3 |
| | 132951 | U04209 | Hs.61418 | microfibrillar-associated protein 1 | 4.3 |
| | 132957 | AA234791 | Hs.61469 | Human gene from PAC 753P9; chromoso | 13.2 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 132959 | AA028103 | Hs.61472 | ESTs; Weakly similar to unknown [S.cere | 18.9 |
| | 132968 | N77151 | Hs.61638 | myosin X | 5.8 |
| | 132984 | H80409 | Hs.62112 | zinc finger protein 207 | 4.3 |
| | 132990 | AA458761 | Hs.18387 | transcription factor AP-2 alpha (activating | 4.2 |
| 5 | 132994 | AA505133 | Hs.279905 | solute carrier family 2 (facilitated glucose | 26.4 |
| | 132998 | Y00062 | Hs.170121 | protein tyrosine phosphatase; receptor typ | 4.4 |
| | 133002 | AF006082 | Hs.42915 | ARP2 (actin-related protein 2; yeast) hom | 4.7 |
| | 133005 | C21400 | Hs.278605 | KIAA0970 protein | 6.6 |
| | 133015 | AA047036 | Hs.246315 | ESTs | 7.9 |
| 10 | 133016 | W81298 | Hs.6289 | growth factor receptor-bound protein 2 | 5.2 |
| | 133039 | X62055 | Hs.63489 | protein tyrosine phosphatase; non-recepto | 4 |
| | 133050 | S67325 | Hs.63788 | propionyl Coenzyme A carboxylase; beta | 5.2 |
| | 133056 | AA071387 | Hs.6396 | jumping translocation breakpoint | 5 |
| | 133062 | R33663 | Hs.64056 | ESTs | 5.4 |
| 15 | 133083 | N70633 | Hs.6456 | chaperonin containing TCP1; subunit 2 (b | 6 |
| | 133091 | AA122147 | Hs.64691 | KIAA0483 protein | 5 |
| | 133093 | AA598749 | Hs.285996 | ESTs | 5.6 |
| | 133124 | AA156049 | Hs.267923 | ESTs | 4.1 |
| | 133126 | D16469 | Hs.6551 | ATPase; H+ transporting; lysosomal (vacu | 6.2 |
| 20 | 133196 | R37367 | Hs.6727 | Ras-GTPase activating protein SH3 doma | 5.1 |
| | 133214 | Y10659 | Hs.285115 | interleukin 13 receptor; alpha 1 | 6.2 |
| | 133225 | Z41415 | Hs.6823 | ESTs; Weakly similar to Intrinsic factor-B | 8.3 |
| | 133228 | N90029 | Hs.6831 | Homo sapiens clone 1400 unknown prote | 4.7 |
| | 133239 | AA059405 | Hs.179882 | Homo sapiens clone 24655 mRNA sequen | 5.5 |
| 25 | 133240 | D31161 | Hs.242894 | ESTs | 9 |
| | 133257 | AF006086 | Hs.6895 | actin related protein 2/3 complex; subunit | 7.7 |
| | 133264 | W72187 | Hs.69192 | ESTs; Weakly similar to cDNA EST yk37 | 6.7 |
| | 133274 | AA488886 | Hs.6949 | ESTs | 4.2 |
| | 133281 | AA421079 | Hs.69594 | ESTs; Weakly similar to Sox-like transcri | 4.9 |
| 30 | 133283 | AA410507 | Hs.6968 | ESTs | 4.3 |
| | 133287 | L15702 | Hs.69771 | B-factor; properdin | 9.3 |
| | 133294 | R79723 | Hs.69997 | zinc finger protein 238 | 30.4 |
| | 133297 | AA600057 | Hs.70266 | KIAA0905 protein | 10.4 |
| | 133318 | AA256168 | Hs.152316 | ESTs | 8.5 |
| 35 | 133362 | H06195 | Hs.7194 | ESTs; Highly similar to CGI-59 protein [H | 14 |
| | 133370 | AA156897 | Hs.72157 | DKFZP56411922 protein | 5 |
| | 133391 | X57579 | Hs.727 | inhibin; beta A (activin A; activin AB alp | 13.9 |
| | 133395 | AA491296 | Hs.72805 | ESTs | 4.3 |
| | 133422 | N79516 | Hs.73287 | ESTs; Weakly similar to eyelid [D.melano | 4.5 |
| 40 | 133431 | AA255438 | Hs.7358 | Homo sapiens mRNA; cDNA DKFZp566 | 8 |
| | 133435 | T23983 | Hs.323966 | ESTs | 5 |
| | 133449 | AA094989 | Hs.7381 | voltage-dependent anion channel 3 | 8.7 |
| | 133468 | X03068 | Hs.73931 | major histocompatibility complex; class II | 5 |
| | 133484 | X78710 | Hs.211581 | metal-regulatory transcription factor 1 | 5.3 |
| 45 | 133506 | AA316868 | Hs.74346 | ESTs; Weakly similar to 140G11.h [D.me | 6.8 |
| | 133517 | X52947 | Hs.74471 | gap junction protein; alpha 1; 43kd (conn | 5.7 |
| | 133551 | D63480 | Hs.278634 | KIAA0146 protein | 4.8 |
| | 133569 | AA313977 | Hs.172772 | transcription elongation factor B (SIII); po | 9.5 |
| | 133572 | W94333 | Hs.279915 | translocase of inner mitochondrial membr | 5 |
| 50 | 133577 | F03717 | Hs.75063 | human immunodeficiency virus type I enh | 7.4 |
| | 133589 | L37368 | Hs.75104 | RNA-binding protein S1; serine-rich dom | 5 |
| | 133608 | D13315 | Hs.75207 | glyoxalase I | 4.2 |
| | 133617 | AA148318 | Hs.75249 | KIAA0069 protein | 4.5 |
| | 133627 | U09587 | Hs.75280 | glycyl-tRNA synthetase | 10 |
| 55 | 133633 | D21262 | Hs.75337 | nucleolar phosphoprotein p130 | 4.5 |
| | 133634 | U24166 | Hs.234279 | microtubule-associated protein; RP/EB fa | 15.2 |
| | 133640 | D83004 | Hs.75355 | ubiquitin-conjugating enzyme E2N (homo | 9.1 |
| | 133644 | D89077 | Hs.75367 | Src-like-adaptor | 6.4 |
| | 133649 | AA479139 | Hs.75393 | acid phosphatase 1; soluble | 4.8 |
| 60 | 133652 | AA287383 | Hs.7540 | ESTs | 4.2 |
| | 133674 | AA458946 | Hs.75497 | ESTs | 4.3 |
| | 133700 | K01396 | Hs.297681 | protease inhibitor 1 (anti-elastase); alpha- | 8.3 |
| | 133705 | N21648 | Hs.75659 | MpV17 transgene; murine homolog; glom | 4.6 |
| | 133716 | Y00282 | Hs.75722 | ribophorin II | 7.5 |
| 65 | 133720 | L27841 | Hs.75737 | pericentriolar material 1 | 9.4 |
| | 133752 | U49278 | Hs.75875 | ubiquitin-conjugating enzyme E2 variant | 4.5 |
| | 133765 | D21255 | Hs.75929 | cadherin 11 (OB-cadherin; osteoblast) | 6.4 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 133772 | W73693 | Hs.76038 | isopentenyl-diphosphate delta isomerase | 7.9 |
| | 133774 | Z23090 | Hs.76067 | heat shock 27kD protein 1 | 4.1 |
| | 133776 | J03473 | Hs.177766 | ADP-ribosyltransferase (NAD+; poly (AD | 13 |
| | 133784 | AA214305 | Hs.301064 | ESTs | 5.2 |
| 5 | 133814 | M33882 | Hs.76391 | myxovirus (influenza) resistance 1; homol | 11.7 |
| | 133829 | AA453783 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564 | 9.4 |
| | 133834 | AA147510 | Hs.288660 | serine protease; umbilical endothelium | 4.8 |
| | 133839 | M59815 | Hs.170250 | complement component 4A | 6.7 |
| | 133842 | U73477 | Hs.285013 | putative human HLA class II associated p | 7.1 |
| 10 | 133845 | T68510 | Hs.76704 | ESTs | 6.3 |
| | 133859 | U86782 | Hs.178761 | 26S proteasome-associated pad1 homolog | 13.7 |
| | 133867 | D43948 | Hs.76989 | KIAA0097 gene product | 4.1 |
| | 133868 | U58090 | Hs.183874 | cullin 4A | 4 |
| | 133871 | AA454597 | Hs.182793 | ESTs | 4.7 |
| 15 | 133893 | X01060 | Hs.77356 | transferrin receptor (p90; CD71) | 8.3 |
| | 133914 | N32811 | Hs.77542 | ESTs | 5 |
| | 133918 | W72783 | Hs.58382 | ESTs; Weakly similar to C13F10.5 [C.ele | 4.5 |
| | 133944 | AA045870 | Hs.7780 | Homo sapiens mRNA; cDNA DKFZp564 | 6.3 |
| | 133946 | AA156565 | Hs.173878 | 4-nitrophenylphosphatase domain and non | 6.4 |
| 20 | 133963 | L34587 | Hs.184693 | transcription elongation factor B (SIII); po | 6.3 |
| | 133980 | D00760 | Hs.250811 | proteasome (prosome; macropain) subunit | 11.9 |
| | 133990 | C02374 | Hs.7822 | Homo sapiens mRNA; cDNA DKFZp564 | 8.2 |
| | 133999 | M28213 | Hs.78305 | RAB2; member RAS oncogene family | 5.2 |
| | 134030 | J03077 | Hs.78575 | prosaposin (variant Gaucher disease and v | 4.6 |
| 25 | 134032 | Z81326 | Hs.78589 | protease inhibitor 12 (neuroserpin) | 6.5 |
| | 134045 | S82470 | Hs.78768 | BB1 | 11.9 |
| | 134046 | D28473 | Hs.172801 | isoleucine-tRNA synthetase | 5.2 |
| | 134064 | D87685 | Hs.78893 | KIAA0244 protein | 7.3 |
| | 134070 | H98621 | Hs.78946 | cullin 3 | 4.7 |
| 30 | 134087 | U51166 | Hs.173824 | thymine-DNA glycosylase | 7 |
| | 134090 | M22382 | Hs.79037 | heat shock 60kD protein 1 (chaperonin) | 4.5 |
| | 134098 | X06323 | Hs.79086 | ribosomal protein; mitochondrial; L3 | 9.4 |
| | 134110 | U41060 | Hs.79136 | LIV-1 protein; estrogen regulated | 4.4 |
| | 134132 | U32519 | Hs.220689 | Ras-GTPase-activating protein SH3-doma | 6.6 |
| 35 | 134168 | AA398908 | Hs.181634 | Human Chromosome 16 BAC clone CIT9 | 8.6 |
| | 134170 | M63138 | Hs.79572 | cathepsin D (lysosomal aspartyl protease) | 9.3 |
| | 134208 | U88871 | Hs.79993 | peroxisomal biogenesis factor 7 | 6.3 |
| | 134258 | L28010 | Hs.808 | heterogeneous nuclear ribonucleoprotein F | 4.3 |
| | 134288 | AA430008 | Hs.8117 | ESTs | 6.9 |
| 40 | 134310 | AA313414 | Hs.8148 | Homo sapiens clone 24856 mRNA sequen | 7.4 |
| | 134326 | U16306 | Hs.81800 | chondroitin sulfate proteoglycan 2 (versic | 6.1 |
| | 134329 | D38551 | Hs.81848 | RAD21 (S. pombe) homolog | 8.6 |
| | 134331 | AA452020 | Hs.111222 | ESTs; Weakly similar to CGI-128 protein | 6.1 |
| | 134351 | R82074 | Hs.82109 | syndecan 1 | 4.4 |
| 45 | 134357 | L43575 | Hs.82171 | Human clone 191B7 placenta expressed m | 6.6 |
| | 134363 | M37033 | Hs.82212 | CD53 antigen | 5.3 |
| | 134367 | X54199 | Hs.82285 | phosphoribosylglycinamide formyltransfe | 4.8 |
| | 134374 | D62633 | Hs.8236 | ESTs | 15.2 |
| | 134375 | AA412720 | Hs.82389 | ESTs; Highly similar to CGI-118 protein | 7.2 |
| 50 | 134376 | X02874 | Hs.82396 | 2';5'-oligoadenylate synthetase 1 | 6.4 |
| | 134381 | U56637 | Hs.184270 | capping protein (actin filament) muscle Z- | 4 |
| | 134388 | M15841 | Hs.82575 | small nuclear ribonucleoprotein polypepti | 5.7 |
| | 134395 | L09717 | Hs.8262 | lysosomal-associated membrane protein 2 | 6.9 |
| | 134399 | H99801 | Hs.82689 | tumor rejection antigen (gp96) 1 | 4.5 |
| 55 | 134401 | AA243746 | Hs.211577 | kinectin 1 (kinesin receptor) | 11.2 |
| | 134405 | J04177 | Hs.82772 | collagen; type XI; alpha 1 | 15.3 |
| | 134415 | AA329274 | Hs.82911 | protein tyrosine phosphatase type IVA; m | 4.1 |
| | 134417 | D87969 | Hs.82921 | solute carrier family 35 (CMP-sialic acid t | 4.2 |
| | 134419 | L08044 | Hs.82961 | trefoil factor 3 (intestinal) | 5.9 |
| 60 | 134421 | AA122386 | Hs.82985 | collagen; type V; alpha 2 | 5.8 |
| | 134423 | W96151 | Hs.83006 | ESTs; Highly similar to CGI-139 protein | 4.4 |
| | 134438 | AA449984 | Hs.246857 | ESTs; Highly similar to protein kinase JN | 7 |
| | 134446 | T25732 | Hs.83419 | KIAA0252 protein | 4.6 |
| | 134453 | X70683 | Hs.83484 | SRY (sex determining region Y)-box 4 | 5.1 |
| 65 | 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 20.3 |
| | 134487 | R38185 | Hs.83954 | Homo sapiens unknown mRNA | 5 |
| | 134495 | D63477 | Hs.84087 | KIAA0143 protein | 16.1 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 134498 | M63180 | Hs.84131 | threonyl-tRNA synthetase | 6.1 |
| | 134506 | U45328 | Hs.84285 | ubiquitin-conjugating enzyme E2I (homol | 4.6 |
| | 134529 | H24460 | Hs.848 | FK506-binding protein 4 (59kD) | 6.2 |
| 5 | 134570 | U66615 | Hs.172280 | SWI/SNF related; matrix associated; actin | 4.8 |
| | 134582 | AA234966 | Hs.86041 | CGG triplet repeat binding protein 1 | 4.7 |
| | 134600 | R68884 | Hs.86347 | ESTs; Weakly similar to predicted using G | 5.8 |
| | 134623 | X74496 | Hs.86978 | prolyl endopeptidase | 4.5 |
| | 134654 | W23625 | Hs.8739 | ESTs; Weakly similar to ORF YGR200c [| 13.7 |
| | 134655 | AA454070 | Hs.123090 | ESTs | 5.8 |
| 10 | 134675 | AA250745 | Hs.87773 | protein kinase; cAMP-dependent; catalyti | 8.9 |
| | 134711 | X04011 | Hs.88974 | cytochrome b-245; beta polypeptide (chro | 6.8 |
| | 134714 | U89922 | Hs.890 | lymphotoxin beta (TNF superfamily; mem | 35.7 |
| | 134722 | W47183 | Hs.284226 | ESTs; Weakly similar to neural F box pro | 8.1 |
| 15 | 134776 | J05582 | Hs.89603 | mucin 1; transmembrane | 6.2 |
| | 134806 | Z49099 | Hs.89718 | spermine synthase | 4.2 |
| | 134810 | M27394 | Hs.89751 | membrane-spanning 4-domains; subfamily | 7 |
| | 134840 | U51477 | Hs.89981 | diacylglycerol kinase; zeta (104kD) | 4.1 |
| | 134843 | H60595 | Hs.90061 | progesterone binding protein | 4.7 |
| 20 | 134853 | D82348 | Hs.90280 | 5-aminimidazole-4-carboxamide ribonuc | 10.2 |
| | 134866 | U84011 | Hs.904 | amylase-1; 6-glucosidase; 4-alpha-glucanotr | 12.1 |
| | 134868 | Z39762 | Hs.90419 | KIAA0882 protein | 6 |
| | 134885 | N27670 | Hs.9071 | progesterone membrane binding protein | 5 |
| | 134982 | N46086 | Hs.92308 | ESTs | 4.1 |
| 25 | 134989 | AA236324 | Hs.92381 | Homo sapiens mRNA; chromosome 1 spe | 16.8 |
| | 134992 | H05625 | Hs.5831 | ESTs | 4 |
| | 134993 | AA282343 | Hs.301005 | purine-rich element binding protein B | 4.4 |
| | 135010 | D59675 | Hs.92927 | ESTs | 7 |
| | 135015 | U54989 | Hs.278338 | LGN protein | 4.8 |
| 30 | 135029 | AA224180 | | ESTs; Moderately similar to 17-beta-hydr | 13.6 |
| | 135032 | AA243497 | Hs.173685 | Human DNA sequence from clone 30M3 | 4 |
| | 135037 | U77948 | Hs.278589 | general transcription factor II; I | 8 |
| | 135059 | AA598449 | Hs.93832 | Homo sapiens clone 24483 unknown mRNA | 5.4 |
| | 135071 | L08069 | Hs.94 | heat shock protein; DNAJ-like 2 | 9.3 |
| 35 | 135083 | AA495950 | Hs.94262 | ESTs | 6.7 |
| | 135117 | W52493 | Hs.94694 | Homo sapiens clone 24837 mRNA sequen | 10.2 |
| | 135144 | AA044842 | Hs.95260 | Homo sapiens mRNA; cDNA DKFZp586 | 6.6 |
| | 135154 | AA126433 | Hs.267812 | sorting nexin 4 | 7.4 |
| | 135218 | D31157 | Hs.324277 | ESTs; Weakly similar to growth factor-res | 6.2 |
| 40 | 135237 | AA454930 | Hs.9691 | ESTs | 19.5 |
| | 135243 | AA215333 | Hs.97101 | putative G protein-coupled receptor | 8.8 |
| | 135335 | H20989 | Hs.198281 | pyruvate kinase; muscle | 12.4 |
| | 135349 | D83174 | Hs.9930 | collagen-binding protein 2 (collagen 2) | 5.5 |
| | 135367 | AA480109 | Hs.9963 | TYRO protein tyrosine kinase binding pro | 5.4 |
| 45 | 135389 | U05237 | Hs.99872 | fetal Alzheimer antigen | 7.8 |
| | 135400 | M23263 | Hs.99915 | androgen receptor (dihydrotestosterone re | 9.1 |
| | 135411 | L10333 | Hs.99947 | reticulum 1 | 5.3 |
| | 300019 | M97935 | | AFFX control: STAT1 | 8.3 |
| | 300021 | M97935 | | AFFX control: STAT1 | 7 |
| | 300022 | M97935 | | AFFX control: STAT1 | 14 |
| 50 | 300089 | AI199738 | Hs.208275 | ESTs; Weakly similar to !!!! ALU CLASS | 9.1 |
| | 300107 | AI694585 | Hs.270464 | ESTs; Weakly similar to !!!! ALU CLASS | 7.4 |
| | 300254 | AW079607 | Hs.188417 | ESTs; Weakly similar to ZnT-3 [H.sapien | 30.1 |
| | 300328 | AW015860 | Hs.224623 | ESTs | 11.9 |
| 55 | 300549 | AA699328 | Hs.298119 | ESTs | 5.5 |
| | 300711 | AI492179 | Hs.166244 | ESTs; Weakly similar to cDNA EST yk40 | 11 |
| | 300921 | AW293224 | Hs.232165 | ESTs | 11 |
| | 301124 | T79326 | Hs.298262 | ESTs; Weakly similar to dJ88J8.1 [H.sapi | 8.8 |
| | 301165 | N85789 | Hs.150186 | ESTs; Weakly similar to PTERIN-4-ALP | 6 |
| 60 | 301576 | AI682905 | Hs.270431 | ESTs; Weakly similar to !!!! ALU SUBFA | 4.7 |
| | 301604 | AA373124 | Hs.24809 | ESTs; Weakly similar to C17G10.1 [C.ele | 8 |
| | 301704 | AA526313 | Hs.293691 | ESTs | 4.2 |
| | 301782 | N99399 | Hs.143046 | EST cluster (not in UniGene) with exon h | 18 |
| | 301884 | AA312082 | Hs.105445 | GNDF family receptor alpha 1 | 20.7 |
| 65 | 301936 | NM_004694 | Hs.114924 | EST cluster (not in UniGene) with exon h | 11.6 |
| | 302002 | AF013956 | Hs.5637 | chromobox homolog 4 (Drosophila Pc cla | 9.2 |
| | 302032 | NM_001992 | Hs.128087 | EST cluster (not in UniGene) with exon h | 4.3 |
| | 302067 | H05698 | Hs.222399 | ESTs; Weakly similar to protein-tyrosine | 7.8 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 302145 | NM_003613 | Hs.151407 | EST cluster (not in UniGene) with exon h | 15.1 |
| | 302236 | AI128606 | Hs.6557 | zinc finger protein 161 | 25.8 |
| | 302276 | NM_004448 | Hs.323910 | EST cluster (not in UniGene) with exon h | 21.6 |
| 5 | 302290 | AL117607 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564 | 41.4 |
| | 302326 | NM_004271 | Hs.184018 | EST cluster (not in UniGene) with exon h | 8.9 |
| | 302342 | AB023141 | Hs.190386 | KIAA0924 protein | 5.4 |
| | 302372 | AL117406 | Hs.200102 | Homo sapiens mRNA; cDNA DKFZp434 | 8.9 |
| | 302422 | AB021227 | Hs.3743 | matrix metalloproteinase 24 (membrane-in | 5.2 |
| | 302431 | AF129530 | Hs.226434 | EST cluster (not in UniGene) with exon h | 5.3 |
| 10 | 302501 | AF022726 | Hs.251446 | EST cluster (not in UniGene) with exon h | 9.9 |
| | 302505 | AL049650 | Hs.247874 | multiple UniGene matches | 4.3 |
| | 302533 | L36149 | Hs.248116 | chemokine (C motif) XC receptor 1 | 4.9 |
| | 302638 | AA463798 | Hs.102696 | ESTs; Weakly similar to C11D2.4 [C.eleg | 5.3 |
| | 302656 | AW293005 | Hs.70704 | ESTs | 8.4 |
| 15 | 302792 | AA343696 | Hs.46821 | ESTs; Weakly similar to putative [H.sapie | 4.5 |
| | 302820 | X04588 | Hs.85844 | EST cluster (not in UniGene) with exon h | 6.8 |
| | 302838 | U66049 | Hs.82171 | EST cluster (not in UniGene) with exon h | 8.4 |
| | 302892 | N58545 | Hs.42346 | histone deacetylase 3 | 22.8 |
| | 302977 | AW263124 | Hs.315111 | EST cluster (not in UniGene) with exon h | 6.8 |
| 20 | 302989 | N46406 | Hs.84700 | EST cluster (not in UniGene) with exon h | 8.9 |
| | 303007 | AA478876 | Hs.317714 | pallid (mouse) homolog; pallidin | 10.1 |
| | 303052 | AF140242 | Hs.279926 | EST cluster (not in UniGene) with exon h | 24.4 |
| | 303131 | AW081061 | Hs.103180 | actin-like 6 | 6.3 |
| | 303132 | AI929819 | Hs.4055 | ESTs | 17.7 |
| 25 | 303153 | U09759 | Hs.246857 | mitogen-activated protein kinase 9 | 11.4 |
| | 303387 | AA908797 | Hs.180799 | ESTs | 15.8 |
| | 303499 | AI815990 | Hs.293515 | ESTs | 7.2 |
| | 303502 | AA488528 | | EST cluster (not in UniGene) with exon h | 5.3 |
| | 303576 | T07216 | Hs.301226 | EST cluster (not in UniGene) with exon h | 16.2 |
| 30 | 303620 | AA397546 | Hs.119151 | ESTs | 8.9 |
| | 303634 | AI953377 | Hs.28444 | ESTs; Weakly similar to predicted using G | 12 |
| | 303642 | AW299459 | Hs.111977 | EST cluster (not in UniGene) with exon h | 4.2 |
| | 303654 | AA436942 | Hs.288529 | ESTs | 8.4 |
| | 303733 | AW502498 | Hs.15220 | ESTs; Weakly similar to zinc finger prote | 5.2 |
| 35 | 303780 | AI424014 | Hs.18995 | ESTs; Moderately similar to KIAA0456 p | 28.4 |
| | 303792 | C75094 | Hs.199839 | ESTs; Highly similar to NG22 [H.sapiens | 4.4 |
| | 303842 | AI337304 | Hs.126268 | ESTs; Weakly similar to similar to PDZ d | 8.1 |
| | 303951 | AW475081 | Hs.172928 | collagen; type I; alpha 1 | 7.5 |
| | 304465 | AA421948 | | EST singleton (not in UniGene) with exon | 6.5 |
| 40 | 304507 | AA456426 | | EST | 5.4 |
| | 304591 | AA505702 | | EST singleton (not in UniGene) with exon | 9.8 |
| | 304601 | AA507875 | | EST singleton (not in UniGene) with exon | 7.5 |
| | 304659 | AA533185 | | EST singleton (not in UniGene) with exon | 7 |
| | 305040 | AA630582 | Hs.169476 | glyceraldehyde-3-phosphate dehydrogena | 12.4 |
| 45 | 305134 | AA653159 | Hs.179661 | EST singleton (not in UniGene) with exon | 8.7 |
| | 305415 | AA725116 | Hs.78465 | EST singleton (not in UniGene) with exon | 5.3 |
| | 305453 | AA738110 | | EST singleton (not in UniGene) with exon | 4.1 |
| | 305898 | AA872838 | | keratin 8 | 7.7 |
| | 305913 | AA876109 | | EST singleton (not in UniGene) with exon | 6.3 |
| 50 | 305950 | AA884479 | | EST singleton (not in UniGene) with exon | 5.6 |
| | 306004 | AA889992 | Hs.2186 | EST singleton (not in UniGene) with exon | 13.2 |
| | 306009 | AA894560 | Hs.283370 | EST singleton (not in UniGene) with exon | 4.4 |
| | 306060 | AA906161 | Hs.76277 | EST singleton (not in UniGene) with exon | 4.6 |
| | 306398 | AA970548 | Hs.297681 | EST singleton (not in UniGene) with exon | 7.6 |
| 55 | 306505 | AA987722 | Hs.172928 | EST singleton (not in UniGene) with exon | 19.7 |
| | 306576 | AA995761 | Hs.276092 | EST singleton (not in UniGene) with exon | 5.5 |
| | 307117 | AI184111 | Hs.76067 | heat shock 27kD protein 1 | 7.7 |
| | 307138 | AI185516 | Hs.172928 | collagen; type I; alpha 1 | 8.8 |
| | 307187 | AI190870 | Hs.276417 | EST singleton (not in UniGene) with exon | 4.1 |
| 60 | 307542 | AI280859 | Hs.62954 | EST singleton (not in UniGene) with exon | 6 |
| | 307554 | AI281603 | Hs.172928 | EST singleton (not in UniGene) with exon | 10.8 |
| | 307806 | AI351739 | Hs.276726 | EST singleton (not in UniGene) with exon | 4.7 |
| | 308079 | AI472733 | Hs.270208 | ESTs | 4.2 |
| | 308307 | AI581398 | Hs.172928 | collagen; type I; alpha 1 | 5.4 |
| 65 | 308511 | AI687580 | Hs.169476 | EST singleton (not in UniGene) with exon | 10.1 |
| | 308615 | AI738593 | Hs.101774 | EST singleton (not in UniGene) with exon | 15.1 |
| | 308677 | AI761173 | | EST singleton (not in UniGene) with exon | 4.6 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 308852 | AI829848 | Hs.182937 | peptidylprolyl isomerase A (cyclophilin A | 5.9 |
| | 308974 | AI872290 | Hs.300697 | immunoglobulin gamma 3 (Gm marker) | 4.5 |
| | 308981 | AI873242 | | EST singleton (not in UniGene) with exon | 7.6 |
| | 308995 | AI880172 | | EST singleton (not in UniGene) with exon | 6.6 |
| 5 | 309177 | AI951118 | | EST singleton (not in UniGene) with exon | 24.3 |
| | 309186 | AI952723 | Hs.90207 | EST singleton (not in UniGene) with exon | 6.1 |
| | 309198 | AI955915 | | major histocompatibility complex; class I; | 5.6 |
| | 309226 | AI969897 | | EST singleton (not in UniGene) with exon | 6.2 |
| | 309279 | AI990102 | | EST singleton (not in UniGene) with exon | 7.9 |
| 10 | 309583 | AW170035 | | EST | 64.5 |
| | 309624 | AW191929 | Hs.252989 | EST | 5.3 |
| | 309629 | AW192764 | Hs.172928 | collagen; type I; alpha 1 | 6.9 |
| | 309641 | AW194230 | Hs.253100 | EST | 11.4 |
| | 309698 | AW238461 | Hs.73742 | ribosomal protein; large; P0 | 4.3 |
| 15 | 309700 | AW241170 | Hs.179661 | Homo sapiens clone 24703 beta-tubulin m | 11.9 |
| | 310073 | AI335004 | Hs.148558 | ESTs | 4.2 |
| | 310094 | AW450967 | Hs.235240 | ESTs | 5.7 |
| | 310373 | AW080778 | Hs.145582 | ESTs | 4.8 |
| | 310438 | AW022192 | Hs.200197 | ESTs | 39.1 |
| 20 | 310470 | AI281848 | Hs.194691 | ESTs | 4.9 |
| | 310583 | AW205632 | Hs.211198 | ESTs | 7 |
| | 310877 | T47784 | Hs.188955 | ESTs | 4.1 |
| | 311067 | AI587332 | Hs.209115 | ESTs | 11.2 |
| | 311166 | AI821294 | Hs.118599 | ESTs | 24.1 |
| 25 | 311199 | T57896 | Hs.191095 | EST cluster (not in UniGene) | 5.7 |
| | 311465 | AI758660 | Hs.206132 | ESTs | 15.7 |
| | 311587 | AI828254 | Hs.271019 | ESTs | 6.4 |
| | 311774 | AA700870 | Hs.14304 | ESTs | 6.2 |
| | 311785 | AI056769 | Hs.133512 | ESTs | 5 |
| 30 | 311923 | T60843 | Hs.189679 | ESTs | 5.9 |
| | 311935 | AA216387 | | EST cluster (not in UniGene) | 5.5 |
| | 311972 | N51511 | Hs.188449 | ESTs | 5.2 |
| | 312014 | AI435650 | Hs.128778 | ESTs | 4.3 |
| | 312047 | AA588275 | Hs.180669 | ESTs | 14.7 |
| 35 | 312147 | T89855 | Hs.195648 | EST cluster (not in UniGene) | 9.8 |
| | 312153 | AA759250 | Hs.153028 | cytochrome b-561 | 27.1 |
| | 312168 | T92251 | Hs.198882 | ESTs | 4.2 |
| | 312172 | AI222168 | Hs.191168 | ESTs | 6.1 |
| | 312226 | AI796815 | Hs.199993 | ESTs; Weakly similar to ubiquitous TPR | 5.5 |
| 40 | 312292 | AW451893 | Hs.151124 | ESTs | 18.4 |
| | 312312 | AI080505 | Hs.134529 | ESTs | 11.9 |
| | 312369 | AA582039 | Hs.173884 | Homo sapiens mRNA; chromosome 1 spe | 4 |
| | 312407 | R46180 | Hs.153485 | ESTs | 13.6 |
| | 312430 | AW139117 | Hs.117494 | ESTs | 4.1 |
| 45 | 312470 | AW451347 | Hs.175862 | ESTs | 4.6 |
| | 312483 | AI417526 | Hs.7753 | ESTs | 15.3 |
| | 312521 | AA033609 | Hs.319093 | ESTs | 12.5 |
| | 312544 | AI498371 | Hs.183526 | ESTs | 14.6 |
| | 312638 | AW439195 | Hs.256880 | ESTs | 5.3 |
| 50 | 312754 | R99834 | Hs.250383 | ESTs | 8.4 |
| | 312772 | H63791 | | EST cluster (not in UniGene) | 4.3 |
| | 312821 | AA699325 | Hs.269880 | ESTs | 8.3 |
| | 312837 | AW292286 | Hs.255058 | ESTs | 7.1 |
| | 312849 | AA846353 | Hs.194054 | ESTs | 5.9 |
| 55 | 312854 | AA828713 | Hs.321058 | EST cluster (not in UniGene) | 4.1 |
| | 312992 | AA088446 | Hs.170298 | ESTs | 7.3 |
| | 313096 | AI422367 | Hs.163533 | ESTs | 6.1 |
| | 313112 | AA732534 | Hs.269099 | ESTs | 4.2 |
| | 313126 | AA720887 | Hs.283313 | EST cluster (not in UniGene) | 18.1 |
| 60 | 313136 | N59284 | Hs.288010 | ESTs | 17 |
| | 313197 | AI738851 | Hs.222487 | ESTs | 12.9 |
| | 313219 | N74924 | Hs.182099 | ESTs | 7.1 |
| | 313258 | AW068358 | Hs.183918 | ESTs | 13.7 |
| | 313328 | AW449211 | Hs.105445 | ESTs | 27.9 |
| 65 | 313352 | AW292127 | Hs.144758 | ESTs | 9.8 |
| | 313417 | AA741151 | Hs.137323 | ESTs | 8.2 |
| | 313455 | AW081702 | Hs.98571 | ESTs | 6.9 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 313590 | AA804410 | Hs.291677 | EST cluster (not in UniGene) | 5.3 |
| | 313663 | AI953261 | Hs.169813 | ESTs | 7.6 |
| | 313667 | U69201 | Hs.13684 | ESTs; Weakly similar to choline kinase is | 12.5 |
| 5 | 313749 | AW450376 | Hs.119004 | ESTs | 5.5 |
| | 313832 | AW271022 | Hs.133294 | ESTs | 4.3 |
| | 313881 | AA535580 | Hs.16331 | ESTs | 7.7 |
| | 313915 | AI969390 | Hs.163443 | ESTs | 27.1 |
| | 313955 | AI858884 | Hs.270647 | ESTs | 5.7 |
| 10 | 313974 | AI310151 | Hs.173524 | ESTs | 4.3 |
| | 314097 | AA648744 | Hs.269493 | ESTs | 14.5 |
| | 314129 | AA228366 | Hs.115122 | ESTs | 9.5 |
| | 314359 | AA205569 | Hs.194193 | ESTs | 5.4 |
| | 314384 | AA535840 | Hs.162203 | ESTs; Weakly similar to alternatively spli | 5.3 |
| | 314394 | AI380563 | Hs.130816 | ESTs | 13.2 |
| 15 | 314462 | AA347951 | Hs.326413 | ESTs | 6.2 |
| | 314465 | AA602917 | Hs.156974 | ESTs | 18.1 |
| | 314470 | AI934422 | Hs.30661 | ESTs | 4.2 |
| | 314488 | AA358265 | Hs.182890 | ESTs | 6.1 |
| 20 | 314506 | AA833655 | Hs.206868 | ESTs | 27.8 |
| | 314510 | AI204418 | Hs.190080 | ESTs | 9.5 |
| | 314558 | AI873274 | Hs.190721 | ESTs | 22.5 |
| | 314661 | AA436432 | Hs.324239 | EST cluster (not in UniGene) | 13.3 |
| | 314691 | AW207206 | Hs.136319 | ESTs | 21.4 |
| | 314754 | AW026761 | Hs.134374 | ESTs | 4.4 |
| 25 | 314775 | AI149880 | Hs.188809 | ESTs | 4.4 |
| | 314943 | AI476797 | Hs.184572 | cell division cycle 2; G1 to S and G2 to M | 18.4 |
| | 314961 | AW008061 | Hs.231994 | ESTs | 10.2 |
| | 314963 | AI689617 | Hs.200934 | ESTs | 5.3 |
| | 315006 | AI538613 | Hs.298241 | ESTs | 20.7 |
| 30 | 315010 | AA531082 | Hs.240049 | ESTs | 5 |
| | 315019 | AA532807 | Hs.105822 | ESTs | 6.1 |
| | 315033 | AI93046 | Hs.146133 | ESTs | 12 |
| | 315036 | AA534953 | Hs.163297 | ESTs | 8.3 |
| 35 | 315037 | AW205863 | Hs.133988 | ESTs; Weakly similar to gene MAC25 pr | 6.1 |
| | 315051 | AW292425 | Hs.163484 | EST | 12.7 |
| | 315054 | AI968598 | Hs.78768 | ESTs | 7.6 |
| | 315073 | AW452948 | Hs.257631 | ESTs | 13.9 |
| | 315080 | AA744550 | Hs.136345 | ESTs | 4.4 |
| | 315083 | AI221325 | Hs.205442 | ESTs | 5.1 |
| 40 | 315088 | AA557351 | Hs.152448 | ESTs; Moderately similar to MULTIFUN | 4.7 |
| | 315175 | AI025842 | Hs.152530 | ESTs | 11.9 |
| | 315196 | AA972756 | Hs.44898 | ESTs | 28.8 |
| | 315296 | AA876905 | Hs.125286 | ESTs | 16.1 |
| 45 | 315303 | AW194364 | Hs.128022 | ESTs; Weakly similar to FIG-1 PROTEIN | 25.7 |
| | 315352 | AA604799 | Hs.136528 | ESTs; Moderately similar to !!!! ALU SU | 12.3 |
| | 315364 | AA643602 | Hs.155485 | ESTs; Highly similar to serine protease [H | 4.6 |
| | 315368 | AW291563 | Hs.104696 | ESTs | 4.8 |
| | 315390 | AI801565 | Hs.200113 | ESTs; Weakly similar to alternatively spli | 4.4 |
| | 315408 | AW273261 | Hs.216292 | ESTs | 5 |
| 50 | 315458 | AA872000 | Hs.116104 | ESTs | 7.6 |
| | 315472 | AA828850 | Hs.165469 | ESTs | 4.9 |
| | 315478 | AA665612 | Hs.120874 | ESTs | 5.2 |
| | 315498 | AA628539 | Hs.116252 | ESTs; Moderately similar to !!!! ALU SU | 4.8 |
| | 315527 | AI791138 | Hs.116768 | ESTs | 4.4 |
| 55 | 315530 | AI200852 | Hs.127780 | ESTs | 22.4 |
| | 315562 | AA737415 | Hs.152826 | ESTs | 5.9 |
| | 315634 | AA837085 | Hs.220585 | ESTs | 8.8 |
| | 315647 | AA648983 | Hs.212911 | ESTs | 15 |
| | 315652 | AI521489 | Hs.3053 | ESTs | 6.3 |
| 60 | 315676 | AW002565 | Hs.124660 | ESTs | 9.2 |
| | 315680 | AA814309 | Hs.123583 | ESTs | 8.1 |
| | 315735 | AI831760 | Hs.155111 | ESTs | 13.4 |
| | 315741 | AA812168 | Hs.122559 | ESTs | 5.4 |
| | 315769 | AA744875 | Hs.189413 | ESTs | 4.4 |
| 65 | 315978 | AA830893 | Hs.119769 | ESTs | 10.4 |
| | 315984 | AI015862 | Hs.131793 | ESTs | 5 |
| | 316042 | AW297979 | Hs.170698 | ESTs | 14.7 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 316136 | AA830808 | Hs.124366 | ESTs | 4 |
| | 316177 | AI908272 | Hs.293102 | EST cluster (not in UniGene) | 32.6 |
| | 316313 | AA741300 | Hs.202599 | ESTs | 4.8 |
| 5 | 316405 | AA757900 | Hs.270823 | ESTs | 4.8 |
| | 316480 | AI749921 | Hs.205377 | ESTs | 12.9 |
| | 316564 | AI743571 | Hs.168799 | ESTs; Weakly similar to !!!! ALU SUBFA | 8.1 |
| | 316714 | AA809792 | Hs.123307 | ESTs | 5 |
| | 316715 | AI440266 | Hs.170673 | ESTs | 4.2 |
| 10 | 316828 | AA828116 | Hs.173076 | ESTs | 5.2 |
| | 316869 | AI954880 | Hs.134604 | ESTs | 13.3 |
| | 316905 | AW138241 | Hs.210846 | ESTs | 6.2 |
| | 316943 | AW014875 | Hs.137007 | ESTs | 5.3 |
| | 316949 | AA856749 | Hs.124620 | ESTs | 7.2 |
| 15 | 317008 | AW051597 | Hs.143707 | ESTs | 4.1 |
| | 317028 | AA962623 | Hs.189144 | ESTs; Weakly similar to RENAL SODIU | 4.2 |
| | 317067 | AI805392 | Hs.325335 | ESTs | 4.5 |
| | 317069 | AI732892 | Hs.190489 | ESTs | 6.4 |
| | 317210 | AA490718 | | EST cluster (not in UniGene) | 4.4 |
| 20 | 317298 | AI922374 | Hs.158549 | ESTs | 5.9 |
| | 317658 | AW139077 | Hs.202217 | ESTs | 4.6 |
| | 317674 | AW294909 | Hs.132208 | ESTs | 5.2 |
| | 317685 | AI798630 | Hs.149997 | ESTs | 4.3 |
| | 317836 | AA983913 | Hs.128929 | ESTs | 12.4 |
| 25 | 317881 | AI827248 | Hs.224398 | ESTs | 12.1 |
| | 317902 | AI828602 | Hs.211265 | ESTs | 8.8 |
| | 317916 | AI565071 | Hs.159983 | ESTs | 12.6 |
| | 318042 | AW294522 | Hs.149991 | ESTs | 5.6 |
| | 318053 | AI074465 | Hs.133469 | ESTs | 4 |
| 30 | 318064 | AW296888 | Hs.170939 | ESTs | 5.2 |
| | 318070 | AI024594 | Hs.248942 | ESTs | 4.7 |
| | 318073 | AW167087 | Hs.131562 | ESTs | 15.7 |
| | 318146 | AI040125 | Hs.150521 | ESTs | 5.9 |
| | 318186 | AW016773 | Hs.3709 | ESTs | 5.3 |
| 35 | 318481 | AI291584 | Hs.145921 | ESTs; Weakly similar to HYPOTHETICA | 7.6 |
| | 318566 | AI335361 | Hs.226376 | ESTs | 5.8 |
| | 318617 | AW247252 | Hs.75514 | nucleoside phosphorylase | 11.1 |
| | 318662 | AI285898 | Hs.294014 | ESTs | 16.3 |
| | 318691 | AW192139 | Hs.181307 | H3 histone; family 3A | 4 |
| 40 | 318740 | NM_002543 | Hs.77729 | EST cluster (not in UniGene) | 21.3 |
| | 318744 | AI793124 | Hs.144479 | ESTs | 35 |
| | 318948 | AA317274 | Hs.13996 | ESTs | 11.7 |
| | 319163 | F15257 | Hs.27 | glycine dehydrogenase (decarboxylating; | 7 |
| | 319478 | RO6841 | Hs.270307 | EST cluster (not in UniGene) | 8.9 |
| 45 | 319545 | R83716 | Hs.14355 | ESTs | 8.2 |
| | 319668 | NM_002731 | Hs.87773 | EST cluster (not in UniGene) | 25.4 |
| | 319763 | AA460775 | Hs.6295 | ESTs | 7 |
| | 319913 | AA179304 | Hs.271586 | ESTs; Moderately similar to !!!! ALU SU | 8.7 |
| | 319936 | W22152 | Hs.282929 | EST cluster (not in UniGene) | 5.6 |
| 50 | 319951 | AA307665 | Hs.14559 | ESTs | 4.9 |
| | 319962 | HO6350 | Hs.135056 | ESTs | 9.2 |
| | 319977 | AA632632 | | EST cluster (not in UniGene) | 4.6 |
| | 320074 | AA321166 | Hs.278233 | EST cluster (not in UniGene) | 16.7 |
| | 320092 | AF022799 | Hs.113292 | calpain 9 (nCL-4) | 5.4 |
| 55 | 320107 | AA836461 | Hs.291712 | EST cluster (not in UniGene) | 5.3 |
| | 320133 | D63271 | | EST cluster (not in UniGene) | 5.5 |
| | 320167 | AA984373 | Hs.90790 | EST cluster (not in UniGene) | 15 |
| | 320187 | T99949 | Hs.303428 | EST cluster (not in UniGene) | 6.7 |
| | 320211 | AL039402 | Hs.125783 | DEME-6 protein | 24.3 |
| 60 | 320401 | U90449 | Hs.152717 | nucleoside diphosphate kinase type 6 (inh | 10 |
| | 320458 | AI884396 | Hs.24131 | ESTs | 5.4 |
| | 320488 | R31386 | Hs.191791 | EST cluster (not in UniGene) | 4.9 |
| | 320521 | N31464 | Hs.24743 | ESTs | 9.5 |
| | 320661 | AA864846 | Hs.115175 | EST cluster (not in UniGene) | 6.6 |
| 65 | 320691 | R61576 | Hs.313951 | hypothetical protein | 5.9 |
| | 320699 | R63161 | Hs.118249 | EST cluster (not in UniGene) | 4 |
| | 320727 | U96044 | Hs.181125 | EST cluster (not in UniGene) | 15.3 |
| | 320993 | AL050145 | Hs.225986 | Homo sapiens mRNA; cDNA DKFZp586 | 7.2 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 321012 | AA737314 | Hs.194324 | EST cluster (not in UniGene) | 6.1 |
| | 321050 | AW393497 | | EST cluster (not in UniGene) | 5 |
| | 321051 | AF134149 | Hs.240395 | EST cluster (not in UniGene) | 11.4 |
| 5 | 321171 | AI769410 | Hs.221461 | ESTs | 7.7 |
| | 321192 | AA295304 | Hs.297939 | ESTs; Weakly similar to neogenin [H.sap | 5.5 |
| | 321354 | AA078493 | | EST cluster (not in UniGene) | 16.9 |
| | 321387 | H68014 | Hs.141278 | ESTs; Weakly similar to !!!! ALU SUBFA | 4.2 |
| | 321412 | AW366305 | Hs.22891 | EST cluster (not in UniGene) | 6.3 |
| 10 | 321489 | AW392474 | Hs.172759 | ESTs; Moderately similar to !!!! ALU SU | 9 |
| | 321539 | N98619 | Hs.42915 | ARP2 (actin-related protein 2; yeast) hom | 11.3 |
| | 321593 | H84762 | Hs.253197 | ESTs | 10.4 |
| | 321666 | D28390 | Hs.272897 | EST cluster (not in UniGene) | 19.9 |
| | 321891 | AW157424 | Hs.165954 | ESTs | 5.6 |
| | 321910 | H67065 | Hs.271530 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.4 |
| 15 | 321953 | AW088268 | Hs.292833 | ESTs; Weakly similar to !!!! ALU CLASS | 6.5 |
| | 321978 | N77342 | Hs.21851 | EST cluster (not in UniGene) | 10.2 |
| | 322017 | AA310039 | Hs.9192 | ESTs | 9.8 |
| | 322026 | AA233527 | Hs.283675 | low density lipoprotein receptor (familial | 27.8 |
| 20 | 322035 | AL137517 | Hs.306201 | EST cluster (not in UniGene) | 40.2 |
| | 322171 | AF085968 | Hs.48474 | EST cluster (not in UniGene) | 5.7 |
| | 322175 | AF085975 | | EST cluster (not in UniGene) | 7.7 |
| | 322236 | AL134970 | Hs.104222 | folistatin-like 1 | 14.4 |
| | 322303 | W07459 | Hs.157601 | EST cluster (not in UniGene) | 13.4 |
| | 322735 | AA086123 | Hs.297856 | EST cluster (not in UniGene) | 7.6 |
| 25 | 322777 | AA679082 | Hs.269947 | ESTs | 4.4 |
| | 322818 | AW043782 | Hs.293616 | ESTs | 21 |
| | 322882 | AW248508 | Hs.279727 | DiGeorge syndrome critical region gene 2 | 15.3 |
| | 322975 | C16391 | | EST cluster (not in UniGene) | 21.3 |
| 30 | 322991 | C18965 | Hs.159473 | ESTs | 11.7 |
| | 323011 | AA580288 | | EST cluster (not in UniGene) | 8.9 |
| | 323091 | AW014094 | Hs.210761 | ESTs | 10.8 |
| | 323107 | AI301107 | Hs.150790 | ESTs | 6.5 |
| | 323136 | AL120351 | Hs.30177 | EST cluster (not in UniGene) | 5.5 |
| 35 | 323168 | AL120862 | Hs.124165 | ESTs | 17.9 |
| | 323195 | AI064982 | Hs.117950 | multifunctional polypeptide similar to SA | 5.8 |
| | 323201 | AL049370 | Hs.13350 | Homo sapiens mRNA; cDNA DKFZp586 | 11.6 |
| | 323203 | AA203135 | Hs.130186 | ESTs | 6.4 |
| | 323243 | W44372 | Hs.110771 | EST cluster (not in UniGene) | 7.3 |
| 40 | 323244 | T70731 | Hs.193620 | EST cluster (not in UniGene) | 15.8 |
| | 323328 | AA228078 | Hs.255096 | EST cluster (not in UniGene) | 4.8 |
| | 323332 | AI829520 | Hs.227513 | ESTs | 20.2 |
| | 323333 | AA228883 | Hs.208558 | EST cluster (not in UniGene) | 8.8 |
| | 323570 | AL038623 | Hs.208752 | ESTs; Weakly similar to !!!! ALU SUBFA | 5 |
| | 323604 | AI751438 | Hs.41271 | ESTs; Weakly similar to !!!! ALU SUBFA | 6.5 |
| 45 | 323685 | AA344205 | Hs.289088 | EST cluster (not in UniGene) | 7.1 |
| | 323753 | AA327102 | Hs.70266 | EST cluster (not in UniGene) | 6.1 |
| | 323817 | AA410943 | | EST cluster (not in UniGene) | 16.8 |
| | 323845 | AI684674 | Hs.41127 | ESTs; Weakly similar to wacław [D.melan | 10.1 |
| 50 | 323930 | AA570698 | Hs.8173 | ESTs | 6.4 |
| | 323997 | AA844907 | Hs.274454 | EST cluster (not in UniGene) | 8 |
| | 324047 | AA378201 | Hs.271340 | EST cluster (not in UniGene) | 6.3 |
| | 324261 | AL044891 | Hs.269350 | EST cluster (not in UniGene) | 50.1 |
| | 324302 | AA543008 | Hs.292471 | ESTs; Weakly similar to !!!! ALU SUBFA | 5.7 |
| 55 | 324338 | AL138357 | Hs.145078 | ESTs | 9.5 |
| | 324344 | AW502000 | Hs.46677 | EST cluster (not in UniGene) | 4.4 |
| | 324432 | AA464510 | Hs.152812 | EST cluster (not in UniGene) | 16.7 |
| | 324495 | AW501411 | Hs.122489 | ESTs; Weakly similar to !!!! ALU CLASS | 5.5 |
| | 324497 | AW152624 | Hs.136340 | ESTs | 5.4 |
| | 324598 | AA502659 | Hs.163986 | ESTs | 8.8 |
| 60 | 324603 | AW016378 | Hs.292934 | ESTs | 23.1 |
| | 324620 | AA448021 | Hs.94109 | EST cluster (not in UniGene) | 21.2 |
| | 324727 | AI610425 | Hs.19597 | ESTs | 5 |
| | 324774 | AI031771 | Hs.132586 | ESTs | 5 |
| | 324783 | AA640770 | Hs.200994 | EST cluster (not in UniGene) | 4.1 |
| 65 | 324824 | AI826999 | Hs.224624 | ESTs | 6.3 |
| | 324826 | AA704806 | Hs.143842 | ESTs | 11.7 |
| | 324902 | D31323 | Hs.271492 | ESTs | 4.8 |

| | | | | | |
|----|--------|------------|---|---|------|
| | 324961 | AA613792 | EST cluster (not in UniGene) | 13.3 | |
| | 324987 | T06882 | Hs.172634 | ESTs | 19.6 |
| | 324988 | T06997 | Hs.121028 | EST cluster (not in UniGene) | 24.5 |
| | 325146 | AI064690 | Hs.171176 | ESTs | 4.6 |
| 5 | 325622 | | CH.14_hs gj 5867000 | | 5.2 |
| | 326213 | | CH.17_hs gj 5867224 | | 8.1 |
| | 326474 | | CH.19_hs gj 5867405 | | 12.7 |
| | 326816 | | CH.20_hs gj 6552458 | | 9.4 |
| | 326817 | | CH.20_hs gj 6552458 | | 11.7 |
| 10 | 327110 | | CH.21_hs gj 6117842 | | 14.7 |
| | 327196 | | CH.01_hs gj 5867446 | | 5.1 |
| | 327283 | | CH.01_hs gj 5867478 | | 4.3 |
| | 327313 | | CH.01_hs gj 5867501 | | 4.8 |
| | 327450 | | CH.02_hs gj 5867766 | | 4.1 |
| 15 | 328059 | | CH.06_hs gj 6117819 | | 6.2 |
| | 328304 | | CH.07_hs gj 6004478 | | 5.4 |
| | 328492 | | CH.07_hs gj 5868455 | | 7 |
| | 328857 | | CH.07_hs gj 6381927 | | 5.2 |
| | 329367 | | CH.X_hs gj 5868842 | | 7.6 |
| 20 | 329373 | | CH.X_hs gj 6682537 | | 12 |
| | 329655 | | CH.14_p2 gj 6448516 | | 4 |
| | 329899 | | CH.15_p2 gj 6563505 | | 4 |
| | 329960 | | CH.16_p2 gj 5091594 | | 7.6 |
| | 330084 | | CH.19_p2 gj 6015302 | | 4 |
| 25 | 330384 | M23263 | androgen receptor (dihydrotestosterone re | | 5.8 |
| | 330385 | AA449749 | ESTs; Highly similar to secreted apoptosi | | 10.2 |
| | 330387 | H14624 | ESTs; Highly similar to secreted apoptosi | | 4.4 |
| | 330388 | X03363 | HER2 receptor tyrosine kinase (c-erbB-2; | | 17.7 |
| | 330409 | D50692 | Hs.78221 | c-myc binding protein | 10.1 |
| 30 | 330460 | TIGR:HT544 | Hs.73946 | Endothelial Cell Growth Factor 1 | 5.5 |
| | 330486 | M13755 | Hs.833 | interferon-stimulated protein; 15 kDa | 67 |
| | 330494 | M29696 | Hs.237868 | Interleukin 7 receptor | 6 |
| | 330500 | M34423 | Hs.79222 | galactosidase; beta 1 | 13.1 |
| | 330510 | M75099 | Hs.227729 | FK506-binding protein 2 (13kD) | 29 |
| 35 | 330513 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 38.5 |
| | 330541 | U22970 | Hs.265827 | multiple UniGene matches | 7.4 |
| | 330542 | U23942 | Hs.226213 | cytochrome P450; 51 (lanosterol 14-alpha | 15 |
| | 330547 | U32989 | Hs.183671 | tryptophan 2;3-dioxygenase | 11 |
| | 330551 | U39840 | Hs.299867 | hepatocyte nuclear factor 3; alpha | 6.5 |
| 40 | 330562 | U49082 | Hs.76460 | transporter protein | 7.7 |
| | 330573 | U62800 | Hs.83393 | cystatin E/M | 4 |
| | 330673 | D57823 | Hs.321403 | Sec23 (S. cerevisiae) homolog A | 10.5 |
| | 330711 | AA164687 | Hs.177576 | mannosyl (alpha-1,3-)-glycoprotein beta-1 | 24.3 |
| | 330814 | AA015730 | Hs.265398 | ESTs; Weakly similar to transformation-r | 44.1 |
| 45 | 330850 | AA075298 | Hs.322710 | ESTs | 4.4 |
| | 330874 | AA127474 | Hs.191157 | ESTs; Weakly similar to !!!! ALU SUBFA | 8.1 |
| | 330884 | AA133457 | Hs.102548 | ESTs | 5.2 |
| | 330912 | AA195936 | Hs.82719 | general transcription factor IIA; 1 (37kD a | 5 |
| | 330924 | AA232136 | Hs.159737 | Homo sapiens mRNA; cDNA DKFZp434 | 9.1 |
| 50 | 330997 | H55762 | Hs.9302 | ESTs | 7.6 |
| | 331014 | H98597 | Hs.30340 | ESTs | 13.5 |
| | 331024 | N32919 | Hs.27931 | ESTs | 9.1 |
| | 331046 | N66563 | Hs.191358 | ESTs | 10.5 |
| | 331135 | R61398 | Hs.4197 | ESTs | 7.4 |
| 55 | 331145 | R72427 | Hs.129873 | ESTs; Weakly similar to CYTOCHROME | 41.9 |
| | 331148 | R73816 | Hs.17385 | ESTs | 4.7 |
| | 331222 | T98531 | Hs.173904 | ESTs | 4.1 |
| | 331230 | W69807 | Hs.16537 | hypothetical protein; similar to (U06944) | 4.9 |
| | 331306 | AA252079 | Hs.63931 | dachshund (Drosophila) homolog | 15.1 |
| 60 | 331327 | AA281076 | Hs.109221 | ESTs | 4.8 |
| | 331337 | AA287662 | Hs.50495 | ESTs | 7.6 |
| | 331341 | AA303125 | Hs.23240 | ESTs; Weakly similar to !!!! ALU SUBFA | 13 |
| | 331344 | AA357927 | Hs.126550 | ESTs | 12.4 |
| | 331362 | AA417956 | Hs.40782 | ESTs | 6.5 |
| 65 | 331363 | AA421562 | Hs.91011 | anterior gradient 2 (Xenopus laevis) homo | 28.2 |
| | 331376 | AA443802 | Hs.41007 | ESTs; Weakly similar to cDNA EST yk47 | 15.1 |
| | 331384 | AA456001 | Hs.93847 | ESTs | 7.9 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 331478 | N26608 | Hs.40639 | ESTs | 7 |
| | 331526 | N49967 | Hs.46624 | ESTs | 19.8 |
| | 331533 | N51517 | Hs.47282 | ESTs | 6.5 |
| 5 | 331681 | W85712 | Hs.119571 | collagen; type III; alpha 1 (Ehlers-Danlos | 13.8 |
| | 331686 | W88502 | Hs.182258 | ESTs | 9.9 |
| | 331750 | AA284372 | Hs.111471 | ESTs | 5.6 |
| | 331751 | AA284840 | Hs.143818 | ESTs | 5.8 |
| | 331760 | AA292721 | Hs.154434 | ESTs; Weakly similar to unknown [H.sap | 7.4 |
| 10 | 331763 | AA312861 | Hs.96704 | ESTs | 7.8 |
| | 331825 | AA411144 | Hs.292882 | ESTs | 15.2 |
| | 331890 | AA432166 | Hs.3577 | succinate dehydrogenase complex; subunit | 24.3 |
| | 331952 | AA454756 | Hs.97837 | ESTs | 5 |
| | 332015 | AA487910 | Hs.208800 | ESTs; Weakly similar to !!!! ALU CLASS | 10.5 |
| | 332043 | AA490831 | Hs.125056 | ESTs | 11.4 |
| 15 | 332060 | AA504779 | Hs.191402 | ESTs | 13.6 |
| | 332071 | AA598594 | Hs.205293 | ESTs | 9.1 |
| | 332093 | AA608794 | Hs.112592 | ESTs | 8.8 |
| | 332139 | AA620669 | Hs.112879 | EST | 9 |
| 20 | 332219 | N22508 | Hs.139315 | ESTs | 7.1 |
| | 332225 | N33213 | Hs.100425 | ESTs | 12.2 |
| | 332246 | N57927 | Hs.120777 | ESTs; Weakly similar to RNA POLYME | 15.6 |
| | 332247 | N58172 | Hs.109370 | ESTs | 16.9 |
| | 332260 | N70088 | Hs.138467 | ESTs | 4 |
| | 332269 | N91279 | Hs.109654 | ESTs; Moderately similar to outer membr | 8.2 |
| 25 | 332336 | T96130 | Hs.137551 | ESTs | 7.7 |
| | 332340 | W15495 | Hs.129781 | chromosome 21 open reading frame 5 | 14.1 |
| | 332347 | W60326 | Hs.288684 | ESTs | 4.4 |
| | 332362 | W93640 | Hs.4779 | ESTs; Moderately similar to similar to AD | 16.9 |
| | 332467 | AA489630 | Hs.119004 | KIAA0665 gene product | 4.8 |
| 30 | 332499 | M12036 | Hs.323910 | Human tyrosine kinase-type receptor (HE | 10.4 |
| | 332513 | AA018182 | Hs.154424 | deiodinase; lodothyronine; type II | 5.8 |
| | 332526 | AA281753 | Hs.77515 | inositol 1;4;5-triphosphate receptor; type | 19 |
| | 332532 | N63192 | Hs.1892 | EST; Highly similar to PHENYLETHAN | 15.3 |
| | 332565 | AA234896 | Hs.25272 | E1A binding protein p300 | 12.3 |
| 35 | 332607 | R41791 | Hs.36566 | LIM domain kinase 1 | 11.1 |
| | 332640 | AA417152 | Hs.5101 | protein regulator of cytokinesis 1 | 18.2 |
| | 332694 | AA262768 | Hs.243901 | KIAA1067 protein | 15.2 |
| | 332702 | H93968 | Hs.75725 | transgelin 2 | 4.7 |
| | 332705 | T59161 | Hs.76293 | thymosin; beta 10 | 5.5 |
| 40 | 332749 | AA479968 | Hs.88251 | arylsulfatase A | 9.8 |
| | 332927 | | | CH22_FGENES.38_1 | 17.7 |
| | 332929 | | | CH22_FGENES.38_3 | 4.7 |
| | 332930 | | | CH22_FGENES.38_4 | 7.4 |
| | 332955 | | | CH22_FGENES.48_12 | 5.4 |
| 45 | 332958 | | | CH22_FGENES.48_15 | 17.8 |
| | 332961 | | | CH22_FGENES.48_18 | 10.6 |
| | 332983 | | | CH22_FGENES.54_5 | 4.3 |
| | 333009 | | | CH22_FGENES.61_1 | 5.2 |
| | 333010 | | | CH22_FGENES.61_2 | 8.1 |
| 50 | 333013 | | | CH22_FGENES.61_5 | 8.5 |
| | 333108 | | | CH22_FGENES.79_14 | 5.6 |
| | 333139 | | | CH22_FGENES.83_16 | 6.3 |
| | 333254 | | | CH22_FGENES.118_2 | 6.8 |
| | 333305 | | | CH22_FGENES.137_2 | 11.4 |
| 55 | 333343 | | | CH22_FGENES.139_12 | 5.1 |
| | 333388 | | | CH22_FGENES.144_3 | 12.7 |
| | 333456 | | | CH22_FGENES.157_5 | 4.2 |
| | 333459 | | | CH22_FGENES.157_8 | 7.6 |
| | 333517 | | | CH22_FGENES.173_2 | 8.2 |
| 60 | 333585 | | | CH22_FGENES.203_4 | 5 |
| | 333679 | | | CH22_FGENES.247_6 | 4.3 |
| | 333743 | | | CH22_FGENES.264_1 | 13.4 |
| | 333758 | | | CH22_FGENES.268_1 | 4 |
| | 333767 | | | CH22_FGENES.271_6 | 5.6 |
| 65 | 333768 | | | CH22_FGENES.271_7 | 12.2 |
| | 333769 | | | CH22_FGENES.271_8 | 48.3 |
| | 333795 | | | CH22_FGENES.275_1 | 6.1 |

| | | | |
|----|--------|--------------------------------|------|
| | 333796 | CH22_FGENES.275_3 | 6.8 |
| | 333892 | CH22_FGENES.292_14 | 4.4 |
| | 333904 | CH22_FGENES.294_2 | 6.5 |
| 5 | 333905 | CH22_FGENES.294_3 | 9.3 |
| | 333921 | CH22_FGENES.296_12 | 9.6 |
| | 333968 | CH22_FGENES.307_4 | 15.9 |
| | 334102 | CH22_FGENES.327_60 | 7.1 |
| | 334222 | CH22_FGENES.360_3 | 6.7 |
| 10 | 334223 | CH22_FGENES.360_4 | 33.5 |
| | 334264 | CH22_FGENES.367_15 | 18.5 |
| | 334343 | CH22_FGENES.375_25 | 6.1 |
| | 334360 | CH22_FGENES.378_5 | 6.1 |
| | 334784 | CH22_FGENES.432_9 | 4.8 |
| 15 | 334789 | CH22_FGENES.432_14 | 5.1 |
| | 334794 | CH22_FGENES.434_2 | 7 |
| | 334889 | CH22_FGENES.452_3 | 12.4 |
| | 335004 | CH22_FGENES.472_8 | 7.9 |
| | 335115 | CH22_FGENES.496_2 | 18.8 |
| 20 | 335287 | CH22_FGENES.526_11 | 4.5 |
| | 335342 | CH22_FGENES.536_1 | 5.3 |
| | 335491 | CH22_FGENES.570_23 | 24 |
| | 335495 | CH22_FGENES.570_28 | 7 |
| | 335498 | CH22_FGENES.571_7 | 12.2 |
| 25 | 335544 | CH22_FGENES.576_5 | 8.4 |
| | 335610 | CH22_FGENES.583_4 | 12.9 |
| | 335653 | CH22_FGENES.590_4 | 6.7 |
| | 335682 | CH22_FGENES.595_2 | 12.1 |
| | 335687 | CH22_FGENES.596_2 | 13.9 |
| 30 | 335755 | CH22_FGENES.604_4 | 11.5 |
| | 335782 | CH22_FGENES.609_4 | 17.9 |
| | 335791 | CH22_FGENES.611_7 | 27.3 |
| | 335809 | CH22_FGENES.617_6 | 19.2 |
| | 335822 | CH22_FGENES.619_7 | 19.1 |
| 35 | 335823 | CH22_FGENES.619_8 | 4.5 |
| | 335824 | CH22_FGENES.619_11 | 40.2 |
| | 335825 | CH22_FGENES.619_12 | 34.3 |
| | 335895 | CH22_FGENES.635_3 | 10.2 |
| | 335917 | CH22_FGENES.636_13 | 6 |
| 40 | 335920 | CH22_FGENES.636_16 | 8.8 |
| | 336035 | CH22_FGENES.678_6 | 5.9 |
| | 336042 | CH22_FGENES.679_4 | 5.8 |
| | 336093 | CH22_FGENES.691_2 | 11.6 |
| | 336096 | CH22_FGENES.691_5 | 7.6 |
| 45 | 336150 | CH22_FGENES.706_6 | 6.3 |
| | 336152 | CH22_FGENES.706_9 | 10.5 |
| | 336416 | CH22_FGENES.823_38 | 5 |
| | 336444 | CH22_FGENES.827_10 | 4.8 |
| | 336449 | CH22_FGENES.829_6 | 13.6 |
| 50 | 336471 | CH22_FGENES.829_30 | 6.9 |
| | 336512 | CH22_FGENES.834_7 | 21.4 |
| | 336558 | CH22_FGENES.842_3 | 8.2 |
| | 336560 | CH22_FGENES.842_5 | 9 |
| | 336676 | CH22_FGENES.43-4 | 9.4 |
| 55 | 336959 | CH22_FGENES.367-13 | 19 |
| | 337968 | CH22_EM:AC005500.GENSCAN.103-2 | 13.4 |
| | 338008 | CH22_EM:AC005500.GENSCAN.127-9 | 15.2 |
| | 338057 | CH22_EM:AC005500.GENSCAN.160-1 | 13.9 |
| | 338410 | CH22_EM:AC005500.GENSCAN.341-6 | 8 |
| 60 | 338451 | CH22_EM:AC005500.GENSCAN.359-3 | 11.6 |
| | 338588 | CH22_EM:AC005500.GENSCAN.432-1 | 10.3 |
| | 338665 | CH22_EM:AC005500.GENSCAN.464-2 | 4.8 |
| | 338689 | CH22_EM:AC005500.GENSCAN.475-3 | 6.7 |
| | 338832 | CH22_DJ246D7.GENSCAN.6-9 | 4.8 |
| 65 | 338980 | CH22_DA59H18.GENSCAN.2-4 | 5.1 |
| | 339352 | CH22_BA354112.GENSCAN.29-7 | 6.9 |
| | 339373 | CH22_BA232E17.GENSCAN.1-29 | 4.3 |

TABLE 13A

Table 13 A shows the accession numbers for those pkeys lacking unigeneID's for Table 13. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT number Accession

| | | |
|--------|------------------|---|
| 123619 | 371681_1 | AA602964 AA609200 |
| 103207 | 30635_4 | X72790 |
| 103349 | 11052_2 | X89059 |
| 110856 | 19346_14 | AA992380 N33063 N21418 H79958 R21911 H79957 |
| 113248 | 328626_1 | T63857 AW971220 AA493469 T63699 |
| 123169 | 44573_2 | AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 |
| | | AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 |
| | | AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 |
| | | AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 |
| | | AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 |
| | | BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 |
| | | AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 |
| | | AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 |
| | | F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 |
| 123533 | genbank_AA608751 | AA608751 |
| 116480 | genbank_C14088 | C14088 |
| 132225 | genbank_AA128980 | AA128980 |
| 125154 | genbank_W38419 | W38419 |
| 118475 | genbank_N66845 | N66845 |
| 102919 | 25180_2 | M21191 AL035748 AA021266 AA323126 AA180515 AI613029 D28356 NM_000034 M11560 AW401425 AW248248 AA012956 |
| | | AA323294 W04965 H38759 AA206622 AA580747 AI541172 AA381075 AA354229 AW402353 AW405575 AW404021 AW406207 |
| | | AA075752 AW176066 AA287222 AA195818 T20243 R87945 AA295539 AA402533 AA232419 AA224515 AW401583 AA331367 |
| | | AW402140 AW249079 R31488 AA075757 X05236 AW239490 AA338036 AW239495 AA357262 AA431005 AA306726 R33804 |
| | | AA216544 AW275288 AA227044 AL038124 AA243300 C03242 AA315615 AL035840 R64336 AA313917 AA018963 AA001385 |
| | | AA054395 H30840 AW498825 AA086141 AI557324 AA121576 H39128 R77161 AA019688 AA380987 AA348140 AA348257 |
| | | AW176086 AA362432 AA171389 AA362416 AA299938 AA319093 AA337972 C04921 AA345696 R89640 AA085425 AA481708 |
| | | AA313637 AL039229 H84490 H86153 F00656 AA326668 AA347304 R65890 H41949 AA339309 AW402002 AW404854 |
| | | AA192582 AA112802 H09248 N83165 H38367 AA356339 AA455763 R66853 AA294935 H85911 AA310414 H93436 N87014 |
| | | AA001186 H83640 AA411328 AA317929 C04192 AW406288 U46335 AA323179 AA427649 AI366131 H14328 AA197161 |
| | | AA379497 AA311816 AA017206 AA001137 AA017420 AA012990 AW163775 AA021397 AA295513 AA355248 AA374921 |
| | | AW380419 AA345864 AA318058 AA371711 AA363255 AA057094 R88057 AA394045 AW362741 AA479579 AW362789 |
| | | AW362775 AA223624 AW362809 AW362746 AW362753 AW380412 AA057104 AA295271 X06352 AW362771 X12447 R59553 |
| | | R87925 AA292864 R83920 F01120 AA496740 AA852551 AL039209 AA093339 AA333961 N86416 C03325 C03831 AA194750 |
| | | AA359270 AA359460 AW245492 AA339400 AA330784 AI908970 N89223 AW361938 AI940063 AA134323 AA371741 F01267 |
| | | AW372970 AA341973 AA346098 AW372969 AA337549 AA327342 H93855 AI074079 F29118 AA852940 F36696 AA345963 |
| | | AA079578 AA113785 C02989 AA095945 C03145 C05199 AA346024 AA190506 AW361659 AI909845 AW374374 AW374382 |
| | | AW374401 AW374373 AW374370 AI909831 AW374367 AA353658 F01041 C02843 AA375948 AW374414 AA213946 AI525039 |
| | | H13744 R31007 AA112044 AA134404 H47935 AW177018 AA429768 AA336873 AA112875 H46393 AA191267 D59131 |
| | | AW406037 AA055244 AA341880 AA179024 AA308537 AW406985 AW327311 H30301 AA300705 H43788 AW364149 |
| | | AA806213 AA481936 C04941 AW375299 M21190 AA4410818 AA250940 AI354547 AA317422 AA250903 AI865497 AA890603 |
| | | AA366197 AW498538 M78072 AW406461 C03092 F00308 H56488 AA336320 AW406501 AA354102 AA382942 AA096393 |
| | | AW376830 AA383446 F01259 AW081388 T94036 AA379643 H43842 AI524063 AA621727 AA379099 AA371417 R66811 |
| | | H44129 N84794 F01135 AA477852 AA293062 AW361595 H27194 AI831650 H43253 H24797 AI564680 AA380090 W20057 |
| | | AI921586 AI192549 AW090808 H25967 AA918121 AI626060 H20221 AA812572 H42178 AA887222 H66000 C03180 F00946 |

5 C03986 AI318091 AI860172 AA582179 AI633388 AA557193 R68075 F24105 AW518239 W56622 AI625219 AI925243
AW468046 AI921828 AA339164 AI144391 AA643334 AA459631 AA873247 AW373432 AA604384 H27600 AI680458 AA159956
AA610836 AA364298 AW373435 AA604225 W73754 AW087924 AA599776 N89227 AI630871 AI633128 AW514329 AA010455
AA563928 AI571596 AI128394 W73707 AI423575 AA583809 AA657988 AI950837 AA169782 AA600009 AI885540 AA771884
AI978829 AA505408 AA533937 AA481469 AA610869 AA775241 AW273870 AW070909 AI905695 AA480115 AA574051
AI889185 AA773167 AA331375 AA001437 AA194324 AA194300 AA558632 AI038538 AA411329 AA781570 AI833176
AA935520 AW074197 AA583063 AW073099 AW001198 AA948025 AA587857 AA191540 AI460085 AA193244 AI538037
AA515572 AA758587 AI149311 AA508610 AA206409 AA534004 AA994600 AA827543 AI916349 AW245129 AW517804 D25663
10 AA781985 AA284536 AI819422 H16040 H27531 AA456564 AA845555 AI423596 AA012908 AA889439 AA716311 AA968868
AA320508 AA725731 AA834202 AA935997 AA724815 AA769353 AA594803 F00827 AI342442 AI003519 AI002503 AI347597
AI040946 AA197162 AA987883 AA292865 AW001944 AI640711 AW244044 AA456784 F30588 AA290829 H24754 AI978683
AA483686 AA583939 AA121382 AA833831 AA477102 AA977322 AA666379 F35456 AA993537 AI749610 AA226934 AA716204
AW513025 AA628543 AA583705 F25702 AI368748 AI124097 AI880086 AA477513 AI758834 AI690753 AA477746 F37761
15 AA642243 AA159957 AA250844 AA459406 AA427566 F25054 AI569314 AA961665 AI922050 AI759000 AA555236 AA514432
AA293474 AA001129 AA826789 AA641390 AA134405 F35585 AA477416 AW193359 AI361315 AA284988 F36340 AI361322
F26969 AA991922 AA021267 F26973 AI361314 F35891 AI918509 AA250964 AA190992 AA577139 AA865535 AA134324
AW192842 AI224046 F18975 AA779626 AA856894 AW269997 AW014614 H95554 F31378 AA374868 F26343 AA654007
AI830942 AA113195 F26432 W56652 AA464690 AA055263 AA340654 AA031448 AA976399 AA972526 AA063476 R83921
20 T16240 AA533290 N91545 H44053 AA883451 AA513761 AA086477 H09249 F20482 F26737 AA054148 AA857063 AA017259
AA179789 AA088908 H43704 AA194320 F35950 AI880127 F20441 F32878 AA962483 H39094 H56489 H46621 F19390
AI302232 F25162 AA826965 AA086052 AA917410 AA454513 R59554 AA196755 AA086369 AA079530 H28106 AA243301
AI025737 AA101239 AA088887 AI214910 AA974886 F16089 F26054 AA515092 F33436 F32829 M78061 AA235645 F19715
F37529 AI811549 AA665180 AA708200 F01124 F32382 AA346220 AA627361 F30741 F30010 F28543 AA211715 F20245
25 AA331222 F25634 F21996 W28215 F21911 R65793 AI192566 H20130 H84491 AA719223 AA557435 F16967 F26989 F30353
AA857159 AA291918 F28234 F20840 F25176 F22437 T27904 AA480355 F19528 R87926 H14286 F27532 AW337864 F28411
H13692 F25651 AA975454 F24229 F29657 F18024 AA464779 F17588 F34954 AA947328 F18063 AA657777 AA459644 N91455
F27850 F29608 F27206 F18418 F31459 F18564 F33496 F16376 F29740 F29843 F29904 F29866 F19135 AW276602 T40337
F24835 F34672 F26474 AI926215 AA464185 F18217 N26193 AL043256 T41197 F33055 F00386 F29500 F34191 F33297
30 AI937207 F22724 F15909 F26232 F18889 AA318627 F29085 AA872104 F17509 F23373 F15660 F17552 F17412 F16863
F34033 F21515 F17364 F18383 F16546 F17561 F17260 AA292000 F15723 T47438 F16798 F18046 F18319 F17978 F17566
F34230 F33258 F20860 F17998 AI695701
118600 genbank_N69222 N69222
118952 genbank_N92966 N92966
120873 genbank_AA358015 AA358015
35 113702 genbank_T97307 T97307
129982 221_267
Z14221 AW381862 M97920 AW401444 Z66542 M29470 AW406502 X61011 M34024 AA327072 Z14166 Z14167 Z14165
AW403806 Z14200 AA383972 Z14205 Z14201 M18513 Z14202 AW403684 X14584 AF062221 U43760 X65892 X65883 X62107
Z80847 X65885 X65893 AF062142 X65891 X17675 Z47274 Z47277 Z47276 X65888 Z47275 X62109 AF062140 L01278
AF062134 AF062139 X81723 Z80840 X81733 X81743 X81744 X81732 Z80843 AW402942 AW403516 X65919 AF062190
40 AF062177 AF062222 AF062115 Z47240 AF062263 AF062261 AF062223 AF062211 Z47238 AW401714 AW404008 AW404991
AF062280 M99595 Z47214 Z47232 Z47218 M26995 AF062184 X65895 L38433 X81731 Z11946 Z47226 AF062205 AF174012
L01276 AF062168 AF062136 X81755 X81748 AF174019 AF062285 L06924 L11699 AW402665 L09070 L28049 L08090
AW407843 Z14171 AW402944 L08083 AW405627 L33035 L26907 M17750 L28052 M17751 AJ239360 U19885 L14821 X56526
45 AB014341 L12087 L12098 U68231 L12184 AF062242 AF022000 U64499 U00570 AI268604 Y15773 X64239 X62969 U00506
X73605 X99360 U00577 D83677 AB021539 AF035796 Z33899 U00588 AJ239353 AF174062 Z33901 X98899 AF174058 X63080
D83676 AB021529 Z18318 U00488 L01412 X81746 U21262 U21272 U00560 AF174060 U00547 U00561 Z18321 S73957
M26435 AF115130 AF115117 Z92896 U21254 Z92895 AF115112 AF062290 T28938 Y09386 AF174067 U27189 Y09384
U77373 AF174057 M17749 X69692 AF174038 U64478 U64486 AF174098 X99365 AF174077 AF174083 AF174089 AF015133
50 AF127792 AJ006171 U00510 U58144 AF004323 AF115109 AF004324 AF015130 AF090414 AF090418 AB021536 AB021519
Z96957 AF021986 Z92898 Z96956 L34164 AF062251 AF052524 U00549 U00541 D83687 AF052522 AF087420 AF052520
AF022011 L43085 U00536 L19915 L43083 AF090420 AB021530 AB021534 Z96955 Z96954 Z33903 X62964 AF103282 U00509
AF062298 AF062289 AF062307 AW408326 L33037 L04337 L04328 X81742 L04336 L03385 AF032360 S56184 AF062191
AF191092 AI906954 AF103184 L04343 AW364860 AF001424 AF103163 Z98717 AF103143 AJ008250 L04323 AF103321
55 AF103335 L04342 L03818 L03817 AW404978 AW403690 U86801 AF103150 AJ010334 AF035027 AJ007327 AF103115
AF017458 AJ008207 AJ008183 AJ008196 AJ008241 AJ008208 AF103210 AF068668 AF068670 AF068671 AF068664
AF068669 AF068666 AF068665 AF068672 AW371244 AW403670 AW408074 AW404575 AW362153 AW403803 AW406702
AW351514 D78345 T29140 J00231 NM_002179 AW405146 AA301091 X04646 H64660 AW402990 AW406534 T93007
AI857980 AW368899 AI905833 AW406586 AA482084 AI872299 AA715266 AW404328 AI831674 AI709348 AA603112
AW514864 AA485775 H64492 AW404789 AA487630 AA715498 AA295885 T27613 T98113
60 115763 genbank_AA421560 AA421560
124357 genbank_N22401 N22401
108733 504187_1 AA121022 AA126422
101544 entrez_M31169 M31169
124447 genbank_N48000 N48000
65 124677 genbank_R01073 R01073
124777 genbank_R41933 R41933
119302 genbank_T25725 T25725

103680 entrez_Z93784Z93784
 135029 H58818_at H58818
 112253 genbank_R51818 R51818
 Pkey CAT number Accession
 5 322175 46877_1 AF085975 H53458 H53459
 323011 139750_1 AA580288 AA315655 AA133031 AA377748
 322975 1510563_1 C16391 C16413
 317210 211994_1 AW881145 AA490718 M85637 AA304575 T06067 AA331991
 10 323817 233566_1 AA410943 AW948953 AA334202 AA332882
 309583 1046029_-2 AW170035
 324961 376239_1 AA613792 AW182329 T05304 AW858385
 303502 325188_1 BE174240 AA488528 AL042253
 320133 447553_1 BE151746 BE336853 D63271 T94955 AA774994
 15 311935 174129_1 AA216387 T63548 AA228676
 321050 502195_1 C05928 AW393497
 319977 345248_1 AA534222 AA632632 T81234
 312772 4380_7 AW962299 AA310349 AW962294 H63791 H63751
 321354 116028_-2 AA078493
 20 336512 CH22_3941FG_834_7_LINK_DJ
 336558 CH22_3992FG_842_3_LINK_DJ
 336560 CH22_3994FG_842_5_LINK_DJ
 329367 c_x_hs
 329373 c_x_hs
 25 336676 CH22_4154FG_43_4_
 338008 CH22_6490FG_LINK_EM:AC00
 338057 CH22_6558FG_LINK_EM:AC00
 329655 c14_p2
 336959 CH22_4764FG_367_13_
 329899 c15_p2
 30 329960 c16_p2
 338410 CH22_7067FG_LINK_EM:AC00
 338451 CH22_7124FG_LINK_EM:AC00
 338588 CH22_7331FG_LINK_EM:AC00
 338665 CH22_7438FG_LINK_EM:AC00
 35 338689 CH22_7464FG_LINK_EM:AC00
 308677 AI761173
 338832 CH22_7678FG_LINK_DJ246D7
 338980 CH22_7859FG_LINK_DA59H18
 333009 CH22_233FG_61_1_LINK_EM:A
 40 333010 CH22_234FG_61_2_LINK_EM:A
 333013 CH22_237FG_61_5_LINK_EM:A
 308981 AI873242
 308995 AI880172
 333108 CH22_336FG_79_14_LINK_EM:
 45 333139 CH22_368FG_83_16_LINK_EM:
 333254 CH22_495FG_118_2_LINK_EM:
 333305 CH22_550FG_137_2_LINK_EM:
 333343 CH22_589FG_139_12_LINK_EM:
 333388 CH22_634FG_144_3_LINK_EM:
 50 326213 c17_hs
 333456 CH22_706FG_157_5_LINK_EM:
 333459 CH22_709FG_157_8_LINK_EM:
 333517 CH22_773FG_173_2_LINK_EM:
 333585 CH22_846FG_203_4_LINK_EM:
 55 333679 CH22_941FG_247_6_LINK_EM:
 326474 c19_hs
 333743 CH22_1009FG_264_1_LINK_EM:
 333758 CH22_1024FG_268_1_LINK_EM:
 333767 CH22_1034FG_271_6_LINK_EM:
 60 333768 CH22_1035FG_271_7_LINK_EM:
 333769 CH22_1036FG_271_8_LINK_EM:
 333795 CH22_1063FG_275_1_LINK_EM:
 333796 CH22_1065FG_275_3_LINK_EM:
 335004 CH22_2326FG_472_8_LINK_EM:
 65 333892 CH22_1163FG_292_14_LINK_E
 335115 CH22_2447FG_496_2_LINK_EM:
 333904 CH22_1176FG_294_2_LINK_EM:

333905 CH22_1177FG_294_3_LINK_EM
 333921 CH22_1194FG_296_12_LINK_E
 333968 CH22_1245FG_307_4_LINK_EM
 328059 c_6_hs
 5 335287 CH22_2629FG_526_11_LINK_E
 326816 c20_hs
 326817 c20_hs
 335342 CH22_2689FG_536_1_LINK_EM
 335491 CH22_2843FG_570_23_LINK_E
 10 335495 CH22_2847FG_570_28_LINK_E
 335498 CH22_2850FG_571_7_LINK_EM
 328304 c_7_hs
 305453 AA738110
 335544 CH22_2899FG_576_5_LINK_EM
 15 335610 CH22_2969FG_583_4_LINK_EM
 335653 CH22_3013FG_590_4_LINK_EM
 335682 CH22_3043FG_595_2_LINK_EM
 335687 CH22_3048FG_596_2_LINK_EM
 328492 c_7_hs
 20 335755 CH22_3122FG_604_4_LINK_EM
 335782 CH22_3151FG_609_4_LINK_EM
 335791 CH22_3160FG_611_7_LINK_EM
 335809 CH22_3181FG_617_6_LINK_EM
 335822 CH22_3195FG_619_7_LINK_EM
 25 335823 CH22_3196FG_619_8_LINK_EM
 335824 CH22_3197FG_619_11_LINK_E
 335825 CH22_3198FG_619_12_LINK_E
 335895 CH22_3272FG_635_3_LINK_EM
 335917 CH22_3294FG_636_13_LINK_E
 30 335920 CH22_3297FG_636_16_LINK_E
 305898 AA872838
 305913 AA876109
 305950 AA884479
 328857 c_7_hs
 35 330084 c19_p2
 337968 CH22_6419FG_LINK_EM:AC00
 309177 AI951118
 309198 AI955915
 309226 AI969897
 40 339352 CH22_8317FG_LINK_BA35411
 309279 AI990102
 339373 CH22_8348FG_LINK_BA232E1
 325622 c14_hs
 45 334102 CH22_1380FG_327_60_LINK_E
 332927 CH22_148FG_38_1_LINK_C20H
 332929 CH22_150FG_38_3_LINK_C20H
 332930 CH22_151FG_38_4_LINK_C20H
 332955 CH22_179FG_48_12_LINK_EM:
 332958 CH22_182FG_48_15_LINK_EM:
 50 332961 CH22_185FG_48_18_LINK_EM:
 332983 CH22_207FG_54_5_LINK_EM:A
 334222 CH22_1506FG_360_3_LINK_EM
 334223 CH22_1507FG_360_4_LINK_EM
 334264 CH22_1551FG_367_15_LINK_E
 55 327110 c21_hs
 334343 CH22_1636FG_375_25_LINK_E
 334360 CH22_1654FG_378_5_LINK_EM
 327196 c_1_hs
 327283 c_1_hs
 60 327313 c_1_hs
 304465 AA421948
 304507 AA456426
 327450 c_2_hs
 304591 AA505702
 65 304601 AA507875
 304659 AA533185
 334784 CH22_2096FG_432_9_LINK_EM

334789 CH22_2101FG_432_14_LINK_E
334794 CH22_2106FG_434_2_LINK_EM
336035 CH22_3420FG_678_6_LINK_DJ
5 336042 CH22_3427FG_679_4_LINK_DJ
336093 CH22_3481FG_691_2_LINK_DJ
336096 CH22_3484FG_691_5_LINK_DJ
334889 CH22_2206FG_452_3_LINK_EM
336150 CH22_3540FG_706_6_LINK_DA
336152 CH22_3543FG_706_9_LINK_DA
10 336416 CH22_3833FG_823_38_LINK_B
336444 CH22_3864FG_827_10_LINK_D
336449 CH22_3870FG_829_6_LINK_DJ
336471 CH22_3894FG_829_30_LINK_D

TABLE 13B

Table 13B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 13B. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|-------------------|--------|-------------------|
| 332955 | Dunham, I. et.al. | Plus | 2508896-2508992 |
| 332958 | Dunham, I. et.al. | Plus | 2516164-2516310 |
| 332961 | Dunham, I. et.al. | Plus | 2521424-2521555 |
| 333139 | Dunham, I. et.al. | Plus | 3369495-3369571 |
| 333254 | Dunham, I. et.al. | Plus | 2521424-2521555 |
| 333305 | Dunham, I. et.al. | Plus | 4630388-4630645 |
| 333388 | Dunham, I. et.al. | Plus | 4913749-4913805 |
| 333517 | Dunham, I. et.al. | Plus | 5570729-5570925 |
| 333585 | Dunham, I. et.al. | Plus | 6234778-6234894 |
| 333679 | Dunham, I. et.al. | Plus | 7068795-7068896 |
| 333767 | Dunham, I. et.al. | Plus | 7694407-7694623 |
| 333768 | Dunham, I. et.al. | Plus | 7695440-7695697 |
| 333769 | Dunham, I. et.al. | Plus | 7696625-7696707 |
| 333795 | Dunham, I. et.al. | Plus | 7807688-7807795 |
| 333796 | Dunham, I. et.al. | Plus | 7808253-7808319 |
| 333892 | Dunham, I. et.al. | Plus | 8156825-8157001 |
| 333921 | Dunham, I. et.al. | Plus | 8380325-8380441 |
| 333968 | Dunham, I. et.al. | Plus | 8681004-8681241 |
| 334102 | Dunham, I. et.al. | Plus | 9995140-9996373 |
| 334264 | Dunham, I. et.al. | Plus | 13234447-13234544 |
| 334343 | Dunham, I. et.al. | Plus | 13655828-13656307 |
| 334794 | Dunham, I. et.al. | Plus | 16374312-16374458 |
| 334889 | Dunham, I. et.al. | Plus | 19286024-19286515 |
| 335287 | Dunham, I. et.al. | Plus | 22299047-22299299 |
| 335491 | Dunham, I. et.al. | Plus | 24128651-24128827 |
| 335495 | Dunham, I. et.al. | Plus | 24140688-24140872 |
| 335498 | Dunham, I. et.al. | Plus | 24172082-24172161 |
| 335653 | Dunham, I. et.al. | Plus | 25329710-25329802 |
| 335687 | Dunham, I. et.al. | Plus | 25445952-25446064 |
| 335809 | Dunham, I. et.al. | Plus | 26310772-26310909 |
| 335822 | Dunham, I. et.al. | Plus | 26364087-26364196 |
| 335823 | Dunham, I. et.al. | Plus | 26365925-26366004 |
| 335824 | Dunham, I. et.al. | Plus | 26376860-26376942 |
| 335825 | Dunham, I. et.al. | Plus | 26378175-26378268 |
| 336035 | Dunham, I. et.al. | Plus | 29016748-29017410 |
| 336093 | Dunham, I. et.al. | Plus | 29556922-29557002 |
| 336096 | Dunham, I. et.al. | Plus | 29578878-29579047 |
| 336444 | Dunham, I. et.al. | Plus | 34190585-34190718 |
| 336959 | Dunham, I. et.al. | Plus | 13233040-13233126 |
| 338008 | Dunham, I. et.al. | Plus | 7697068-7697236 |
| 338057 | Dunham, I. et.al. | Plus | 8526397-8526522 |
| 338410 | Dunham, I. et.al. | Plus | 19292807-19292916 |
| 338588 | Dunham, I. et.al. | Plus | 22896767-22896920 |
| 338665 | Dunham, I. et.al. | Plus | 24472654-24472853 |
| 338832 | Dunham, I. et.al. | Plus | 27775128-27775290 |
| 338980 | Dunham, I. et.al. | Plus | 29896789-29896874 |
| 339352 | Dunham, I. et.al. | Plus | 33544784-33545121 |

| | | | | |
|----|--------|-------------------|-------|-------------------|
| | 332929 | Dunham, I. et.al. | Minus | 2020758-2020664 |
| | 332930 | Dunham, I. et.al. | Minus | 2022565-2022497 |
| | 332983 | Dunham, I. et.al. | Minus | 2631933-2631797 |
| | 333009 | Dunham, I. et.al. | Minus | 2766043-2765856 |
| 5 | 333010 | Dunham, I. et.al. | Minus | 2766207-2766119 |
| | 333013 | Dunham, I. et.al. | Minus | 2772278-2772039 |
| | 333108 | Dunham, I. et.al. | Minus | 3240494-3240389 |
| | 333343 | Dunham, I. et.al. | Minus | 4692886-4692753 |
| | 333456 | Dunham, I. et.al. | Minus | 2631933-2631797 |
| 10 | 333459 | Dunham, I. et.al. | Minus | 5144548-5144344 |
| | 333743 | Dunham, I. et.al. | Minus | 7573218-7573060 |
| | 333758 | Dunham, I. et.al. | Minus | 7666413-7666091 |
| | 333904 | Dunham, I. et.al. | Minus | 8217374-8217261 |
| | 333905 | Dunham, I. et.al. | Minus | 8217796-8217670 |
| 15 | 334222 | Dunham, I. et.al. | Minus | 12732417-12732289 |
| | 334223 | Dunham, I. et.al. | Minus | 12734365-12734269 |
| | 334360 | Dunham, I. et.al. | Minus | 13728850-13728751 |
| | 334784 | Dunham, I. et.al. | Minus | 16294548-16294360 |
| | 334789 | Dunham, I. et.al. | Minus | 16306095-16305996 |
| 20 | 335004 | Dunham, I. et.al. | Minus | 20581911-20581794 |
| | 335115 | Dunham, I. et.al. | Minus | 21388250-21388146 |
| | 335342 | Dunham, I. et.al. | Minus | 22597448-22597284 |
| | 335544 | Dunham, I. et.al. | Minus | 24650505-24650403 |
| | 335610 | Dunham, I. et.al. | Minus | 25068943-25068841 |
| 25 | 335682 | Dunham, I. et.al. | Minus | 25421215-25421093 |
| | 335755 | Dunham, I. et.al. | Minus | 25763806-25763747 |
| | 335782 | Dunham, I. et.al. | Minus | 25908578-25908440 |
| | 335791 | Dunham, I. et.al. | Minus | 25948563-25948411 |
| | 335895 | Dunham, I. et.al. | Minus | 26975307-26975239 |
| 30 | 335917 | Dunham, I. et.al. | Minus | 27028481-27028377 |
| | 335920 | Dunham, I. et.al. | Minus | 27034927-27034811 |
| | 336042 | Dunham, I. et.al. | Minus | 29041694-29041500 |
| | 336150 | Dunham, I. et.al. | Minus | 30150423-30150256 |
| | 336152 | Dunham, I. et.al. | Minus | 30156053-30155870 |
| 35 | 336416 | Dunham, I. et.al. | Minus | 34047408-34047311 |
| | 336449 | Dunham, I. et.al. | Minus | 34204707-34204577 |
| | 336471 | Dunham, I. et.al. | Minus | 34215091-34214978 |
| | 336512 | Dunham, I. et.al. | Minus | 34278373-34278275 |
| | 336558 | Dunham, I. et.al. | Minus | 34375825-34375698 |
| 40 | 336560 | Dunham, I. et.al. | Minus | 34376814-34376596 |
| | 336676 | Dunham, I. et.al. | Minus | 2022565-2022497 |
| | 337968 | Dunham, I. et.al. | Minus | 7095797-7095680 |
| | 338451 | Dunham, I. et.al. | Minus | 20174286-20174193 |
| | 338689 | Dunham, I. et.al. | Minus | 24893073-24892972 |
| 45 | 339373 | Dunham, I. et.al. | Minus | 33860127-33860047 |
| | 325622 | 5867000 | Plus | 69994-70075 |
| | 329655 | 6448516 | Minus | 35565-35843 |
| | 329899 | 6563505 | Minus | 111058-111783 |
| | 329960 | 5091594 | Minus | 1031-1162 |
| 50 | 326213 | 5867224 | Minus | 60751-60927 |
| | 326474 | 5867405 | Plus | 16995-18101 |
| | 330084 | 6015302 | Minus | 57019-59337 |
| | 326816 | 6552458 | Plus | 198354-198436 |
| | 326817 | 6552458 | Plus | 199909-200001 |
| 55 | 327110 | 6117842 | Plus | 94608-94785 |
| | 327196 | 5867446 | Plus | 180921-181333 |
| | 327283 | 5867478 | Minus | 567-962 |
| | 327313 | 5867501 | Minus | 89734-89838 |
| | 327450 | 5867766 | Minus | 47928-48076 |
| 60 | 328059 | 6117819 | Plus | 37052-37204 |
| | 328492 | 5868455 | Minus | 46094-46241 |
| | 328304 | 6004478 | Minus | 3884-3952 |
| | 328857 | 6381927 | Minus | 80557-81051 |
| | 329367 | 5868842 | Minus | 87201-87587 |
| 65 | 329373 | 6682537 | Minus | 38950-39301 |

TABLE 14: Table 2 from BRCA 001-5 US

5 **Table 14, a subset of table 13, depicts a preferred group of genes highly upregulated in breast cancer cells.**

| | | | | | |
|----|----------------|---|------------|---|------|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal breast tissue | | | |
| 15 | Pkey | ExAccn | UniGene ID | Unigene Title | R1 |
| 20 | 100038 | M97935 | | AFFX control: STAT1 | 16.7 |
| | 100114 | D00596 | Hs.82962 | thymidylate synthetase | 15.9 |
| | 100975 | J02923 | Hs.76506 | lymphocyte cytosolic protein 1 (L-plastin) | 30.1 |
| | 101031 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B; 9 | 37.2 |
| | 101104 | L07615 | Hs.169266 | Human neuropeptide Y receptor Y1 (NPYY | 18.3 |
| 25 | 101143 | L12723 | Hs.90093 | heat shock 70kD protein 4 | 17.4 |
| | 101332 | L47276 | Hs.156346 | Homo sapiens (cell line HL-6) alpha topois | 18.9 |
| | 101378 | M13755 | Hs.833 | interferon-stimulated protein; 15 kDa | 18.1 |
| | 101809 | M86849 | Hs.323733 | Homo sapiens connexin 26 (GJB2) mRNA | 22.5 |
| | 102618 | U65932 | Hs.81071 | extracellular matrix protein 1 | 23.2 |
| 30 | 102721 | U79241 | Hs.118666 | Human clone 23759 mRNA; partial cds | 15 |
| | 102817 | U90904 | Hs.83724 | Human clone 23773 mRNA sequence | 15.2 |
| | 102907 | X06985 | Hs.202833 | heme oxygenase (decycling) 1 | 22.7 |
| | 102985 | X17644 | Hs.2707 | G1 to S phase transition 1 | 20.6 |
| | 103060 | X57766 | Hs.155324 | matrix metalloproteinase 11 (stromelysin 3 | 17.8 |
| 35 | 103180 | X69433 | Hs.5337 | isocitrate dehydrogenase 2 (NADP+); mito | 18.9 |
| | 103206 | X72755 | Hs.77367 | monokine induced by gamma interferon | 15.1 |
| | 103821 | AA157623 | Hs.198793 | KIAA0750 gene product | 23.3 |
| | 104115 | AA428090 | Hs.26102 | ESTs | 28.7 |
| | 104667 | AA007234 | Hs.30098 | ESTs | 16.6 |
| 40 | 105186 | AA191512 | Hs.28005 | Homo sapiens mRNA; cDNA DKFZp564G | 19.3 |
| | 106103 | AA421104 | Hs.12094 | ESTs | 15.4 |
| | 107151 | AA621169 | Hs.8687 | ESTs | 19 |
| | 109415 | AA227219 | Hs.110826 | trinucleotide repeat containing 9 | 20.1 |
| | 110189 | H20543 | Hs.6278 | DKFZP586B1621 protein | 16.6 |
| 45 | 110561 | H59617 | Hs.5199 | ESTs; Weakly similar to UBIQUITIN-CON | 19.5 |
| | 110734 | H98714 | Hs.24131 | ESTs | 30.2 |
| | 110915 | N46252 | Hs.29724 | ESTs | 23.2 |
| | 111179 | N67239 | Hs.10760 | ESTs | 37 |
| | 111357 | N91023 | Hs.87128 | ESTs | 15 |
| 50 | 112134 | R46025 | Hs.7413 | ESTs | 17.4 |
| | 113970 | W86748 | Hs.8109 | ESTs | 15 |
| | 114124 | Z38595 | Hs.125019 | ESTs; Highly similar to KIAA0886 protein | 22 |
| | 114292 | Z40715 | Hs.184641 | delta-6 fatty acid desaturase | 19.4 |
| | 114901 | AA236276 | Hs.196437 | ESTs; Weakly similar to R26660_1; partial | 16.9 |
| 55 | 114965 | AA250737 | Hs.72472 | ESTs | 35.1 |
| | 115652 | AA405098 | Hs.38178 | ESTs | 16.1 |
| | 115875 | AA433943 | Hs.43946 | ESTs; Weakly similar to Weak similarity t | 33.5 |
| | 116790 | H29532 | Hs.101174 | microtubule-associated protein tau | 22.2 |
| | 116921 | H72948 | Hs.821 | biglycan | 20.7 |
| 60 | 117412 | N26722 | Hs.42645 | ESTs | 18.1 |
| | 120241 | Z41815 | Hs.65946 | ESTs | 15.6 |
| | 120325 | AA195651 | Hs.104106 | ESTs | 15.2 |
| | 121596 | AA416740 | Hs.174104 | ESTs | 22.6 |
| | 123619 | AA609200 | | ESTs | 23.1 |
| | 124006 | D60302 | Hs.270016 | ESTs | 20.6 |
| | 125852 | H09290 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B | 25.9 |
| | 126160 | N90960 | Hs.265398 | ESTs; Weakly similar to transformation-rel | 16.4 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 127677 | AA916752 | Hs.264190 | ESTs; Highly similar to MEM3 [M.muscul | 17.3 |
| | 128595 | U31875 | Hs.152677 | short-chain alcohol dehydrogenase family m | 27.1 |
| | 128717 | T30617 | Hs.104222 | Homo sapiens mRNA; cDNA DKFZp566L | 24.5 |
| 5 | 129124 | AA234530 | Hs.108802 | N-ethylmaleimide-sensitive factor | 20.7 |
| | 129366 | H18027 | Hs.184697 | plexin C1 | 18.2 |
| | 130455 | X17059 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acetyl | 26.4 |
| | 130604 | X03635 | Hs.1657 | estrogen receptor 1 | 39.9 |
| | 130913 | W03592 | Hs.21198 | translocase of outer mitochondrial membra | 20.9 |
| 10 | 130944 | M97935 | Hs.21486 | signal transducer and activator of transcript | 18.8 |
| | 131472 | AA608962 | Hs.27258 | calyculin binding protein | 18.1 |
| | 131562 | U90551 | Hs.28777 | H2A histone family; member L | 18.8 |
| | 132180 | AA405569 | Hs.418 | fibroblast activation protein; alpha; seprase | 15.4 |
| | 132406 | F09979 | Hs.4774 | ESTs | 15 |
| | 132465 | AA047896 | Hs.49169 | ESTs | 15.4 |
| 15 | 132994 | AA505133 | Hs.279905 | solute carrier family 2 (facilitated glucose t | 26.4 |
| | 133294 | R79723 | Hs.69997 | zinc finger protein 238 | 30.4 |
| | 133534 | U24166 | Hs.234279 | microtubule-associated protein; RP/EB fam | 15.2 |
| | 134374 | D62633 | Hs.8236 | ESTs | 15.2 |
| 20 | 134405 | J04177 | Hs.82772 | collagen; type XI; alpha 1 | 15.3 |
| | 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 20.3 |
| | 134495 | D63477 | Hs.84087 | KIAA0143 protein | 16.1 |
| | 134714 | U89922 | Hs.890 | lymphotoxin beta (TNF superfamily; memb | 35.7 |
| | 135237 | AA454930 | Hs.9691 | ESTs | 19.5 |
| 25 | 301884 | AA312082 | Hs.105445 | GDNF family receptor alpha 1 | 20.7 |
| | 302276 | NM_004448 | Hs.323910 | EST cluster (not in UniGene) with exon hit | 21.6 |
| | 302290 | AL117607 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N | 41.4 |
| | 309177 | AI951118 | | EST singleton (not in UniGene) with exon | 24.3 |
| | 309583 | AW170035 | | EST | 64.5 |
| 30 | 310438 | AW022192 | Hs.200197 | ESTs | 39.1 |
| | 311166 | AI821294 | Hs.118599 | ESTs | 24.1 |
| | 312153 | AA759250 | Hs.153028 | cytochrome b-561 | 27.1 |
| | 313915 | AI969390 | Hs.163443 | ESTs | 27.1 |
| | 314506 | AA833655 | Hs.206868 | ESTs | 27.8 |
| 35 | 314558 | AI873274 | Hs.190721 | ESTs | 22.5 |
| | 314691 | AW207206 | Hs.136319 | ESTs | 21.4 |
| | 314943 | AI476797 | Hs.184572 | cell division cycle 2; G1 to S and G2 to M | 18.4 |
| | 315196 | AA972756 | Hs.44898 | ESTs | 28.8 |
| | 316177 | AI908272 | Hs.293102 | EST cluster (not in UniGene) | 32.6 |
| 40 | 318073 | AW167087 | Hs.131562 | ESTs | 15.7 |
| | 318662 | AI285898 | Hs.294014 | ESTs | 16.3 |
| | 318740 | NM_002543 | Hs.77729 | EST cluster (not in UniGene) | 21.3 |
| | 318744 | AI793124 | Hs.144479 | ESTs | 35 |
| | 319668 | NM_002731 | Hs.87773 | EST cluster (not in UniGene) | 25.4 |
| 45 | 320074 | AA321166 | Hs.278233 | EST cluster (not in UniGene) | 16.7 |
| | 320211 | AL039402 | Hs.125783 | DEME-6 protein | 24.3 |
| | 320727 | U96044 | Hs.181125 | EST cluster (not in UniGene) | 15.3 |
| | 322818 | AW043782 | Hs.293616 | ESTs | 21 |
| | 322882 | AW248508 | Hs.279727 | DiGeorge syndrome critical region gene 2 | 15.3 |
| 50 | 324261 | AL044891 | Hs.269350 | EST cluster (not in UniGene) | 50.1 |
| | 324432 | AA464510 | Hs.152812 | EST cluster (not in UniGene) | 16.7 |
| | 324603 | AW016378 | Hs.292934 | ESTs | 23.1 |
| | 324620 | AA448021 | Hs.94109 | EST cluster (not in UniGene) | 21.2 |
| | 324988 | T06997 | Hs.121028 | EST cluster (not in UniGene) | 24.5 |
| 55 | 330388 | X03363 | | HER2 receptor tyrosine kinase (c-erbB-2; E | 17.7 |
| | 330486 | M13755 | Hs.833 | interferon-stimulated protein; 15 kDa | 67 |
| | 330814 | AA015730 | Hs.265398 | ESTs; Weakly similar to transformation-rel | 44.1 |
| | 331145 | R72427 | Hs.129873 | ESTs; Weakly similar to CYTOCHROME | 41.9 |
| | 331306 | AA252079 | Hs.63931 | dachshund (Drosophila) homolog | 15.1 |
| 60 | 331890 | AA432166 | Hs.3577 | succinate dehydrogenase complex; subunit | 24.3 |
| | 332526 | AA281753 | Hs.77515 | inositol 1,4;5-triphosphate receptor; type 3 | 19 |
| | 332532 | N63192 | Hs.1892 | EST; Highly similar to PHENYLETHANO | 15.3 |
| | 332694 | AA262768 | Hs.243901 | KIAA1067 protein | 15.2 |
| | 332958 | | | CH22_FGENES.48_15 | 17.8 |
| | 333769 | | | CH22_FGENES.271_8 | 48.3 |
| 65 | 333968 | | | CH22_FGENES.307_4 | 15.9 |
| | 334223 | | | CH22_FGENES.360_4 | 33.5 |
| | 334264 | | | CH22_FGENES.367_15 | 18.5 |

| | | |
|--------|--------------------------------|------|
| 335791 | CH22_FGENES.611_7 | 27.3 |
| 336512 | CH22_FGENES.834_7 | 21.4 |
| 338008 | CH22_EM:AC005500.GENSCAN.127-9 | 15.2 |

TABLE 14A

Table 14A shows the accession numbers for those pkeys lacking unigeneID's for Table 14. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|---------------------------|-------------------|
| 309583 | 1046029_-2 | AW170035 |
| 336512 | CH22_3941FG_834_7_LINK_DJ | |
| 338008 | CH22_6490FG_LINK_EM:AC00 | |
| 333769 | CH22_1036FG_271_8_LINK_EM | |
| 333968 | CH22_1245FG_307_4_LINK_EM | |
| 335791 | CH22_3160FG_611_7_LINK_EM | |
| 309177 | AI951118 | |
| 332958 | CH22_182FG_48_15_LINK_EM: | |
| 334223 | CH22_1507FG_360_4_LINK_EM | |
| 334264 | CH22_1551FG_367_15_LINK_E | |
| 123619 | 371681_1 | AA602964 AA609200 |

TABLE 14B

5 **Table 14B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al, Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 15 NT_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NT_position |
|-----------|-------------------|--------|-------------------|
| 332958 | Dunham, I. et.al. | Plus | 2516164-2516310 |
| 20 333769 | Dunham, I. et.al. | Plus | 7696625-7696707 |
| 333968 | Dunham, I. et.al. | Plus | 8681004-8681241 |
| 334264 | Dunham, I. et.al. | Plus | 13234447-13234544 |
| 338008 | Dunham, I. et.al. | Plus | 7697068-7697236 |
| 334223 | Dunham, I. et.al. | Minus | 12734365-12734269 |
| 25 335791 | Dunham, I. et.al. | Minus | 25948563-25948411 |
| 336512 | Dunham, I. et.al. | Minus | 34278373-34278275 |

TABLE 15: Table 3 from BRCA 001-5 US

Table 15 shows genes downregulated in breast cancer cells.

5

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 10 Unigene Title: Unigene gene title
 R1: Ratio of normal breast tissue to tumor

| 15 | Pkey | ExAccn | UniGene ID | Unigene Title | R1 |
|----|--------|-------------|------------|--|-----|
| | 100115 | D00632 | Hs.172153 | glutathione peroxidase 3 (plasma) | 1.7 |
| | 100499 | TIGR:HT1428 | Hs.283108 | Globin, Beta | 1.5 |
| | 100502 | TIGR:HT1496 | Hs.169228 | Adrenal-Specific Protein Pg2 | 2.3 |
| | 100815 | TIGR:HT4268 | Hs.9739 | L-Glycerol-3-Phosphate:Nad+ Oxidoreduct | 1.7 |
| 20 | 101125 | L10373 | Hs.82749 | transmembrane 4 superfamily member 2 | 1.5 |
| | 101367 | M12963 | Hs.4 | alcohol dehydrogenase 1 (class I); alpha po | 2.9 |
| | 101397 | M15856 | Hs.180878 | lipoprotein lipase | 1.6 |
| | 101883 | M98399 | Hs.75613 | CD36 antigen (collagen type I receptor; thr | 1.6 |
| | 102227 | U25138 | Hs.93841 | potassium large conductance calcium-activ | 1.6 |
| 25 | 102857 | X00129 | Hs.76461 | retinol-binding protein 4; interstitial | 3 |
| | 103211 | X73079 | Hs.288579 | polymeric immunoglobulin receptor | 1.8 |
| | 103496 | Y09267 | Hs.132821 | flavin containing monooxygenase 2 | 1.5 |
| | 103562 | Z21966 | Hs.2815 | POU domain; class 6; transcription factor 1 | 1.8 |
| | 104672 | AA007629 | | glycerol-3-phosphate dehydrogenase 1 (sol | 2.4 |
| 30 | 105083 | AA146619 | Hs.18791 | ESTs; Weakly similar to CALCIUM-BIND | 1.7 |
| | 105138 | AA164519 | Hs.15248 | ESTs | 1.5 |
| | 106075 | AA417915 | Hs.25930 | ESTs | 1.5 |
| | 106870 | AA487576 | Hs.26530 | serum deprivation response (phosphatidyls | 1.6 |
| | 107099 | AA609645 | Hs.211568 | eukaryotic translation initiation factor 4 gam | 2.7 |
| 35 | 107616 | AA004901 | Hs.261164 | ESTs | 1.6 |
| | 107997 | AA037388 | Hs.82223 | Human DNA sequence from clone 141H5 o | 1.7 |
| | 108604 | AA099820 | Hs.49696 | ESTs | 2.4 |
| | 111130 | N64265 | Hs.19515 | yz44h12.s1 Morton Fetal Cochlea Homo sa | 1.7 |
| | 111837 | R36447 | Hs.24453 | ESTs | 1.6 |
| 40 | 112538 | R70255 | | ESTs | 1.9 |
| | 112808 | R97970 | Hs.281022 | EST | 1.5 |
| | 113086 | T40652 | Hs.209100 | DKFZP434C171 protein | 1.9 |
| | 115740 | AA418033 | Hs.283559 | ESTs | 1.6 |
| | 115949 | AA443800 | Hs.43125 | ESTs | 2 |
| 45 | 115965 | AA446661 | Hs.173233 | ESTs | 2.2 |
| | 117224 | N20300 | Hs.218707 | ESTs | 1.7 |
| | 117513 | N32174 | Hs.44317 | SRY (sex-determining region Y)-box 10 | 1.7 |
| | 119059 | R15436 | Hs.77889 | Friedreich ataxia region gene X123 | 1.7 |
| | 119175 | R71792 | Hs.301002 | ESTs; Weakly similar to cell death activato | 2.8 |
| 50 | 119359 | T71021 | Hs.285681 | ESTs; Highly similar to WS basic-helix-loo | 1.9 |
| | 119798 | W73386 | Hs.249129 | ESTs | 3 |
| | 120889 | AA365784 | Hs.97044 | ESTs | 1.6 |
| | 121381 | AA405747 | Hs.97984 | ESTs; Weakly similar to WASP-family pro | 1.8 |
| | 121750 | AA421184 | Hs.97549 | ESTs | 1.5 |
| 55 | 122127 | AA434447 | Hs.106771 | ESTs | 2.5 |
| | 122348 | AA443695 | Hs.293410 | ESTs | 2.1 |
| | 122485 | AA448300 | Hs.160318 | phospholemman | 1.5 |
| | 123443 | AA598841 | Hs.167382 | natriuretic peptide receptor A/guanylate cy | 1.8 |
| | 123505 | AA600135 | | ESTs; Moderately similar to !!! ALU SUB | 1.5 |
| 60 | 125284 | W94688 | Hs.103253 | perlepin | 1.7 |
| | 126300 | D81972 | HUM427D08B | Human fetal brain (TFU)w | 1.8 |
| | 126747 | R72515 | Hs.160318 | phospholemman | 1.6 |
| | 127218 | AA309765 | Hs.116017 | ESTs; Weakly similar to KIAA0795 protei | 1.5 |
| | 127357 | AA452788 | Hs.75432 | zx39g11.r1 Soares_tota fetus_Nb2HF8_9 | 1.7 |

| | | | | | |
|----|--------|----------|-----------|--|-----|
| | 127638 | AA634405 | Hs.122608 | ESTs | 1.5 |
| | 128213 | AA972780 | Hs.129194 | ESTs; Weakly similar to IIII ALU SUBFA | 1.5 |
| | 128351 | AI092391 | Hs.134886 | ESTs | 1.5 |
| | 128842 | N44757 | Hs.20340 | ESTs | 1.6 |
| 5 | 128870 | R71403 | Hs.75309 | eukaryotic translation elongation factor 2 | 1.7 |
| | 129146 | AA459944 | Hs.108924 | DKFZP586P1422 protein | 1.5 |
| | 129285 | T62068 | Hs.11006 | ESTs | 2.1 |
| | 129331 | N93465 | Hs.279772 | ESTs; Highly similar to CGI-38 protein [H | 1.5 |
| | 130085 | M62402 | Hs.274313 | insulin-like growth factor binding protein 6 | 1.7 |
| 10 | 130400 | M25079 | Hs.283108 | hemoglobin; beta | 1.7 |
| | 131267 | AA211776 | Hs.2504 | myomesin 1 (skelemin) (185kD) | 3.8 |
| | 131277 | AA131466 | Hs.23767 | ESTs | 1.9 |
| | 131282 | M12272 | Hs.4 | alcohol dehydrogenase 3 (class I); gamma p | 2.2 |
| | 131304 | AA295848 | Hs.25475 | aquaporin 7 | 1.7 |
| 15 | 131810 | D49487 | Hs.194236 | leptin (murine obesity homolog) | 2.5 |
| | 132788 | AA045503 | Hs.56874 | ESTs; Weakly similar to Homo sapiens p2 | 1.6 |
| | 132931 | Z41452 | Hs.6090 | deleted in bladder cancer chromosome regl | 1.5 |
| | 133120 | X64559 | Hs.65424 | tetranectin (plasminogen-binding protein) | 2 |
| | 133314 | U95367 | Hs.70725 | gamma-aminobutyric acid (GABA) A recep | 1.5 |
| 20 | 133507 | X74295 | Hs.74369 | integrin; alpha 7 | 1.7 |
| | 133601 | S95936 | Hs.284176 | transferrin | 2.3 |
| | 133702 | N56898 | Hs.75652 | glutathione S-transferase M5 | 1.9 |
| | 134111 | N79674 | Hs.8022 | TU3A protein | 4.6 |
| | 134699 | U56814 | Hs.88646 | deoxyribonuclease I-like 3 | 1.5 |
| 25 | 134749 | L10955 | Hs.89485 | carbonic anhydrase IV | 1.6 |
| | 135173 | M72885 | Hs.95910 | Human G0S2 protein gene; complete cds | 1.9 |
| | 300132 | AW027556 | Hs.156286 | ESTs | 1.7 |
| | 300732 | AI369956 | Hs.257891 | ESTs | 1.5 |
| | 300750 | AA514805 | Hs.293055 | ESTs | 1.8 |
| 30 | 301140 | AI807692 | Hs.129129 | ESTs | 1.6 |
| | 301396 | AA923549 | Hs.224121 | ESTs | 2.1 |
| | 302910 | N77976 | Hs.251577 | hemoglobin; alpha 1 | 1.8 |
| | 303798 | V00505 | Hs.36977 | hemoglobin; delta | 1.6 |
| | 303831 | T04868 | Hs.46780 | EST cluster (not in UniGene) with exon hit | 1.7 |
| 35 | 303844 | U94362 | Hs.58589 | glycogenin 2 | 1.5 |
| | 304182 | H91086 | | EST singleton (not in UniGene) with exon | 1.5 |
| | 304622 | AA516384 | | EST singleton (not in UniGene) with exon | 1.5 |
| | 304682 | AA550994 | | EST singleton (not in UniGene) with exon | 1.7 |
| 40 | 305612 | AA782347 | Hs.272572 | EST singleton (not in UniGene) with exon | 1.5 |
| | 306193 | AA923457 | | EST singleton (not in UniGene) with exon | 1.5 |
| | 307206 | AI192534 | | EST singleton (not in UniGene) with exon | 1.6 |
| | 307377 | AI222691 | | EST singleton (not in UniGene) with exon | 1.5 |
| | 308023 | AI452732 | Hs.251577 | EST singleton (not in UniGene) with exon | 1.9 |
| | 308359 | AI612774 | Hs.79372 | retinoid X receptor; beta | 1.5 |
| 45 | 309838 | AW296073 | Hs.255504 | EST | 1.5 |
| | 310403 | AI720978 | Hs.148006 | ESTs; Moderately similar to alternatively s | 1.8 |
| | 311671 | AW241947 | Hs.232478 | ESTs | 1.6 |
| | 311794 | AW238092 | Hs.254759 | ESTs | 2.1 |
| | 312082 | T79860 | Hs.118180 | ESTs | 1.9 |
| 50 | 312575 | H25237 | Hs.306814 | ESTs | 2.3 |
| | 313076 | N49684 | Hs.143040 | ESTs | 1.8 |
| | 313283 | W32480 | Hs.157099 | ESTs | 2.2 |
| | 313374 | AW328672 | Hs.132760 | ESTs | 1.9 |
| | 314701 | AI754634 | Hs.131987 | ESTs | 1.7 |
| 55 | 315391 | AA759098 | Hs.192007 | ESTs | 1.8 |
| | 315688 | AA680055 | Hs.264885 | ESTs | 1.5 |
| | 316249 | AA948612 | Hs.130414 | ESTs | 1.6 |
| | 316586 | AI205077 | Hs.294085 | ESTs | 1.7 |
| | 316890 | AA837079 | Hs.24647 | ESTs | 1.5 |
| 60 | 316983 | AI480204 | Hs.177131 | ESTs | 1.5 |
| | 317604 | AI650625 | Hs.300756 | ESTs | 1.6 |
| | 317951 | AW206520 | Hs.129621 | ESTs | 1.5 |
| | 319400 | W26902 | Hs.154085 | ESTs | 1.7 |
| | 320757 | H22654 | Hs.6382 | EST cluster (not in UniGene) | 1.5 |
| 65 | 321594 | AA021402 | Hs.11067 | ESTs | 1.7 |
| | 322102 | H45589 | | EST cluster (not in UniGene) | 1.5 |
| | 322814 | AI824495 | Hs.211038 | ESTs | 2.2 |

| | | | | | |
|----|--------|----------|--------------------------------|---------------------------------------|-----|
| | 322929 | AI365585 | Hs.146246 | ESTs | 2.3 |
| | 323831 | AA335715 | Hs.200299 | ESTs | 1.7 |
| | 324044 | AL045752 | Hs.22350 | ESTs | 1.8 |
| | 324675 | AW014734 | Hs.157969 | ESTs | 2.2 |
| 5 | 325272 | | CH.11_hs gij5866902 | | 1.5 |
| | 325558 | | CH.12_hs gij6066302 | | 1.6 |
| | 325656 | | CH.14_hs gij6056305 | | 1.6 |
| | 326120 | | CH.17_hs gij5867194 | | 1.5 |
| | 326139 | | CH.17_hs gij5867203 | | 1.5 |
| 10 | 326855 | | CH.20_hs gij6552460 | | 1.5 |
| | 327438 | | CH.02_hs gij6004454 | | 1.6 |
| | 329733 | | CH.14_p2 gij6065783 | | 1.6 |
| | 330931 | F01443 | Hs.284256 | ESTs | 4.6 |
| | 331591 | N71677 | Hs.42146 | ESTs | 1.9 |
| 15 | 332159 | AA621393 | Hs.112984 | EST | 1.5 |
| | 332364 | W94688 | Hs.103253 | perilipin | 2.1 |
| | 332502 | H21819 | Hs.14896 | Homo sapiens clone 24590 mRNA sequenc | 1.5 |
| | 334175 | | CH22_FGENES.349_10 | | 1.5 |
| | 334347 | | CH22_FGENES.375_31 | | 1.8 |
| 20 | 334737 | | CH22_FGENES.424_12 | | 1.8 |
| | 335352 | | CH22_FGENES.539_5 | | 1.5 |
| | 335639 | | CH22_FGENES.584_19 | | 1.6 |
| | 336244 | | CH22_FGENES.746_2 | | 1.5 |
| | 336336 | | CH22_FGENES.814_8 | | 1.7 |
| 25 | 336865 | | CH22_FGENES.305-1 | | 1.6 |
| | 337494 | | CH22_FGENES.799-12 | | 1.6 |
| | 337764 | | CH22_EM:AC000097.GENSCAN.119-1 | | 1.8 |
| | 337983 | | CH22_EM:AC005500.GENSCAN.110-1 | | 2 |
| | 338192 | | CH22_EM:AC005500.GENSCAN.228-1 | | 1.5 |
| 30 | 339366 | | CH22_BA354112.GENSCAN.34-2 | | 1.5 |

TABLE 15A

Table 15A shows the accession numbers for those pkeys lacking unigeneID's for Table 15.

- 5 For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15

Pkey CAT number Accession

20

126300 250375_2 D81972 BE003132
 112538 504579_1 AA908813 R70255
 123505 genbank_AA600135 AA600135
 104672 6735_7 AA349096 AI368018 F21390 F17759 R48772 AI421485 AI300352 H43971 AI378525 F33652 R47898 AI264177 F22289 N28263
 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375
 H45809 F33447 AA774528 AA007629 H42537 C01077 F32386

25

322102 46708_1 H45589 H19807 AF075038 H19808 H42437

30

336865 CH22_4590FG_305_1_
 338192 CH22_6755FG_LINK_EM:AC00
 329733 c14_p2
 326120 c17_hs
 326139 c17_hs
 326855 c20_hs

35

335352 CH22_2699FG_539_5_LINK_EM
 335639 CH22_2999FG_584_19_LINK_E
 307206 AI192534

40

307377 AI222691
 337494 CH22_5727FG_799_12_
 337764 CH22_6115FG_LINK_EM:AC00
 337983 CH22_6438FG_LINK_EM:AC00
 339366 CH22_8336FG_LINK_BA35411

45

325272 c11_hs
 325558 c12_hs
 325656 c14_hs
 334175 CH22_1455FG_349_10_LINK_E
 304182 H91086

50

334347 CH22_1640FG_375_31_LINK_E
 327438 c_2_hs
 304622 AA516384
 334737 CH22_2049FG_424_12_LINK_E
 304682 AA550994
 336244 CH22_3642FG_746_2_LINK_DA
 306193 AA923457
 336336 CH22_3746FG_814_8_LINK_BA

TABLE 15B

5 **Table 15B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

| Pkey | Ref | Strand | Nt_position |
|-----------|-------------------|--------|-------------------|
| 334347 | Dunham, I. et.al. | Plus | 13663814-13663926 |
| 334737 | Dunham, I. et.al. | Plus | 15998517-15998685 |
| 20 335639 | Dunham, I. et.al. | Plus | 25173591-25173696 |
| 337494 | Dunham, I. et.al. | Plus | 33339024-33339148 |
| 334175 | Dunham, I. et.al. | Minus | 11668659-11668597 |
| 335352 | Dunham, I. et.al. | Minus | 22681512-22681384 |
| 336244 | Dunham, I. et.al. | Minus | 31402729-31402583 |
| 25 336336 | Dunham, I. et.al. | Minus | 33797209-33797076 |
| 336865 | Dunham, I. et.al. | Minus | 8622405-8622289 |
| 337764 | Dunham, I. et.al. | Minus | 4035640-4035446 |
| 337983 | Dunham, I. et.al. | Minus | 7275495-7275271 |
| 338192 | Dunham, I. et.al. | Minus | 13248453-13248277 |
| 30 339366 | Dunham, I. et.al. | Minus | 33647431-33647293 |
| 325272 | 5866902 | Minus | 13247-13312 |
| 325558 | 6056302 | Plus | 70930-71030 |
| 325656 | 6056305 | Minus | 78190-78707 |
| 329733 | 6065783 | Plus | 163237-163450 |
| 35 326120 | 5867194 | Plus | 36116-36276 |
| 326139 | 5867203 | Minus | 218901-218960 |
| 326855 | 6552460 | Minus | 111390-111463 |
| 327438 | 6004454 | Minus | 199569-199692 |

TABLE 16: Table 4 from BRCA 001-5 US

Table 16, a subset of table 15, depicts a preferred group of genes highly downregulated in breast cancer cells.

| | | | | | |
|----|----------------|---|------------|--|-----|
| 10 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigenelD: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of normal breast tissue to tumor | | | |
| 15 | Pkey | ExAccn | UniGene ID | Unigene Title | R1 |
| 20 | 100502 | TIGR:HT1496 | Hs.169228 | Adrenal-Specific Protein Pg2 | 2.3 |
| | 101367 | M12963 | Hs.4 | alcohol dehydrogenase 1 (class I); alpha | 2.9 |
| | 102857 | X00129 | Hs.76461 | retinol-binding protein 4; interstitial | 3 |
| | 104672 | AA007629 | | glycerol-3-phosphate dehydrogenase 1 | 2.4 |
| | 107099 | AA609645 | Hs.211568 | eukaryotic translation initiation factor 4 gam | 2.7 |
| 25 | 108604 | AA099820 | Hs.49696 | ESTs | 2.4 |
| | 115949 | AA443800 | Hs.43125 | ESTs | 2 |
| | 115965 | AA446661 | Hs.173233 | ESTs | 2.2 |
| | 119175 | R71792 | Hs.301002 | ESTs; Weakly similar to cell death activator | 2.8 |
| | 119798 | W73386 | Hs.249129 | ESTs | 3 |
| 30 | 122127 | AA434447 | Hs.106771 | ESTs | 2.5 |
| | 122348 | AA443695 | Hs.293410 | ESTs | 2.1 |
| | 129285 | T62068 | Hs.11006 | ESTs | 2.1 |
| | 131267 | AA211776 | Hs.2504 | myomesin 1 (skelemin) (185kD) | 3.8 |
| | 131282 | M12272 | Hs.4 | alcohol dehydrogenase 3 (class I); gamma | 2.2 |
| 35 | 131810 | D49487 | Hs.194236 | leptin (murine obesity homolog) | 2.5 |
| | 133120 | X64559 | Hs.65424 | tetranectin (plasminogen-binding protein) | 2 |
| | 133601 | S95936 | Hs.284176 | transferrin | 2.3 |
| | 134111 | N79674 | Hs.8022 | TU3A protein | 4.6 |
| | 301396 | AA923549 | Hs.224121 | ESTs | 2.1 |
| 40 | 311794 | AW238092 | Hs.254759 | ESTs | 2.1 |
| | 312575 | H25237 | Hs.306814 | ESTs | 2.3 |
| | 313283 | W32480 | Hs.157099 | ESTs | 2.2 |
| | 322814 | AI824495 | Hs.211038 | ESTs | 2.2 |
| | 322929 | AI365585 | Hs.146246 | ESTs | 2.3 |
| 45 | 324675 | AW014734 | Hs.157969 | ESTs | 2.2 |
| | 330931 | F01443 | Hs.284256 | ESTs | 4.6 |
| | 332364 | W94688 | Hs.103253 | perilipin | 2.1 |
| | 337983 | | | CH22_EM:AC005500.GENSCAN.110-1 | 2 |

TABLE 16A

Table 16A shows the accession numbers for those pkeys lacking unigeneID's for Table 16. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT number Accession

104672 6735_7 AA349096 AI368018 F21390 F17759 R48772 AI421485 AI300352 H43971 AI378525 F33652 R47898 AI264177 F22289 N28263
 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375
 H45809 F33447 AA774528 AA007629 H42537 C01077 F32386

TABLE 17: Table 1 from BRCA 014 P

5 **Table 17** shows accession numbers representing 759 sequences of breast cancer genes or fragments thereof encoding breast cancer modulating proteins. For each overexpressed gene identified, a ratio of the relative amount of expression in breast tumors versus normal breast tissue.

10

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 15 R1: Ratio of tumor to normal breast tissue

| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|----|--------|-----------|-----------|--|------|
| 20 | 100227 | AV654694 | Hs.82316 | interferon-induced, hepatitis C-associated | 3 |
| | 100405 | AW291587 | Hs.82733 | nidogen 2 | 3.2 |
| | 100406 | AI962060 | Hs.118397 | AE-binding protein 1 | 3.6 |
| | 100420 | D86983 | Hs.118893 | Melanoma associated gene | 3.2 |
| | 100911 | X83300 | Hs.289103 | SMA4 | 5.2 |
| 25 | 100960 | J00124 | Hs.117729 | keratin 14 (epidermolysis bullosa simple | 4.3 |
| | 101011 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 3 |
| | 101183 | AA442324 | Hs.795 | H2A histone family, member O | 3.2 |
| | 101194 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 3 |
| | 101329 | U66042 | Hs.82171 | Homo sapiens clone 191B7 placenta expres | 4.1 |
| 30 | 101378 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 5.3 |
| | 101474 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 3.9 |
| | 101491 | M25809 | Hs.64173 | ATPase, H+ transporting, lysosomal (vacu | 4.5 |
| | 101530 | M29874 | Hs.1360 | cytochrome P450, subfamily IIB (phenobar | 9 |
| | 101602 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 3.4 |
| 35 | 101663 | NM_003528 | Hs.2178 | H2B histone family, member Q | 5.6 |
| | 101758 | BE019494 | Hs.79217 | pyrroline-5-carboxylate reductase 1 | 3.6 |
| | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 12 |
| | 101817 | M89907 | Hs.152292 | SWI/SNF related, matrix associated, acti | 3.2 |
| 40 | 101851 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 4.1 |
| | 101878 | M97815 | Hs.183650 | cellular retinoic acid-binding protein 2 | 6.5 |
| | 102209 | NM_002038 | Hs.265827 | Interferon, alpha-inducible protein (clo | 3 |
| | 102214 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 3 |
| | 102297 | NM_001504 | Hs.198252 | G protein-coupled receptor 9 | 3.7 |
| | 102299 | NM_005824 | Hs.155545 | 37 kDa leucine-rich repeat (LRR) protein | 3.7 |
| 45 | 102301 | NM_005651 | Hs.183671 | tryptophan 2,3-dioxygenase | 5.2 |
| | 102305 | AL043202 | Hs.90073 | chromosome segregation 1 (yeast homolog) | 3.5 |
| | 102369 | U39840 | Hs.299867 | hepatocyte nuclear factor 3, alpha | 3.9 |
| | 102591 | U62325 | Hs.324125 | amyloid beta (A4) precursor protein-bind | 4 |
| | 102721 | H16646 | Hs.118666 | hypothetical protein PP591 | 3.5 |
| 50 | 102739 | AA363025 | Hs.155572 | Human clone 23801 mRNA sequence | 3.2 |
| | 102791 | AF080229 | | gb:Human endogenous retrovirus K clone 1 | 3 |
| | 102804 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 3.2 |
| | 102903 | M73779 | Hs.250505 | retinoic acid receptor, alpha | 3.3 |
| | 103010 | X52509 | Hs.161640 | tyrosine aminotransferase | 12.4 |
| 55 | 103042 | T81656 | Hs.252259 | ribosomal protein S3 | 4.5 |
| | 103117 | X63578 | Hs.295449 | parvalbumin | 3 |
| | 103207 | X72790 | | gb:Human endogenous retrovirus mRNA for | 5.9 |
| | 103282 | BE390551 | Hs.77628 | steroidogenic acute regulatory protein r | 3.9 |
| | 103284 | AI751601 | Hs.8375 | TNF receptor-associated factor 4 | 3.3 |
| 60 | 103329 | X85134 | Hs.72984 | retinoblastoma-binding protein 5 | 3.1 |
| | 103364 | X90872 | Hs.279929 | gp25L2 protein | 3 |
| | 103385 | NM_007069 | Hs.37189 | similar to rat HREV107 | 3.4 |
| | 103456 | AA496425 | Hs.9629 | papillary renal cell carcinoma (transloc | 3.2 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 103498 | Y09306 | Hs.30148 | homeodomain-interacting protein kinase 3 | 3.4 |
| | 103558 | BE616547 | Hs.2785 | keratin 17 | 3.7 |
| | 103563 | L02911 | Hs.150402 | Activin A receptor, type I (ACVR1) (ALK | 3.2 |
| | 103612 | BE336654 | Hs.70937 | H3 histone family, member A | 4.5 |
| 5 | 103825 | AI571835 | Hs.55468 | ESTs | 4 |
| | 104073 | AW779318 | Hs.88417 | ESTs | 3.8 |
| | 104103 | AW021102 | Hs.21509 | ESTs | 4.3 |
| | 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal | 7.6 |
| | 104168 | AA461618 | Hs.31704 | ESTs, Weakly similar to KIAA0227 [H.sapi | 3.6 |
| 10 | 104173 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 4 |
| | 104181 | AF173296 | Hs.283740 | DC6 protein | 3 |
| | 104189 | AB040927 | Hs.301804 | KIAA1494 protein | 3.2 |
| | 104269 | AI559444 | Hs.293960 | ESTs | 4.3 |
| | 104307 | AI929700 | Hs.111680 | endosulfine alpha | 3.1 |
| 15 | 104518 | H20816 | Hs.112423 | Homo sapiens mRNA; cDNA DKFZp58611420 (f | 3.2 |
| | 104556 | AV650851 | Hs.96900 | hypothetical protein; KIAA1830 protein | 4.4 |
| | 104658 | AA360954 | Hs.27268 | Homo sapiens cDNA: FLJ21933 fis, clone H | 3.2 |
| | 104748 | AA015879 | Hs.33536 | ESTs | 3.2 |
| | 104755 | T49951 | Hs.9029 | DKFZP434G032 protein | 4.5 |
| 20 | 104825 | AA035613 | Hs.141883 | ESTs | 6.9 |
| | 104830 | AW294092 | Hs.21594 | hypothetical protein MGC15754 | 11.1 |
| | 104865 | T79340 | Hs.22575 | B-cell CLL/lymphoma 6, member B (zinc fi | 3.5 |
| | 104906 | BE298684 | Hs.26802 | protein kinase domains containing protei | 6.5 |
| | 104961 | H78517 | Hs.33905 | ESTs | 3.6 |
| 25 | 105038 | AW503733 | Hs.9414 | KIAA1488 protein | 4.5 |
| | 105088 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fis, clone PL | 3.8 |
| | 105092 | AA148982 | Hs.29068 | ESTs | 3 |
| | 105093 | AL137566 | Hs.32405 | Homo sapiens mRNA; cDNA DKFZp586G0321 (f | 4.8 |
| | 105304 | AW134924 | Hs.190325 | ESTs | 8.2 |
| 30 | 105397 | AA814807 | Hs.7395 | hypothetical protein FLJ23182 | 3.1 |
| | 105409 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 4.2 |
| | 105431 | AA252033 | Hs.242413 | hypothetical protein DKFZp434K1421 | 4.4 |
| | 105552 | AA256750 | Hs.28802 | centaurin-alpha 2 protein | 3.2 |
| | 105598 | AA279439 | Hs.279763 | hypothetical protein FLJ10504 | 3.5 |
| 35 | 105650 | W16741 | Hs.25635 | HSPC003 protein | 3.7 |
| | 105688 | AI299139 | Hs.17517 | ESTs | 5.5 |
| | 105808 | AI133161 | Hs.286131 | CGI-101 protein | 3.5 |
| | 105809 | AW973653 | Hs.20104 | hypothetical protein FLJ00052 | 3.3 |
| | 105909 | AA195191 | Hs.5111 | hypothetical protein FLJ20729 | 3.2 |
| 40 | 105965 | AA131657 | Hs.23830 | ESTs | 3.3 |
| | 106135 | AL117474 | Hs.41181 | Homo sapiens mRNA; cDNA DKFZp727C191 (fr | 3.2 |
| | 106184 | W28948 | Hs.10762 | ESTs | 3.3 |
| | 106293 | N39842 | Hs.301444 | KIAA1673 | 4.1 |
| | 106400 | BE397649 | Hs.94109 | Homo sapiens cDNA FLJ13634 fis, clone PL | 3.1 |
| 45 | 106474 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 3.2 |
| | 106484 | AA351978 | Hs.4943 | hepatocellular carcinoma associated prot | 7.8 |
| | 106533 | AL134708 | Hs.145998 | ESTs | 3 |
| | 106614 | AA648459 | Hs.335951 | hypothetical protein AF301222 | 3.8 |
| | 106636 | AW958037 | Hs.286 | ribosomal protein L4 | 3.3 |
| 50 | 106661 | AW499914 | Hs.7579 | hypothetical protein FLJ10402 | 3 |
| | 106743 | BE613328 | Hs.21938 | hypothetical protein FLJ12492 | 4.2 |
| | 106844 | AA485055 | Hs.158213 | sperm associated antigen 6 | 3.4 |
| | 106864 | AI311928 | | gb:qo89h04.x1 NCL_CGAP_Kid5 Homo sapiens | 4.4 |
| | 106865 | AW192535 | Hs.19479 | ESTs | 3.6 |
| 55 | 106871 | AW472981 | Hs.321130 | hypothetical protein MGC2771 | 4.1 |
| | 106942 | AA995351 | Hs.31314 | retinoblastoma-binding protein 7 | 3.6 |
| | 106968 | AF216751 | Hs.26813 | CDA14 | 5.3 |
| | 107105 | AW963419 | Hs.155223 | stanniocalcin 2 | 3.4 |
| | 107158 | N32849 | Hs.31844 | hypothetical protein FLJ12586 | 3.1 |
| 60 | 107248 | AW263124 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 5.9 |
| | 107265 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 3.9 |
| | 107630 | AW961576 | Hs.60178 | ESTs | 4.6 |
| | 107710 | AI955040 | Hs.265398 | ESTs, Weakly similar to transformation-r | 3 |
| | 107890 | AA025386 | Hs.61311 | ESTs, Weakly similar to S10590 cysteine | 3.1 |
| 65 | 107985 | T40064 | Hs.71968 | Homo sapiens mRNA; cDNA DKFZp564F053 (fr | 4.8 |
| | 108000 | AI263307 | Hs.239884 | H2B histone family, member L | 3.3 |
| | 108217 | AA058686 | Hs.62588 | ESTs | 3.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 108435 | T82427 | Hs.194101 | Homo sapiens cDNA: FLJ20869 fis, clone A | 3 |
| | 108591 | AB033073 | Hs.43857 | similar to glucosamine-6-sulfatases | 3.3 |
| | 108733 | AA121022 | | gb:zn84f10.r1 Stratagene lung carcinoma | 3.9 |
| 5 | 108771 | AF068290 | Hs.79741 | hypothetical protein FLJ10116 | 6.1 |
| | 108819 | AA011449 | Hs.271627 | ESTs | 3.6 |
| | 108912 | AA136674 | Hs.118681 | EST | 3.9 |
| | 109086 | AF186114 | Hs.270737 | tumor necrosis factor (ligand) superfam | 3.7 |
| | 109124 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 3.1 |
| 10 | 109132 | AI970536 | Hs.16603 | hypothetical protein FLJ13163 | 3.7 |
| | 109163 | N23235 | Hs.30567 | ESTs, Weakly similar to B34087 hypotheti | 4.5 |
| | 109277 | AA196443 | Hs.86043 | Homo sapiens cDNA FLJ13558 fis, clone PL | 3.7 |
| | 109410 | AW504732 | Hs.21275 | hypothetical protein FLJ11011 | 4.6 |
| | 109454 | AA232255 | Hs.295232 | ESTs, Moderately similar to A46010 X-lin | 6.4 |
| | 109514 | AA234087 | Hs.262346 | ESTs, Weakly similar to S72482 hypotheti | 4.8 |
| 15 | 109581 | R45584 | Hs.23025 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.3 |
| | 109632 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 3 |
| | 109644 | AW973964 | Hs.291531 | ESTs, Highly similar to 1203217A dehydro | 3 |
| | 109700 | F09609 | | gb:HSC33H092 normalized infant brain cDN | 3.2 |
| | 109768 | F06838 | Hs.14763 | ESTs | 3.2 |
| 20 | 109807 | R43646 | Hs.12422 | ESTs | 3.8 |
| | 109842 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 3.3 |
| | 109895 | AK001680 | Hs.30488 | DKFZP434F091 protein | 3.6 |
| | 110024 | AW973152 | Hs.31050 | ESTs | 4.2 |
| | 110561 | AA379597 | Hs.5199 | HSPC150 protein similar to ublquitin-con | 5.1 |
| 25 | 110675 | H89355 | Hs.249159 | adrenergic, alpha-2A-, receptor | 5.3 |
| | 110707 | AI239832 | Hs.15617 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 3.7 |
| | 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 3.7 |
| | 111139 | N64683 | Hs.290943 | ESTs | 4 |
| | 111155 | N66563 | Hs.191358 | ESTs | 3.1 |
| 30 | 111199 | AI767435 | Hs.29822 | ESTs | 4.5 |
| | 111336 | AI457338 | Hs.29894 | ESTs | 5.4 |
| | 111510 | R07856 | Hs.16355 | ESTs | 3.2 |
| | 111532 | R08440 | | gb:yf19f09.s1 Soares fetal liver spleen | 3.1 |
| | 111689 | AA602004 | Hs.23260 | ESTs | 3.2 |
| 35 | 111823 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 3.3 |
| | 111876 | R38239 | Hs.293246 | ESTs, Weakly similar to putative p150 [H | 3.1 |
| | 111892 | AA421081 | Hs.12388 | ESTs | 3.4 |
| | 111893 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 3.3 |
| 40 | 112125 | AW379029 | Hs.118338 | ESTs, Weakly similar to unnamed protein | 4.4 |
| | 112170 | BE246743 | Hs.288529 | hypothetical protein FLJ22635 | 7.3 |
| | 112287 | AB033064 | Hs.334806 | KIAA1238 protein | 3.2 |
| | 112300 | H24334 | Hs.26125 | ESTs | 4.4 |
| | 112303 | R54797 | | gb:yg87b07.s1 Soares infant brain 1N1B H | 3.4 |
| | 112478 | R66067 | Hs.28664 | ESTs | 8.2 |
| 45 | 112561 | AI791493 | Hs.129873 | ESTs, Weakly similar to A36036 cytochrom | 5.5 |
| | 112631 | R82040 | | gb:yj06b06.s1 Soares placenta Nb2HP Homo | 3.9 |
| | 112637 | R82331 | Hs.164599 | ESTs | 5.4 |
| | 112657 | AW844878 | Hs.19769 | hypothetical protein MGC4174 | 3.2 |
| | 112678 | AI418466 | Hs.33665 | ESTs | 4.7 |
| 50 | 112917 | AA082465 | Hs.125031 | choline/ethanolaminephosphotransferase | 3.7 |
| | 113070 | AB032977 | Hs.6298 | KIAA1151 protein | 3.1 |
| | 113095 | AA828380 | Hs.126733 | ESTs | 3.4 |
| | 113117 | AW813731 | Hs.159153 | ESTs, Moderately similar to S65657 alpha | 3.4 |
| | 113187 | BE613410 | Hs.31575 | SEC63, endoplasmic reticulum translocon | 3.2 |
| 55 | 113200 | T57773 | Hs.10263 | ESTs | 3.5 |
| | 113206 | BE262470 | Hs.241471 | RNB6 | 6.2 |
| | 113374 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.7 |
| | 113440 | U54727 | Hs.191445 | ESTs | 3 |
| | 113494 | T91451 | Hs.86538 | ESTs | 3.4 |
| 60 | 113518 | AW367788 | Hs.323954 | postmeiotic segregation increased 2-like | 3.1 |
| | 113571 | AI702609 | Hs.15713 | hypothetical protein MGC2776 | 3.1 |
| | 113822 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 3.9 |
| | 113835 | AI912410 | Hs.27475 | Homo sapiens cDNA FLJ12749 fis, clone NT | 3 |
| | 113938 | W81598 | | gb:zd88g02.s1 Soares_fetal_heart_NbHH19W | 4.6 |
| 65 | 113947 | W84768 | | gb:zh53d03.s1 Soares_fetal_liver_spleen_ | 3.1 |
| | 113970 | W27249 | Hs.8109 | hypothetical protein FLJ21080 | 6.9 |
| | 114086 | AA378776 | Hs.288649 | hypothetical protein MGC3077 | 4.3 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 114148 | AW470411 | Hs.288433 | neurotrimin | 4.1 |
| | 114424 | AW780192 | Hs.267596 | ESTs | 3.4 |
| | 114518 | AW163267 | Hs.106469 | suppressor of var1 (S.cerevisiae) 3-like | 3.1 |
| | 114563 | AI979168 | Hs.82226 | glycoprotein (transmembrane) nmb | 4.8 |
| 5 | 114965 | AI733881 | Hs.72472 | BMP-R1B | 10.1 |
| | 114995 | AA769266 | Hs.193657 | ESTs | 3.6 |
| | 115121 | AI634549 | Hs.88155 | ESTs | 3.2 |
| | 115134 | AW968073 | Hs.194331 | ESTs, Highly similar to A55713 inositol | 4.2 |
| | 115167 | AA749209 | Hs.43728 | hypothetical protein | 3 |
| 10 | 115253 | BE149845 | Hs.289038 | hypothetical protein MGC4126 | 3.6 |
| | 115277 | AA814100 | Hs.86693 | ESTs | 3.9 |
| | 115327 | N46436 | Hs.109221 | ESTs | 3.4 |
| | 115354 | AA281636 | Hs.334827 | ESTs | 4.8 |
| | 115657 | AA405620 | Hs.55158 | ESTs, Weakly similar to T29520 hypotheti | 3.5 |
| | 115676 | AA953006 | Hs.88143 | ESTs | 9.3 |
| | 115709 | AW293849 | Hs.58279 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.4 |
| | 115729 | AA417812 | Hs.38775 | ESTs | 4 |
| | 115787 | AI126772 | Hs.40479 | ESTs | 3.1 |
| | 115830 | AW970529 | Hs.86434 | hypothetical protein FLJ21816 | 3.6 |
| 20 | 115835 | AA521410 | Hs.41371 | ESTs | 3.1 |
| | 115850 | NM_014937 | Hs.52463 | KIAA0966 protein | 3 |
| | 115900 | AK001500 | Hs.165186 | hypothetical protein FLJ13852 | 3.2 |
| | 115935 | AA354549 | Hs.41181 | Homo sapiens mRNA; cDNA DKFZp727C191 (fr | 3 |
| | 115948 | AL042465 | Hs.43445 | poly(A)-specific ribonuclease (deadenyla | 3.1 |
| 25 | 116092 | AB041035 | Hs.93847 | NM_016931:Homo sapiens NADPH oxidase 4 (| 6.7 |
| | 116115 | AL042355 | Hs.70202 | WD repeat domain 10 | 3.6 |
| | 116184 | AW450737 | Hs.128791 | CGI-09 protein | 3.1 |
| | 116192 | AA464976 | Hs.62528 | ESTs, Moderately similar to A46010 X-tin | 3.3 |
| | 116208 | AI219083 | Hs.42532 | ESTs, Moderately similar to ALU8_HUMAN A | 3.2 |
| 30 | 116246 | AF265555 | Hs.250646 | baculoviral IAP repeat-containing 6 | 3.6 |
| | 116443 | AW962196 | Hs.321264 | LBP protein 32 | 4.1 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 4.1 |
| | 116726 | AK001114 | Hs.53913 | hypothetical protein FLJ10252 | 8.6 |
| | 116845 | AA649530 | | gb:ns44k05.s1 NCI_CGAP_Alv1 Homo sapiens | 3.2 |
| 35 | 117026 | H88256 | Hs.50456 | ESTs, Moderately similar to ZN75_HUMAN Z | 3.5 |
| | 117216 | AI569804 | Hs.42792 | ESTs, Weakly similar to I78885 serine/th | 3.1 |
| | 117296 | AL133427 | Hs.42506 | Homo sapiens mRNA full length insert cDN | 3.2 |
| | 117403 | H84455 | Hs.40639 | ESTs | 4.7 |
| | 117691 | AB040959 | Hs.93836 | DKFZP434N014 protein | 3 |
| 40 | 118229 | AW968941 | Hs.166254 | hypothetical protein DKFZp566I133 | 3.3 |
| | 118363 | AI183838 | Hs.48938 | hypothetical protein FLJ21802 | 4.3 |
| | 118416 | N66028 | Hs.49105 | FKBP-associated protein | 3.1 |
| | 118470 | AW970584 | Hs.291033 | ESTs | 3.4 |
| | 118502 | AL157488 | Hs.50150 | Homo sapiens mRNA; cDNA DKFZp564B182 (fr | 5.2 |
| 45 | 118695 | AK000465 | Hs.50081 | KIAA1199 protein | 3.4 |
| | 118925 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN A | 3.3 |
| | 119025 | BE003760 | Hs.55209 | Homo sapiens mRNA; cDNA DKFZp434K0514 (f | 19.7 |
| | 119036 | R95872 | Hs.117572 | chemokine binding protein 2 | 3.7 |
| | 119063 | R16833 | Hs.53106 | ESTs, Moderately similar to ALU1_HUMAN A | 4.1 |
| 50 | 119075 | M10905 | Hs.287820 | fibronectin 1 | 3.2 |
| | 119620 | W47620 | Hs.56009 | 2'-5'-oligoadenylate synthetase 3 (100 k | 3.3 |
| | 119741 | AF041853 | Hs.43670 | kinesin family member 3A | 3.1 |
| | 119747 | AI970797 | Hs.64859 | ESTs | 5 |
| | 119754 | AL037824 | Hs.194695 | ras homolog gene family, member I | 3.8 |
| 55 | 119905 | AW449064 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 3.1 |
| | 120084 | W94472 | Hs.59529 | ESTs, Moderately similar to ALU1_HUMAN A | 8.4 |
| | 120241 | AA825686 | Hs.321176 | ESTs, Weakly similar to S65824 reverse t | 3.6 |
| | 120326 | AA196300 | Hs.21145 | hypothetical protein RG083M05.2 | 3.2 |
| | 120742 | AA225084 | | gb:nc21d06.r1 NCI_CGAP_Pr1 Homo sapiens | 3.6 |
| 60 | 120870 | AA357172 | Hs.292581 | ESTs, Moderately similar to ALU1_HUMAN A | 5.8 |
| | 120885 | AA365515 | Hs.301872 | hypothetical protein MGC4840 | 3 |
| | 120970 | AA398118 | Hs.97579 | ESTs, Weakly similar to A46010 X-linked | 3.7 |
| | 121054 | AW976570 | Hs.97387 | ESTs | 5.3 |
| | 121095 | AA320134 | Hs.196029 | Homo sapiens mRNA for KIAA1657 protein, | 4 |
| 65 | 121103 | AA398936 | Hs.97697 | EST | 3.5 |
| | 121121 | AA399371 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 6.3 |
| | 121337 | AW885727 | Hs.301570 | ESTs | 4.7 |

| | | | | | |
|----|--------|-----------|----------------------------|--|-----|
| | 121351 | AW206227 | Hs.287727 | hypothetical protein FLJ23132 | 5 |
| | 121611 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 3.6 |
| | 121643 | AA640987 | Hs.193767 | ESTs | 5.6 |
| | 121770 | NM_015902 | Hs.278428 | progesterone induced protein | 3.4 |
| 5 | 122125 | AK000492 | Hs.98806 | hypothetical protein | 4.1 |
| | 122338 | AA443311 | Hs.98998 | ESTs | 3 |
| | 122417 | AA446965 | Hs.112092 | ESTs | 4.7 |
| | 122513 | AI767879 | Hs.99214 | ESTs | 3.8 |
| | 122544 | AW973253 | Hs.292689 | ESTs | 3 |
| 10 | 122655 | AA323296 | Hs.97837 | Homo sapiens mRNA; cDNA DKFZp547J047 (fr | 5.6 |
| | 122805 | AA526911 | Hs.82772 | collagen, type XI, alpha 1 | 3.2 |
| | 122851 | AW205931 | Hs.99598 | hypothetical protein MGC5338 | 8.6 |
| | 123105 | AA487809 | Hs.166011 | catenin (cadherin-associated protein), d | 3 |
| | 123111 | AA228776 | Hs.191721 | ESTs | 6.9 |
| 15 | 123249 | AA371307 | Hs.125056 | ESTs | 3.6 |
| | 123273 | AA491253 | Hs.173611 | Empirically selected from AFFX single pr | 7 |
| | 123385 | BE149685 | Hs.17767 | KIAA1554 protein | 3.1 |
| | 123419 | T66087 | Hs.112482 | Homo sapiens unknown mRNA sequence | 3.4 |
| | 123485 | AI308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 3.1 |
| 20 | 123645 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 3.8 |
| | 123819 | AA580082 | Hs.112264 | ESTs | 4.7 |
| | 124012 | AA352723 | Hs.241471 | RNB6 | 3.8 |
| | 124243 | H69125 | Hs.133525 | ESTs | 4.1 |
| | 124357 | N22401 | gb:yw37g07.s1 | Morton Fetal Cochlea Homo | 4.1 |
| 25 | 124359 | N22508 | Hs.139315 | Homo sapiens cDNA: FLJ21479 fis, clone C | 3.6 |
| | 124567 | AW451645 | Hs.151504 | Homo sapiens cDNA FLJ11973 fis, clone HE | 3.1 |
| | 124911 | N34151 | Hs.174195 | interferon induced transmembrane protein | 3.5 |
| | 124972 | R41396 | Hs.101774 | hypothetical protein FLJ23045 | 4.3 |
| | 125006 | BE065136 | Hs.145696 | splicing factor (CC1.3) | 6 |
| 30 | 125042 | T78906 | Hs.269432 | ESTs, Moderately similar to ALU1_HUMAN A | 8.1 |
| | 125184 | W60326 | Hs.288684 | Homo sapiens cDNA FLJ11750 fis, clone HE | 4.7 |
| | 125243 | AW970536 | Hs.105413 | ESTs | 3.1 |
| | 125286 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 3.3 |
| | 125304 | AL359573 | Hs.124940 | GTP-binding protein | 3 |
| 35 | 125330 | AW880562 | Hs.114574 | ESTs | 3 |
| | 125331 | AI422996 | Hs.161378 | ESTs | 3.2 |
| | 125685 | AI924630 | Hs.4943 | hepatocellular carcinoma associated prot | 3.2 |
| | 126257 | N99638 | gb:za39g11.r1 | Soares fetal liver spleen | 4 |
| | 126474 | AW975814 | Hs.326714 | Homo sapiens clone IMAGE:713177, mRNA se | 4 |
| 40 | 126666 | AA648886 | Hs.151999 | ESTs | 3.8 |
| | 126872 | AW450979 | gb:UH-BI3-ala-a-12-0-UI.s1 | NCI_CGAP_Su | 3 |
| | 127431 | AW771958 | Hs.175437 | ESTs, Moderately similar to PC4259 femi | 3.6 |
| | 127980 | AA961459 | Hs.125644 | ESTs | 4.1 |
| | 127997 | AW068311 | Hs.311054 | Homo sapiens mRNA full length insert cDN | 3.3 |
| 45 | 128420 | AA650274 | Hs.41296 | fibronectin leucine rich transmembrane p | 4.6 |
| | 128609 | NM_003616 | Hs.102456 | survival of motor neuron protein Interac | 3.9 |
| | 128946 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | 3.1 |
| | 128955 | AA775076 | Hs.185807 | Homo sapiens, Similar to PRO0478 protein | 3.9 |
| | 129092 | D56365 | Hs.63525 | poly(rC)-binding protein 2 | 3.3 |
| 50 | 129270 | AA357185 | Hs.109918 | ras homolog gene family, member H | 3.1 |
| | 129301 | AF182277 | Hs.330780 | cytochrome P450, subfamily IIB (phenobar | 3.9 |
| | 129385 | AA172106 | Hs.110950 | Rag C protein | 6.2 |
| | 129619 | AA209534 | Hs.284243 | tetraspan NET-6 protein | 3.4 |
| | 129629 | AK000398 | Hs.11747 | hypothetical protein FLJ20391 | 3 |
| 55 | 129725 | X56411 | Hs.1219 | alcohol dehydrogenase 4 (class II), pi p | 3.2 |
| | 130069 | AI754813 | Hs.146428 | collagen, type V, alpha 1 | 5.4 |
| | 130092 | X03363 | Hs.323910 | v-erb-b2 avian erythroblastic leukemia v | 4.4 |
| | 130298 | AI347487 | Hs.132781 | class I cytokine receptor | 4.6 |
| | 130382 | NM_003450 | Hs.155204 | zinc finger protein 174 | 5.6 |
| 60 | 130622 | AI582291 | Hs.16846 | ESTs, Weakly similar to O4HUD1 debrisoku | 3 |
| | 130703 | R77776 | Hs.18103 | ESTs | 3.8 |
| | 130881 | AA809875 | Hs.25933 | ESTs | 4.2 |
| | 130954 | AB014544 | Hs.21572 | KIAA0644 gene product | 4.7 |
| | 131095 | AI399653 | Hs.22917 | ESTs | 4.3 |
| 65 | 131153 | H09048 | Hs.23606 | ESTs | 3.8 |
| | 131253 | R71802 | Hs.24853 | ESTs | 3.5 |
| | 131372 | AW293399 | Hs.144904 | nuclear receptor co-repressor 1 | 3.6 |

| | | | | | |
|----|--------|-----------|---|--|------|
| | 131507 | AI826268 | Hs.27769 | ESTs, Weakly similar to MCAT_HUMAN MITOC | 3.2 |
| | 131587 | AI695549 | Hs.183868 | glucuronidase, beta | 3.1 |
| | 131739 | AF017986 | Hs.31386 | secreted frizzled-related protein 2 | 3.2 |
| | 131795 | BE501849 | Hs.32317 | high-mobility group 20B | 3.2 |
| 5 | 131970 | D86960 | Hs.3610 | KIAA0205 gene product | 3.6 |
| | 131986 | NM_002314 | Hs.36566 | LIM domain kinase 1 | 3.2 |
| | 132093 | AA400091 | Hs.39421 | ESTs | 3.2 |
| | 132122 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 3 |
| | 132159 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 3.2 |
| 10 | 132333 | AA192669 | Hs.45032 | ESTs | 3.5 |
| | 132406 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (f | 9.2 |
| | 132482 | AV660345 | Hs.238126 | CGI-49 protein | 8.2 |
| | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 3.4 |
| | 132624 | AA326108 | Hs.33829 | bHLH protein DEC2 | 3.2 |
| 15 | 132700 | AA319233 | Hs.5521 | ESTs | 4.8 |
| | 132725 | NM_006276 | Hs.184167 | splicing factor, arginine/serine-rich 7 | 3.6 |
| | 132799 | W73311 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 3.2 |
| | 132847 | T48195 | Hs.58189 | eukaryotic translation initiation factor | 3.5 |
| | 132857 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 4.4 |
| 20 | 132936 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transl | 4.8 |
| | 133130 | AI128606 | Hs.6557 | zinc finger protein 161 | 3.3 |
| | 133142 | AW952412 | Hs.65874 | ESTs, Weakly similar to A40348 Elav/Sex- | 3.5 |
| | 133167 | AW162840 | Hs.6641 | kinesin family member 5C | 4.5 |
| | 133225 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 3.3 |
| 25 | 133274 | AA085191 | Hs.6949 | hypothetical protein MGC11275 | 3 |
| | 133275 | Z93241 | Hs.239934 | CGI-96 protein | 4.5 |
| | 133287 | AW797437 | Hs.69771 | B-factor, properdin | 4.1 |
| | 133376 | BE618768 | Hs.7232 | acetyl-Coenzyme A carboxylase alpha | 5.1 |
| | 133462 | AW675064 | Hs.73875 | fumarylacetoacetate hydrolase (fumarylac | 3 |
| 30 | 133740 | AW162919 | Hs.170160 | RAB2, member RAS oncogene family-like | 3.4 |
| | 133831 | BE274552 | Hs.76578 | protein inhibitor of activated STAT3 | 3.9 |
| | 133976 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 6.2 |
| | 134666 | BE391929 | Hs.8752 | transmembrane protein 4 | 3.1 |
| | 134710 | AI433797 | Hs.8889 | serine hydroxymethyltransferase 1 (solub | 3 |
| 35 | 134731 | D89377 | Hs.89404 | msh (Drosophila) homeo box homolog 2 | 5.8 |
| | 134776 | J05582 | Hs.89603 | mucin 1, transmembrane | 4 |
| | 135230 | AF064804 | Hs.96757 | suppressor of Ty (S.cerevisiae) 3 homolo | 3.2 |
| | 135303 | R61253 | Hs.98265 | KIAA1877 protein | 3.3 |
| | 135400 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 4.8 |
| 40 | 135411 | L10333 | Hs.99947 | reticulon 1 | 3.8 |
| | 300089 | AI199738 | Hs.208275 | ESTs, Weakly similar to ALUA_HUMAN !!!! | 3.8 |
| | 300233 | AW614220 | Hs.189402 | ESTs | 4.2 |
| | 300254 | AW183618 | Hs.55610 | solute carrier family 30 (zinc transport | 9.9 |
| | 300256 | AW591433 | Hs.298241 | Transmembrane protease, serine 3 | 4.9 |
| 45 | 300378 | Z45270 | Hs.235873 | hypothetical protein FLJ22672 | 3.4 |
| | 300973 | AA572949 | Hs.207566 | ESTs | 3.5 |
| | 301111 | R10799 | Hs.191990 | ESTs | 3.8 |
| | 301341 | AA887801 | Hs.208229 | G protein-coupled receptor | 13.9 |
| | 301548 | AI091631 | Hs.203845 | two pore potassium channel KT3.3 | 4.4 |
| 50 | 301884 | AA312082 | Hs.105445 | GDNF family receptor alpha 1 | 5.7 |
| | 301936 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | 8.6 |
| | 301976 | T97905 | gb:ye54c10.r1 Soares fetal liver spleen | | 3.9 |
| | 302001 | AB020711 | Hs.278346 | KIAA0904 protein | 7.7 |
| | 302067 | BE542706 | Hs.222399 | CEGP1 protein | 7.3 |
| 55 | 302094 | AW749321 | Hs.6786 | ESTs | 3.3 |
| | 302099 | AL049670 | Hs.137576 | ribosomal protein L34 pseudogene 1 | 4.2 |
| | 302145 | NM_003613 | Hs.151407 | cartilage intermediate layer protein, nu | 7.9 |
| | 302235 | AL049987 | Hs.166361 | Homo sapiens mRNA; cDNA DKFZp564F112 (fr | 5.6 |
| | 302276 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 5.4 |
| 60 | 302290 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 34.1 |
| | 302372 | AL117406 | Hs.200102 | ATP-binding cassette transporter MRP8 | 6.7 |
| | 302378 | AL109712 | Hs.296506 | Homo sapiens mRNA full length insert cDN | 4 |
| | 302384 | AI678059 | Hs.202676 | synaptonemal complex protein 2 | 4.3 |
| | 302385 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | 13.8 |
| 65 | 302680 | AW192334 | Hs.38218 | ESTs | 9.6 |
| | 302830 | AI038997 | Hs.132921 | ESTs | 5 |
| | 302857 | AF282265 | Hs.44836 | inner centromere protein antigens (135kD | 3.4 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 302892 | AW176909 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 3.4 |
| | 302970 | W05608 | Hs.312679 | ESTs, Weakly similar to A49019 dynein he | 5.1 |
| | 303271 | AA652687 | Hs.96151 | Human DNA sequence from clone RP5-1103G7 | 3.7 |
| | 303289 | AL121460 | Hs.272673 | hypothetical protein FLJ20508 | 4.1 |
| 5 | 303357 | AW006352 | Hs.159643 | ESTs, Weakly similar to T32554 hypotheti | 4.2 |
| | 303540 | AA355607 | Hs.309490 | ESTs, Weakly similar to putative WHSC1 p | 4.3 |
| | 303563 | AA367699 | Hs.10082 | potassium intermediate/small conductance | 3.3 |
| | 303642 | AW299459 | | gb:xs50d08.x1 NCI_CGAP_Kid11 Homo sapien | 4.2 |
| | 303780 | AI424014 | Hs.18995 | KIAA1304 protein | 3.6 |
| 10 | 303797 | AW629759 | | gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens | 4.9 |
| | 303852 | R53434 | Hs.90207 | hypothetical protein MGC11138 | 3.7 |
| | 304328 | AA149951 | Hs.62112 | zinc finger protein 207 | 3 |
| | 304782 | AA582081 | | gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapiens | 4.1 |
| | 305913 | AA876109 | | gb:nx24h01.s1 NCI_CGAP_GC3 Homo sapiens | 3 |
| 15 | 305917 | AA876469 | | gb:oe48b04.s1 NCI_CGAP_Pr25 Homo sapiens | 3.1 |
| | 307010 | AI140014 | | gb:qa68f09.x1 Soares_fetal_heart_NbHH19W | 3.5 |
| | 307041 | AI144243 | | gb:qb85b12.x1 Soares_fetal_heart_NbHH19W | 3.9 |
| | 308106 | AI476803 | | gb:ij77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S | 4.3 |
| | 308307 | AI581398 | Hs.172928 | collagen, type I, alpha 1 | 4.6 |
| 20 | 308615 | AK000142 | Hs.101774 | hypothetical protein FLJ23045 | 4.4 |
| | 309177 | AI951118 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 17.3 |
| | 309328 | AW024348 | Hs.233191 | EST, Weakly similar to A27217 glucose tr | 3.2 |
| | 309574 | AW168083 | | gb:xg59g04.x1 NCI_CGAP_Ut4 Homo sapiens | 3.1 |
| | 309583 | AW170035 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 57.6 |
| 25 | 310064 | AI199712 | Hs.148486 | ESTs, Weakly similar to 1917210A Pro/Arg | 4.6 |
| | 310098 | AI685841 | Hs.161354 | ESTs | 3.6 |
| | 310438 | AW022192 | Hs.200197 | ESTs | 4.6 |
| | 310683 | AI939456 | Hs.160870 | ESTs | 3.2 |
| | 310727 | AK000703 | Hs.323822 | Homo sapiens mRNA for KIAA1551 protein, | 3.6 |
| 30 | 310781 | AI380797 | Hs.158992 | ESTs | 10.2 |
| | 310895 | AI955121 | Hs.165724 | N-acetylgalactosamine-4-O-sulfotransfera | 3.4 |
| | 310955 | AI476732 | Hs.263912 | ESTs | 10.9 |
| | 311117 | AI671439 | Hs.196029 | Homo sapiens mRNA for KIAA1657 protein, | 3.1 |
| | 311166 | AI821005 | Hs.118599 | ESTs | 10.8 |
| 35 | 311237 | AA641098 | Hs.208809 | ESTs, Moderately similar to ALU1_HUMAN A | 4.3 |
| | 311465 | AI758660 | Hs.206132 | ESTs | 4.4 |
| | 311587 | AI828254 | Hs.271019 | ESTs, Weakly similar to A47582 B-cell gr | 5.1 |
| | 311598 | AW023595 | Hs.232048 | ESTs | 5.8 |
| | 311774 | AA700870 | Hs.14304 | ESTs | 3.3 |
| 40 | 311785 | AI056769 | Hs.133512 | ESTs | 3.9 |
| | 311872 | R12375 | Hs.194600 | ESTs | 3.3 |
| | 311889 | AA767342 | Hs.122483 | ESTs, Weakly similar to PSF_HUMAN PTB-AS | 3 |
| | 311913 | AI358522 | Hs.270188 | ESTs | 3 |
| | 311923 | T60843 | Hs.189679 | ESTs | 5.6 |
| 45 | 311935 | AA216387 | | gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sapiens | 5.2 |
| | 312019 | AA373630 | Hs.188750 | ESTs | 3 |
| | 312021 | AA759263 | Hs.14041 | ESTs | 3.4 |
| | 312067 | T78968 | Hs.14411 | ESTs | 3.5 |
| | 312090 | T80177 | Hs.118064 | similar to rat nuclear ubiquitous casein | 3.8 |
| 50 | 312147 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheti | 4.4 |
| | 312153 | BE261944 | Hs.118625 | hexokinase 1 | 5.2 |
| | 312168 | T92251 | Hs.198882 | ESTs | 3.3 |
| | 312182 | T94344 | Hs.326263 | ESTs | 3.3 |
| | 312187 | AA700439 | Hs.188490 | ESTs | 3.4 |
| 55 | 312199 | AW438602 | Hs.191179 | ESTs | 3.9 |
| | 312219 | H73505 | Hs.117874 | ESTs | 4 |
| | 312226 | AA315703 | Hs.199993 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 4.9 |
| | 312299 | AA972712 | Hs.269737 | ESTs | 5.7 |
| | 312544 | AA516420 | Hs.183526 | ESTs, Weakly similar to I38022 hypotheti | 6.3 |
| 60 | 312638 | AW439195 | Hs.256880 | ESTs, Weakly similar to S65657 alpha-1C- | 4.9 |
| | 312826 | AW291545 | Hs.185018 | ESTs | 4.9 |
| | 312837 | AW292286 | Hs.255058 | ESTs | 4.4 |
| | 312980 | AA497043 | Hs.115685 | ESTs | 3.1 |
| | 313070 | AI422023 | Hs.161338 | ESTs | 4.3 |
| 65 | 313079 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 3.3 |
| | 313089 | AF026944 | Hs.293797 | ESTs | 5.8 |
| | 313096 | AW073310 | Hs.163533 | Homo sapiens cDNA FLJ14142 fis, clone MA | 4.5 |

| | | | | | |
|----|--------|----------|--|--|------|
| | 313126 | AA746503 | Hs.283313 | ESTs | 10 |
| | 313166 | AI801098 | Hs.151500 | ESTs | 3.5 |
| | 313197 | AW979008 | Hs.222487 | ESTs | 3.3 |
| | 313280 | AW960454 | Hs.222830 | ESTs | 4.7 |
| 5 | 313325 | AI420611 | Hs.127832 | ESTs | 3.4 |
| | 313328 | AW449211 | Hs.105445 | GDNF family receptor alpha 1 | 12.4 |
| | 313352 | AW150945 | Hs.144758 | ESTs | 4.1 |
| | 313385 | AI032087 | Hs.269819 | ESTs | 3 |
| | 313393 | AI674685 | Hs.200141 | ESTs | 5.2 |
| 10 | 313417 | AA741151 | Hs.137323 | ESTs | 3.5 |
| | 313434 | W92070 | gb:zh48g05.r1 Soares_fetal_liver_spleen_ | | 3.7 |
| | 313569 | AI273419 | Hs.135146 | hypothetical protein FLJ13984 | 3 |
| | 313591 | AA046309 | gb:zf12f01.s1 Soares_fetal_heart_NbHH19W | | 5.6 |
| | 313615 | AI540978 | Hs.301997 | hypothetical protein FLJ13033 | 3.2 |
| 15 | 313915 | C18863 | Hs.163443 | Homo sapiens cDNA FLJ11576 fis, clone HE | 26.3 |
| | 313975 | AW175896 | Hs.65114 | keratin 18 | 3 |
| | 313979 | AI535895 | Hs.221024 | ESTs | 4.9 |
| | 313997 | AV657317 | Hs.288649 | hypothetical protein MGC3077 | 3.9 |
| | 314043 | AA827082 | Hs.291872 | ESTs | 3.1 |
| 20 | 314078 | AW129357 | Hs.329700 | ESTs | 8.3 |
| | 314097 | AA648744 | Hs.269493 | ESTs | 6.6 |
| | 314121 | AI732083 | Hs.187619 | ESTs | 6.2 |
| | 314129 | AA228366 | Hs.115122 | ESTs | 4 |
| | 314138 | AA740616 | gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens | | 5.9 |
| 25 | 314236 | AA743396 | Hs.189023 | ESTs | 3.1 |
| | 314244 | AL036450 | Hs.103238 | ESTs | 4 |
| | 314305 | AI280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fis, clone OV | 8 |
| | 314306 | AI697901 | Hs.192425 | ESTs | 3.7 |
| | 314322 | AA907153 | Hs.190060 | ESTs | 3.3 |
| 30 | 314394 | AW961597 | Hs.130816 | ESTs, Moderately similar to I38022 hypot | 4.2 |
| | 314401 | AI660412 | Hs.234557 | ESTs | 3.3 |
| | 314465 | AA602917 | Hs.156974 | ESTs | 4.7 |
| | 314506 | AA833655 | Hs.206868 | Homo sapiens cDNA FLJ14056 fis, clone HE | 8.5 |
| | 314510 | AI204418 | Hs.190080 | ESTs | 4 |
| 35 | 314546 | AW007211 | Hs.16131 | hypothetical protein FLJ12876 | 3.4 |
| | 314547 | AA399272 | Hs.144341 | ESTs | 6.7 |
| | 314558 | AI873274 | Hs.190721 | ESTs | 27.4 |
| | 314627 | AA425310 | Hs.155766 | ESTs, Weakly similar to A47582 B-cell gr | 4.4 |
| | 314648 | AW979268 | gb:EST391378 MAGE resequences, MAGP Homo | | 4.6 |
| 40 | 314691 | AW207206 | Hs.136319 | ESTs | 20.7 |
| | 314729 | AA457367 | Hs.191638 | ESTs | 3.6 |
| | 314754 | AW026761 | Hs.134374 | ESTs | 3.6 |
| | 314814 | BE350122 | Hs.157367 | ESTs, Weakly similar to I78885 serine/th | 4.9 |
| | 314864 | AW971198 | Hs.294068 | ESTs | 4.3 |
| 45 | 314881 | AI095087 | Hs.152299 | ESTs, Moderately similar to S65657 alpha | 3.7 |
| | 314882 | AA828032 | Hs.189076 | ESTs | 3.1 |
| | 314981 | AW972359 | Hs.293334 | ESTs | 3 |
| | 315006 | AI538613 | Hs.298241 | Transmembrane protease, serine 3 | 10.9 |
| | 315021 | AA533447 | Hs.312989 | ESTs | 5.3 |
| 50 | 315051 | AW292425 | Hs.163484 | ESTs | 12.9 |
| | 315060 | AA551104 | Hs.189048 | ESTs, Moderately similar to ALUC_HUMAN I | 5.8 |
| | 315073 | AW452948 | Hs.257631 | ESTs | 4.2 |
| | 315080 | AA744550 | Hs.136345 | ESTs | 3.7 |
| | 315175 | AI025842 | Hs.152530 | ESTs | 6 |
| 55 | 315183 | AW136134 | Hs.220277 | ESTs | 3.9 |
| | 315193 | AI241331 | Hs.131765 | ESTs, Moderately similar to I38937 DNA/R | 4.4 |
| | 315196 | AI367347 | Hs.44898 | Homo sapiens clone TCCCTA00151 mRNA sequ | 8.2 |
| | 315198 | AI741506 | Hs.165900 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 |
| | 315240 | R38772 | Hs.172619 | myelin transcription factor 1-like | 3.4 |
| 60 | 315263 | AW510994 | Hs.220740 | ESTs | 3.4 |
| | 315282 | AI222165 | Hs.144923 | ESTs | 4.9 |
| | 315296 | AA876905 | Hs.125286 | ESTs | 4 |
| | 315368 | AB037745 | Hs.104696 | KIAA1324 protein | 4.7 |
| | 315397 | AA218940 | Hs.137516 | fidgetin-like 1 | 3.1 |
| 65 | 315489 | AI378817 | Hs.191847 | ESTs | 3.1 |
| | 315498 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 3.2 |
| | 315526 | AI193043 | Hs.128685 | ESTs, Weakly similar to T17226 hypotheti | 4.1 |

| | | | | | |
|----|--------|-----------|--|--|------|
| | 315530 | AW015415 | Hs.127780 | ESTs | 8.9 |
| | 315562 | AA737415 | Hs.152826 | ESTs | 5.5 |
| | 315634 | AA837085 | Hs.220585 | ESTs | 6.3 |
| | 315647 | AA648983 | Hs.212911 | ESTs | 3.6 |
| 5 | 315707 | AI418055 | Hs.161160 | ESTs | 5.1 |
| | 315772 | AW515373 | Hs.271249 | Homo sapiens cDNA FLJ13580 fis, clone PL | 3.1 |
| | 315850 | AW270550 | Hs.116957 | ESTs | 3.8 |
| | 315858 | AA737345 | Hs.294041 | ESTs | 5 |
| | 315878 | AA683336 | Hs.189046 | ESTs | 3.1 |
| 10 | 315977 | AW865916 | Hs.151206 | ESTs | 4.7 |
| | 315978 | AA830893 | Hs.119769 | ESTs | 4.1 |
| | 315995 | AI217477 | Hs.194591 | ESTs | 4.1 |
| | 316012 | AA764950 | Hs.119898 | ESTs | 7 |
| | 316042 | AI469960 | Hs.170698 | ESTs | 4.9 |
| 15 | 316052 | AI962796 | Hs.136754 | ESTs | 4.1 |
| | 316072 | AW517524 | Hs.135201 | NOD2 protein | 3.2 |
| | 316074 | AW975114 | Hs.293273 | ESTs | 3.8 |
| | 316100 | AW203986 | Hs.213003 | ESTs | 3.2 |
| | 316133 | AI187742 | Hs.125562 | ESTs | 3.7 |
| 20 | 316177 | AI904982 | Hs.293102 | ESTs, Moderately similar to ALU1_HUMAN A | 30.7 |
| | 316186 | AI433540 | gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien | | 3.1 |
| | 316244 | AI640761 | Hs.224988 | ESTs | 3.5 |
| | 316303 | AA740994 | Hs.209609 | ESTs | 3.8 |
| | 316313 | AA741300 | Hs.202599 | ESTs, Weakly similar to I38022 hypotheti | 4.4 |
| 25 | 316364 | AA747807 | Hs.149500 | ESTs | 3.2 |
| | 316580 | AA938198 | Hs.146123 | poly(A) polymerase gamma | 9.4 |
| | 316697 | AW293174 | Hs.252627 | ESTs | 4.4 |
| | 316715 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypotheti | 3 |
| | 316868 | AI660898 | Hs.195602 | ESTs | 3.2 |
| 30 | 316869 | AI954880 | Hs.134604 | ESTs | 3.2 |
| | 316886 | AA836331 | Hs.134981 | ESTs | 4.4 |
| | 316897 | AA838114 | Hs.221612 | ESTs | 3.7 |
| | 316943 | AW014875 | Hs.137007 | ESTs | 4.6 |
| | 317069 | AI732892 | Hs.190489 | ESTs | 5.9 |
| 35 | 317194 | AW445167 | Hs.126036 | ESTs | 4.1 |
| | 317360 | AI125252 | Hs.126419 | ESTs | 3.5 |
| | 317404 | AI806867 | Hs.126594 | ESTs | 5.1 |
| | 317452 | AA972965 | Hs.135568 | ESTs | 6.9 |
| | 317501 | AI822034 | Hs.137097 | ESTs | 4.6 |
| 40 | 317674 | AW294909 | Hs.132208 | ESTs | 4.3 |
| | 317803 | AW664964 | Hs.128899 | ESTs | 6.1 |
| | 317834 | X56348 | Hs.287270 | ret proto-oncogene (multiple endocrine n | 3.1 |
| | 317850 | AI681545 | Hs.152982 | hypothetical protein FLJ13117 | 3.4 |
| | 317881 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fis, clone HE | 9.6 |
| 45 | 317902 | AW102941 | Hs.211265 | ESTs | 4.1 |
| | 317916 | AI565071 | Hs.159983 | ESTs | 10.3 |
| | 318042 | AW294522 | Hs.149991 | ESTs | 3.1 |
| | 318223 | AI077540 | Hs.134090 | ESTs | 3.9 |
| | 318327 | AW294013 | Hs.200942 | ESTs | 3 |
| 50 | 318332 | AI093930 | Hs.163440 | Homo sapiens cDNA: FLJ21000 fis, clone C | 4.4 |
| | 318418 | AF107493 | Hs.118498 | Homo sapiens LUCA-15 protein mRNA, splic | 5.4 |
| | 318558 | AW402677 | Hs.146381 | RNA binding motif protein, X chromosome | 4.4 |
| | 318625 | AA526235 | Hs.193162 | Homo sapiens cDNA FLJ11983 fis, clone HE | 5.9 |
| | 318634 | T49598 | Hs.156832 | ESTs | 4 |
| 55 | 318740 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 7.3 |
| | 318744 | AI793124 | Hs.144479 | ESTs | 17.8 |
| | 318781 | F11802 | Hs.6818 | ESTs | 3 |
| | 319191 | NM_012391 | Hs.79414 | prostate epithelium-specific Ets transcr | 3.6 |
| | 319478 | AI524124 | Hs.270307 | ESTs | 4.6 |
| 60 | 319510 | W88532 | Hs.254562 | ESTs | 3.3 |
| | 319551 | AA761668 | gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens | | 3.2 |
| | 319745 | T79366 | Hs.108258 | actin binding protein; macrophin (microf | 3.3 |
| | 319834 | AA071267 | gb:zm61g01.r1 Stratagene fibroblast (937 | | 6.2 |
| | 319840 | C19035 | Hs.164259 | ESTs | 3.3 |
| 65 | 319977 | AA534222 | gb:nj21d02.s1 NCL_CGAP_AA1 Homo sapiens | | 4.3 |
| | 320074 | AA321166 | Hs.278233 | ESTs | 3.4 |
| | 320167 | AA984373 | Hs.90790 | Homo sapiens cDNA: FLJ22930 fis, clone K | 4.1 |

| | | | | | |
|----|--------|----------|---|--|------|
| | 320187 | T99949 | Hs.303428 | Homo sapiens cDNA FLJ14832 fis, clone OV | 5.3 |
| | 320211 | AL039402 | Hs.125783 | DEME-6 protein | 9.2 |
| | 320416 | AI026984 | Hs.293662 | ESTs | 3.1 |
| 5 | 320588 | U78082 | Hs.167738 | RNA polymerase II transcriptional regula | 3.1 |
| | 320635 | N50617 | Hs.80506 | small nuclear ribonucleoprotein polypept | 6.1 |
| | 320654 | AI160015 | Hs.118112 | ESTs | 3.5 |
| | 320742 | AI601188 | Hs.120910 | ESTs | 3 |
| | 320832 | AA214584 | Hs.290167 | ESTs | 3.7 |
| 10 | 320915 | AI359144 | Hs.143688 | Homo sapiens cDNA: FLJ23031 fis, clone L | 3.1 |
| | 321016 | BE144167 | Hs.49994 | hypothetical protein similar to RNA-bind | 3.3 |
| | 321107 | AI732643 | Hs.144151 | ESTs | 12.3 |
| | 321171 | AI769410 | Hs.221461 | ESTs | 3.3 |
| | 321253 | AA610649 | Hs.333239 | ESTs | 3 |
| 15 | 321318 | AB033041 | Hs.137507 | vang (van gogh, Drosophila)-like 2 | 3.9 |
| | 321642 | AI432199 | Hs.247084 | ESTs | 3 |
| | 321644 | AW975944 | Hs.237396 | ESTs | 11.7 |
| | 321683 | AI471598 | Hs.197531 | ESTs | 3.8 |
| | 321758 | U29112 | Hs.196151 | ESTs | 4.4 |
| 20 | 321811 | D80630 | gb:HUM091D02B Human fetal brain (TFuji)wa | 3.2 | |
| | 321828 | R59890 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 3.1 |
| | 321910 | H67065 | Hs.271530 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 4.7 |
| | 321937 | AL049351 | Hs.302058 | Homo sapiens mRNA; cDNA DKFZp566C093 (fr | 3.5 |
| | 321978 | N77342 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 5 |
| 25 | 322035 | AL137517 | Hs.334473 | hypothetical protein DKFZp564O1278 | 19 |
| | 322136 | AF075083 | gb:Homo sapiens full length insert cDNA | 3.6 | |
| | 322258 | BE265745 | Hs.194359 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3 |
| | 322296 | W76326 | gb:zd60d04.r1 Soares_fetal_heart_NBHH19W | 4.4 | |
| | 322303 | AI357412 | Hs.157601 | ESTs | 11.5 |
| 30 | 322476 | AW963372 | Hs.46677 | PRO2000 protein | 3 |
| | 322520 | T55958 | gb:yb35f05.r1 Stratagene fetal spleen (9 | 3 | |
| | 322521 | AF147347 | gb:Homo sapiens full length insert cDNA | 4.2 | |
| | 322567 | AF155108 | Hs.256150 | Homo sapiens, Similar to RIKEN cDNA 2810 | 4 |
| | 322595 | W92147 | Hs.118394 | ESTs | 5.4 |
| 35 | 322675 | AA017656 | gb:ze39h01.r1 Soares retina N2b4HR Homo | 3.1 | |
| | 322766 | AW068805 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.2 |
| | 322818 | AW043782 | Hs.293616 | ESTs | 7.6 |
| | 322882 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 5.9 |
| | 322975 | C16391 | gb:C16391 Clontech human aorta polyA mRNA | 16.5 | |
| 40 | 323091 | AI902456 | Hs.210761 | ESTs, Weakly similar to I38022 hypotheti | 4 |
| | 323131 | AK002088 | Hs.270124 | Homo sapiens cDNA FLJ11226 fis, clone PL | 3.3 |
| | 323168 | AL120862 | Hs.124165 | programmed cell death 9 (PDCD9) | 6.3 |
| | 323244 | AW675572 | Hs.193620 | ESTs | 4.6 |
| | 323262 | AL133990 | Hs.190642 | ESTs | 10.5 |
| 45 | 323332 | AI829520 | gb:w19c06.x1 NCI_CGAP_Ut1 Homo sapiens | 6.2 | |
| | 323333 | AV651680 | Hs.208558 | ESTs | 4.3 |
| | 323335 | AI655499 | Hs.161712 | ESTs | 9.2 |
| | 323645 | AW445014 | Hs.197746 | ESTs | 3.1 |
| | 323663 | BE081058 | Hs.243023 | ESTs | 4 |
| 50 | 323693 | AA317962 | Hs.249721 | ESTs, Moderately similar to PC4259 femi | 3 |
| | 323782 | AW961560 | Hs.97600 | ESTs | 3.2 |
| | 323817 | AA410943 | BMP-R1B | 8.4 | |
| | 323930 | AL043683 | Hs.8173 | hypothetical protein FLJ10803 | 3.3 |
| | 323974 | AI825204 | Hs.211408 | ESTs | 4.5 |
| 55 | 324001 | AL044949 | Hs.116298 | ESTs | 4.5 |
| | 324036 | AI472078 | Hs.303662 | ESTs | 8.4 |
| | 324261 | BE069341 | gb:QV3-BT0381-270100-073-c08 BT0381 Homo | 49.4 | |
| | 324285 | AA431159 | Hs.122954 | ESTs | 3 |
| | 324296 | AI524039 | Hs.192524 | ESTs | 3 |
| 60 | 324305 | AA642007 | Hs.116369 | ESTs | 3.3 |
| | 324432 | AA464510 | Hs.152812 | ESTs | 16.5 |
| | 324585 | AI823969 | Hs.132678 | ESTs | 3.3 |
| | 324598 | AW972227 | Hs.163986 | Homo sapiens cDNA: FLJ22765 fis, clone K | 5 |
| | 324603 | AW993522 | Hs.292934 | ESTs | 10.4 |
| | 324631 | AA937116 | Hs.293683 | ESTs, Weakly similar to I54374 gene NF2 | 3.3 |
| 65 | 324716 | BE169746 | Hs.12504 | likely ortholog of mouse Arkadia | 3.2 |
| | 324748 | AW974941 | Hs.292385 | ESTs, Weakly similar to I78885 serine/th | 3 |
| | 324771 | AA631739 | Hs.335440 | EST | 3 |

| | | | | | | |
|----|--------|---------------|-----------|--|------|--|
| | 324774 | AI031771 | Hs.132586 | ESTs | 4.2 | |
| | 324823 | AW516704 | Hs.208726 | ESTs | 3.4 | |
| | 324824 | AI826999 | Hs.224624 | ESTs | 3.1 | |
| | 324826 | AA704806 | Hs.143842 | ESTs, Weakly similar to 2004399A chromos | 4.4 | |
| 5 | 324961 | AA613792 | | gb:nc97h03.s1 NCL_CGAP_Pr2 Homo sapiens | 3.9 | |
| | 324987 | AI375572 | Hs.172634 | ESTs | 18.8 | |
| | 324994 | AI805416 | Hs.213897 | ESTs | 3.3 | |
| | 325146 | AI064690 | Hs.171176 | ESTs | 4.2 | |
| | 325372 | | | Phase 2 & 3 Exons | 4.4 | |
| 10 | 325544 | | | Phase 2 & 3 Exons | 5.7 | |
| | 327075 | | | Phase 2 & 3 Exons | 3.8 | |
| | 332798 | | | C22000007.gij12314195 emb CAB99338.1 (A | 4.3 | |
| | 334223 | | | NM_005080*:Homo sapiens X-box binding pr | 26.2 | |
| | 334447 | | | NM_012429*:Homo sapiens SEC14 (S. cerevi | 3.9 | |
| 15 | 335809 | | | NM_014509*:Homo sapiens kraken-like (BK1 | 10.1 | |
| | 335824 | | | ENSP00000249072*:DJ222E13.1 (N-TERMINAL | 20 | |
| | 338255 | | | NM_014323*:Homo sapiens zinc finger prot | 9 | |
| | 409430 | R21945 | Hs.166975 | splicing factor, arginine/serine-rich 5 | 4 | |
| | 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to I38022 hypot | 4.6 | |
| 20 | 432558 | R97268 | Hs.177269 | ESTs | 3.2 | |
| | 436808 | AA731602 | Hs.120266 | ESTs | 3.9 | |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 4.1 | |
| | 453542 | AW836724 | Hs.339660 | Homo sapiens mRNA expressed only in plac | 3.7 | |
| | | M97935 | | AFFX control: STAT1 | 3.2 | |
| 25 | | M97935 | | AFFX control: STAT1 | 3 | |
| | | M55150 | | fumarylacetoacetate | 3 | |
| | | M13755 | | interferon stimulated protein; 15 kDa | 4.5 | |
| | | AI052047 | | ESTs | 6.7 | |
| | | AA252033 | | ESTs; Weakly similar to I!!! ALU SUBFAMILY J | 3.2 | |
| 30 | | AA401739 | | ESTs | 3.3 | |
| | | H18459 | | hepatocellular carcinoma associated protein; | 3 | |
| | | R48744 | | ESTs | 4.2 | |
| | | M31682 | | inhibin; beta B (activin AB beta polypeptide) | 3 | |
| | | AA416873 | | ESTs | 3 | |
| 35 | | D80240 | | HUM5G11A Human fetal brain (TFujitwara) Homo | 4 | |
| | | R49590 | | ESTs | 3.2 | |
| | | | | CH22_FGENES.678_5 | 16.8 | |
| | | | | CH22_FGENES.619_7 | 12.9 | |
| | | | | CH22_FGENES.619_12 | 11.3 | |
| 40 | | | | CH22_EM:AC005500.GENSCAN.127 9 | 9.2 | |
| | | | | CH22_EM:AC005500.GENSCAN.304 2 | 8.5 | |
| | | | | CH22_FGENES.271_8 | 8.4 | |
| | | | | CH22_FGENES.619_13 | 8 | |
| | | | | CH22_FGENES.271_7 | 7.3 | |
| 45 | | | | CH22_FGENES.617_7 | 7.2 | |
| | | | | CH.07_hs gjl6004473 | 7.1 | |
| | | | | CH22_FGENES.264_1 | 6.8 | |
| | | X03363 | | HER2 receptor tyrosine kinase (c erbB 2; ERBB2; neu) | 6.6 | |
| | | | | CH22_FGENES.617_9 | 6.5 | |
| 50 | | | | CH.07_hs gjl5868264 | 5.8 | |
| | | | | CH.19_hs gjl5867439 | 5.7 | |
| | | | | CH22_FGENES.6 3 | 5.3 | |
| | | | | CH.17_hs gjl5867230 | 5.1 | |
| | | | | CH.20_hs gjl6552458 | 5.1 | |
| 55 | | | | CH22_EM:AC005500.GENSCAN.148 22 | 4.7 | |
| | | | | CH22_FGENES.669_10 | 4.6 | |
| | | AA034918 | | KIAA1028 protein | 4.6 | |
| | | | | CH22_FGENES.48_12 | 4.5 | |
| | | | | CH22_FGENES.118_2 | 4.5 | |
| 60 | | AF049569 | | ESTs | 4.4 | |
| | | M13955 | | multiple UniGene matches | 4.3 | |
| | | | | CH22_FGENES.619_8 | 4.3 | |
| | | | | CH22_FGENES.13 7 | 4.3 | |
| | | HG4126 HT4396 | | Zinc Finger Protein Hzf4 | 4.3 | |
| 65 | | | | CH22_FGENES.360_3 | 4.3 | |
| | | | | CH22_FGENES.706_9 | 4.3 | |
| | | | | CH.21_hs gjl6531965 | 4.2 | |

| | | | | |
|----|---------------|---|---|-----|
| | | CH.17_hs gij5867215 | 4.1 | |
| | | CH22_FGENES.669_8 | 4.1 | |
| | HG2614 HT2710 | | Collagen, Type VIII, Alpha 1 | 4.1 |
| 5 | X83535 | CH22_FGENES.48_18 | 4.1 | |
| | | matrix metalloproteinase 14 (membrane inserted) | 4 | |
| | | CH22_FGENES.271_6 | 3.9 | |
| | | CH22_FGENES.617_3 | 3.9 | |
| | | CH22_FGENES.290_8 | 3.8 | |
| 10 | HG4716 HT5158 | | Guanosine 5' Monophosphate Synthase | 3.8 |
| | | CH22_FGENES.13_5 | 3.8 | |
| | | CH22_FGENES.13_2 | 3.8 | |
| | | CH.14_hs gij6682474 | 3.8 | |
| | | CH.02_hs gij5867750 | 3.8 | |
| 15 | HG4677 HT5102 | CH22_FGENES.617_8 | 3.7 | |
| | | Oncogene Ret/Ptc2, Fusion Activated | 3.7 | |
| | | CH22_DJ32110.GENSCAN.23_39 | 3.7 | |
| | | CH22_FGENES.543_20 | 3.7 | |
| | | CH22_EM:AC005500.GENSCAN.96_1 | 3.7 | |
| 20 | | CH22_FGENES.204_2 | 3.5 | |
| | | CH22_FGENES.619_4 | 3.5 | |
| | | CH.16_hs gij5867087 | 3.5 | |
| | AA714311 | EST cluster (not in UniGene) | 3.4 | |
| | | CH22_EM:AC005500.GENSCAN.149_9 | 3.4 | |
| 25 | | CH22_EM:AC005500.GENSCAN.421_5 | 3.4 | |
| | | CH22_FGENES.13_4 | 3.3 | |
| | | CH.07_hs gij6004478 | 3.3 | |
| | | CH22_FGENES.360_1 | 3.3 | |
| | HG2465 HT4871 | | Dna Binding Protein Ap 2, Alt. Splice 3 | 3.3 |
| 30 | | CH22_FGENES.6_2 | 3.3 | |
| | | CH22_C20H12.GENSCAN.16_2 | 3.2 | |
| | | CH22_C65E1.GENSCAN.8_1 | 3.2 | |
| | AA707750 | ESTs; Weakly similar to cis Golgi matrix | 3.1 | |
| | | CH22_FGENES.307_4 | 3.1 | |
| 35 | | CH22_EM:AC005500.GENSCAN.248_14 | 3.1 | |
| | | CH.06_hs gij5902482 | 3.1 | |
| | | CH22_FGENES.669_5 | 3.1 | |
| | | CH22_DJ32110.GENSCAN.19_8 | 3.1 | |
| | | CH22_FGENES.527_6 | 3.1 | |
| 40 | | CH22_FGENES.330_10 | 3.1 | |
| | | CH22_FGENES.14_2 | 3.1 | |
| | AA976074 | ESTs | 3 | |
| | | CH22_FGENES.226_7 | 3 | |
| | | CH22_FGENES.13_3 | 3 | |
| 45 | | CH22_EM:AC005500.GENSCAN.209_12 | 3 | |
| | | CH22_FGENES.271_3 | 3 | |

TABLE 17A

Table 17A shows the accession numbers for those pkeys lacking unigeneID's for Table 17. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|----------------|---|
| 116845 | 393481_1 | AA649530 AA659316 H64973 |
| 103207 | 30635_4 | X72790 |
| 126257 | 182217_1 | N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815 |
| 102791 | 37186_1 | AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 |
| | | AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 |
| | | N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833 |
| | | AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 |
| | | AI652535 BE465762 AA206331 AW451866 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 |
| | | AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 |
| | | AA348354 AI493192 |
| 126872 | 142696_1 | AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 |
| | | BE011367 BE011368 BE011362 BE011215 BE011365 BE011363 |
| 112631 | 1746257_1 | R82040 R70934 |
| 120742 | 176835_1 | AA225084 AA302713 |
| 106864 | 324239_1 | AI311928 AA936030 T51931 AA609816 AA487195 AA664207 |
| 109700 | genbank_F09609 | F09609 |
| 111532 | genbank_R08440 | R08440 |
| 113938 | genbank_W81598 | W81598 |
| 113947 | genbank_W84768 | W84768 |
| 124357 | genbank_N22401 | N22401 |
| 108733 | 504187_1 | AA121022 AA126422 |
| 112303 | genbank_R54797 | R54797 |
| 322136 | 46802_1 | AF075083 H52291 H52528 |
| 322296 | 47334_1 | W76326 AF086341 W72300 |
| 321811 | 1527481_1 | D80630 D80896 D80895 |
| 314648 | 293660_1 | AW979268 AA878419 AA431342 AA431628 |
| 322520 | 38916_1 | T55958 T57205 AF147346 |
| 322521 | 38917_1 | AF147347 T55426 T55503 |
| 322675 | 86787_1 | AA017656 AA017374 AA019761 |
| 323332 | 179142_1 | AI829520 AI791832 AA228414 AI791823 AA229211 AA229315 |
| 316186 | 425440_1 | AI433540 AA728984 AA804981 |
| 322975 | 1510563_1 | C16391 C16413 |
| 324261 | 273265_1 | BE069341 AW748403 AL044891 AI908240 AA393080 |
| 323817 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| 301976 | 128835_1 | T97905 AA101672 |
| 324961 | 376239_1 | AA613792 AW182329 T05304 AW858385 |
| 303642 | 284260_1 | AW299459 AA417112 |
| 303797 | 386364_1 | AW629759 AW749955 AA633408 AI651005 |
| 319551 | 357371_1 | AA761668 AA573621 R92814 R09670 |
| 311935 | 174129_1 | AA216387 T63548 AA228676 |
| 319834 | 112523_1 | AA071267 T65940 T64515 AA071334 |
| 319977 | 345248_1 | AA534222 AA632632 T81234 |
| 314138 | 179960_1 | AA740616 AA654854 AA229923 |
| 313591 | 103087_1 | AA046309 AI263500 AA046397 |

308106 AI476803
338255 CH22_6856FG_LINK_EM:AC00
335809 CH22_3181FG_617_6_LINK_EM
335824 CH22_3197FG_619_11_LINK_E
5 307010 AI140014
307041 AI144243
305913 AA876109
305917 AA876469
309574 AW168083
10 325372 c12_hs
325544 c12_hs
332798 CH22_14FG_6_5_LINK_C4G1.G
334223 CH22_1507FG_360_4_LINK_EM
327075 c21_hs
15 334447 CH22_1746FG_387_7_LINK_EM
304782 AA582081
313434 441798_1 W92070 AW019952 W92053

TABLE 17B

5 **Table 17B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 17. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

| Pkey | Ref | Strand | Nt_position |
|-----------|-------------------|--------|-------------------|
| 334447 | Dunham, I. et.al. | Plus | 14308764-14308824 |
| 335809 | Dunham, I. et.al. | Plus | 26310772-26310909 |
| 20 335824 | Dunham, I. et.al. | Plus | 26376860-26376942 |
| 332798 | Dunham, I. et.al. | Minus | 232147-231974 |
| 334223 | Dunham, I. et.al. | Minus | 12734365-12734269 |
| 338255 | Dunham, I. et.al. | Minus | 15242294-15242231 |
| 325372 | 5866920 | Minus | 1117061-1117304 |
| 25 325544 | 6682452 | Plus | 171228-171286 |
| 327075 | 6531965 | Plus | 4041318-4041431 |

TABLE 18: Table 2 from BRCA 014 P

Table 18 shows genes with atleast five times the expression in breast tumor tissue than is expressed in normal body tissues.

| | | | | | |
|----|----------------|---|-----------|--|------|
| | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| 10 | UnigenelD: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal body tissue | | | |
| 15 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 101378 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 5.3 |
| | 101530 | M29874 | Hs.1360 | cytochrome P450, subfamily IIB (phenobar | 9 |
| | 101767 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 12 |
| 20 | 101878 | M97815 | Hs.183650 | cellular retinoic acid-binding protein 2 | 6.5 |
| | 103010 | X52509 | Hs.161640 | tyrosine aminotransferase | 12.4 |
| | 104115 | AF183810 | Hs.26102 | opposite strand to trichorhinophalangeal | 7.6 |
| | 104825 | AA035613 | Hs.141883 | ESTs | 6.9 |
| | 107105 | AW963419 | Hs.155223 | stannocalcin 2 | 5.3 |
| 25 | 108819 | AA011449 | Hs.271627 | ESTs | 6.1 |
| | 112287 | AB033064 | Hs.334806 | KIAA1238 protein | 7.3 |
| | 112561 | A1791493 | Hs.129873 | ESTs, Weakly similar to A36036 cytochrom | 8.2 |
| | 112637 | R82331 | Hs.164599 | ESTs | 5.4 |
| | 113206 | BE262470 | Hs.241471 | RNB6 | 6.2 |
| 30 | 113970 | W27249 | Hs.8109 | hypothetical protein FLJ21080 | 6.9 |
| | 114965 | A1733881 | Hs.72472 | BMP-R1B | 10.1 |
| | 118925 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN A | 19.7 |
| | 119905 | AW449064 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 8.4 |
| 35 | 121611 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 5.6 |
| | 129301 | AF182277 | Hs.330780 | cytochrome P450, subfamily IIB (phenobar | 6.2 |
| | 133976 | A1908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 6.2 |
| | 134731 | D89377 | Hs.89404 | msh (Drosophila) homeo box homolog 2 | 5.8 |
| | 300254 | AW183618 | Hs.55610 | solute carrier family 30 (zinc transport | 9.9 |
| 40 | 301884 | AA312082 | Hs.105445 | GDNF family receptor alpha 1 | 5.7 |
| | 302001 | AB020711 | Hs.278346 | KIAA0904 protein | 7.7 |
| | 302067 | BE542706 | Hs.222399 | CEGP1 protein | 7.3 |
| | 302276 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 5.4 |
| | 302290 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f34.1 | 6.7 |
| 45 | 302372 | AL117406 | Hs.200102 | ATP-binding cassette transporter MRP8 | 6.7 |
| | 302385 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | 13.8 |
| | 309177 | A1951118 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 17.3 |
| | 309583 | AW170035 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 57.6 |
| | 310781 | A1380797 | Hs.158992 | ESTs | 10.2 |
| | 311166 | A1821005 | Hs.118599 | ESTs | 10.8 |
| 50 | 311935 | AA216387 | | gb:nc16b02.s1 NCL_CGAP_Pr1 Homo sapiens | 5.2 |
| | 312153 | BE261944 | Hs.118625 | hexokinase 1 | 5.2 |
| | 313328 | AW449211 | Hs.105445 | GDNF family receptor alpha 1 | 12.4 |
| | 313915 | C18863 | Hs.163443 | Homo sapiens cDNA FLJ11576 fis, clone HE | 26.3 |
| | 314097 | AA648744 | Hs.269493 | ESTs | 6.6 |
| 55 | 314138 | AA740616 | | gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens | 5.9 |
| | 314506 | AA833655 | Hs.206868 | Homo sapiens cDNA FLJ14056 fis, clone HE | 8.5 |
| | 314558 | A1873274 | Hs.190721 | ESTs | 27.4 |
| | 314691 | AW207206 | Hs.136319 | ESTs | 20.7 |
| | 315006 | A1538613 | Hs.298241 | Transmembrane protease, serine 3 | 10.9 |
| 60 | 315021 | AA533447 | Hs.312989 | ESTs | 5.3 |
| | 315051 | AW292425 | Hs.163484 | ESTs | 12.9 |
| | 315060 | AA551104 | Hs.189048 | ESTs, Moderately similar to ALUC_HUMAN I | 5.8 |

| | | | | | | |
|----|----------|-----------|-----------|---|------|--|
| | 315196 | AI367347 | Hs.44898 | Homo sapiens clone TCCCTA00151 mRNA sequ | 8.2 | |
| | 315530 | AW015415 | Hs.127780 | ESTs | 8.9 | |
| | 315634 | AA837085 | Hs.220585 | ESTs | 6.3 | |
| 5 | 316012 | AA764950 | Hs.119898 | ESTs | 7 | |
| | 316177 | AI904982 | Hs.293102 | ESTs, Moderately similar to ALLU1_HUMAN A | 30.7 | |
| | 316580 | AA938198 | Hs.146123 | poly(A) polymerase gamma | 9.4 | |
| | 317803 | AW664964 | Hs.128899 | ESTs | 6.1 | |
| | 317881 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fis, clone HE | 9.6 | |
| 10 | 318740 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 7.3 | |
| | 318744 | AI793124 | Hs.144479 | ESTs | 17.8 | |
| | 320211 | AL039402 | Hs.125783 | DEME-6 protein | 9.2 | |
| | 321107 | AI732643 | Hs.144151 | ESTs | 12.3 | |
| | 321644 | AW975944 | Hs.237396 | ESTs | 11.7 | |
| 15 | 321978 | N77342 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 5 | |
| | 322035 | AL137517 | Hs.334473 | hypothetical protein DKFZp564O1278 | 19 | |
| | 322766 | AW068805 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.2 | |
| | 322818 | AW043782 | Hs.293616 | ESTs | 7.6 | |
| | 322975 | C16391 | | gb:C16391 Clontech human aorta polyA mRN | 16.5 | |
| 20 | 323262 | AL133990 | Hs.190642 | ESTs | 10.5 | |
| | 323332 | AI829520 | | gb:wl19c06.x1 NCI_CGAP_Ut1 Homo sapiens | 6.2 | |
| | 323817 | AA410943 | | BMP-R1B | 8.4 | |
| | 324261 | BE069341 | | gb:QV3-BT0381-270100-073-c08 BT0381 Homo | 49.4 | |
| | 324432 | AA464510 | Hs.152812 | ESTs | 16.5 | |
| 25 | 324598 | AW972227 | Hs.163986 | Homo sapiens cDNA: FLJ22765 fis, clone K | 5 | |
| | 324603 | AW993522 | Hs.292934 | ESTs | 10.4 | |
| | 324987 | AI375572 | Hs.172634 | ESTs | 18.8 | |
| | 325544 | | | Phase 2 & 3 Exons | 5.7 | |
| | 330388 | | Hs.46 | HER2 receptor tyrosine kinase (c-erb-b2, | 6.6 | |
| 30 | 334223 | | | NM_005080*:Homo sapiens X-box binding pr | 26.2 | |
| | 335809 | | | NM_014509*:Homo sapiens kraken-like (BK1 | 10.1 | |
| | 335824 | | | ENSP00000249072*:DJ222E13.1 (N-TERMINAL | 20 | |
| | AI052047 | | | ESTs; Weakly similar to CYTOCHROME P450 | 6.7 | |
| | R72427 | | | CH22_EM:AC005500.GENSCAN.127 9 | 5.5 | |
| 35 | | | | CH22_FGENES.619_13 | 9.2 | |
| | | | | CH22_FGENES.617_9 | 8 | |
| | | | | CH22_FGENES.271_7 | 6.5 | |
| | | | | CH22_FGENES.619_7 | 7.3 | |
| | | | | CH22_FGENES.271_8 | 12.9 | |
| 40 | | | | CH22_FGENES.619_12 | 8.4 | |
| | | | | CH22_EM:AC005500.GENSCAN.304 2 | 11.3 | |
| | | | | CH.07_hs gll6004473 | 8.5 | |
| | | | | CH22_FGENES.617_7 | 7.1 | |
| | | | | CH22_FGENES.678_5 | 7.2 | |
| | | | | CH22_FGENES.678_5 | 16.8 | |

TABLE 18A

Table 18A shows the accession numbers for those pkeys lacking unigeneID's for Table 18. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|---------------------------|---|
| 323332 | 179142_1 | AI829520 AI791832 AA228414 AI791823 AA229211 AA229315 |
| 322975 | 1510563_1 | C16391 C16413 |
| 324261 | 273265_1 | BE069341 AW748403 AL044891 AI908240 AA393080 |
| 323817 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| 311935 | 174129_1 | AA216387 T63548 AA228676 |
| 314138 | 179960_1 | AA740616 AA654854 AA229923 |
| 335809 | CH22_3181FG_617_6_LINK_EM | |
| 335824 | CH22_3197FG_619_11_LINK_E | |
| 325544 | c12_hs | |
| 334223 | CH22_1507FG_360_4_LINK_EM | |

TABLE 18B

5 **Table 18B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 18. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 15 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|-------------------|--------|-------------------|
| 335809 | Dunham, I. et.al. | Plus | 26310772-26310909 |
| 335824 | Dunham, I. et.al. | Plus | 26376860-26376942 |
| 334223 | Dunham, I. et.al. | Minus | 12734365-12734269 |
| 325544 | 6682452 | Plus | 171228-171286 |

20

**TABLE 19: 1045 GENES UP-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT TISSUES**

- 5 **Table 19** shows 1045 genes up-regulated in breast cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" breast cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" breast cancer level was set to the 90th percentile value. The "average" normal adult tissue level was set to the 90th percentile value amongst 144 non-
- 10 malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 144 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

- 15 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
20 R1: Ratio of tumor to normal body tissue

| | Pkey | ExAccn | UnigeneID | UnigeneTitle | R1 |
|----|--------|-----------|-----------|--|-------|
| | 408591 | AF015224 | Hs.46452 | mammaglobin 1 | 137.6 |
| 25 | 406964 | M21305 | | gb:Human alpha satellite and satellite 3 | 71.0 |
| | 400291 | AA401369 | Hs.190721 | ESTs | 68.4 |
| | 407277 | AW170035 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 54.2 |
| | 449746 | AI668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 46.4 |
| | 426878 | BE069341 | | gb:QV3-BT0381-270100-073-c08 BT0381 Homo | 44.8 |
| 30 | 400292 | AA250737 | Hs.72472 | BMP-R1B | 37.4 |
| | 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 32.9 |
| | 408045 | AW138959 | Hs.245123 | ESTs | 31.9 |
| | 407178 | AA195651 | Hs.104106 | ESTs | 30.4 |
| | 407377 | C16391 | | gb:C16391 Clontech human aorta polyA mRN | 27.7 |
| 35 | 450705 | U90304 | Hs.25351 | iroquois homeobox protein 5 | 24.8 |
| | 407212 | AA412108 | Hs.269350 | ESTs | 22.0 |
| | 428848 | NM_000230 | Hs.194236 | leptin (murine obesity homolog) | 21.9 |
| | 404561 | | | trichorhinophalangeal syndrome I (TRPS1) | 21.8 |
| | 407980 | AA046309 | | gb:zf12f01.s1 Soares_fetal_heart_NbHH19W | 19.8 |
| 40 | 447350 | AI375572 | Hs.172634 | ESTs | 17.3 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 16.6 |
| | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | 16.5 |
| | 435496 | AW840171 | Hs.265398 | ESTs, Weakly similar to transformation-r | 16.0 |
| | 453160 | AI263307 | Hs.239884 | H2B histone family, member L | 15.8 |
| 45 | 420813 | X51501 | Hs.99949 | prolactin-induced protein | 15.8 |
| | 415989 | AI267700 | Hs.317584 | ESTs | 15.5 |
| | 422505 | AL120862 | Hs.124165 | programmed cell death 9 (PDCD9) | 14.8 |
| | 424399 | AI905687 | Hs.2533 | aldehyde dehydrogenase 9 family, member | 14.5 |
| | 423575 | C18863 | Hs.163443 | Homo sapiens cDNA FLJ11576 fis, clone HE | 13.7 |
| 50 | 429441 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | 13.6 |
| | 431474 | AL133990 | Hs.190642 | ESTs | 13.5 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 13.0 |
| | 427217 | AA399272 | Hs.144341 | ESTs | 12.8 |
| | 402578 | | | C1001134:gil2117372 pir l65981 fatty ac | 12.6 |
| 55 | 422805 | AA436989 | Hs.121017 | H2A histone family, member A | 12.2 |
| | 424634 | NM_003613 | Hs.151407 | cartilage intermediate layer protein, nu | 12.0 |
| | 456207 | AA193450 | | gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi | 11.9 |
| | 424086 | AI351010 | Hs.102267 | lysyl oxidase | 11.9 |
| | 459587 | AA031956 | | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 11.5 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 416208 | AW291168 | Hs.41295 | ESTs, Weakly similar to MUC2_HUMAN MUCIN | 11.5 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 11.5 |
| | 407276 | AI951118 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 11.4 |
| 5 | 434377 | AW137148 | Hs.306593 | Homo sapiens cDNA FLJ11382 fis, clone HE | 11.3 |
| | 448390 | AL035414 | Hs.21068 | hypothetical protein | 11.1 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 11.0 |
| | 421037 | AI684808 | Hs.197653 | programmed cell death 9 (PDCD9) | 10.9 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 10.7 |
| 10 | 443348 | AW873596 | Hs.182278 | calmodulin 2 (phosphorylase kinase, delt | 10.6 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | 10.5 |
| | 402606 | | NM_024626 | Homo sapiens hypothetical prot | 10.4 |
| | 409269 | AA576953 | Hs.22972 | hypothetical protein FLJ13352 | 10.4 |
| | 447268 | AI370413 | Hs.36563 | hypothetical protein FLJ22418 | 10.3 |
| | 447033 | AI357412 | Hs.157601 | ESTs | 10.2 |
| 15 | 400295 | W72838 | Hs.2533 | aldehyde dehydrogenase 9 family, member | 10.1 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 10.1 |
| | 432441 | AW292425 | Hs.163484 | ESTs | 9.9 |
| | 427365 | AI873274 | Hs.190721 | ESTs | 9.9 |
| | 438950 | H23789 | Hs.144530 | EST | 9.8 |
| 20 | 422835 | BE218705 | Hs.121378 | metallothionein-like 5, testis-specific | 9.7 |
| | 425692 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 9.7 |
| | 411869 | W20027 | Hs.23439 | ESTs | 9.6 |
| | 439820 | AL360204 | Hs.283853 | Homo sapiens mRNA full length insert cDN | 9.6 |
| | 445730 | AI624342 | Hs.170042 | ESTs | 9.5 |
| 25 | 459583 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 9.3 |
| | 452744 | AI267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 9.2 |
| | 432596 | AJ224741 | Hs.278461 | matrilin 3 | 9.1 |
| | 400297 | AI127076 | Hs.334473 | hypothetical protein DKFZp564O1278 | 9.1 |
| | 449448 | D60730 | Hs.57471 | ESTs | 9.1 |
| 30 | 423945 | AA410943 | | gb:zt32h03.r1 Soares ovary tumor NbHOT H | 9.1 |
| | 406348 | | | Target Exon | 9.0 |
| | 424735 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | 9.0 |
| | 453392 | U23752 | Hs.32964 | SRX (sex determining region Y)-box 11 | 9.0 |
| | 433365 | AF026944 | Hs.293797 | ESTs | 8.8 |
| 35 | 405654 | NA | | C12001521:g 7513934 pir T31081 cca3 pr | 8.8 |
| | 418601 | AA279490 | Hs.86368 | calmeglin | 8.8 |
| | 451110 | AI955040 | Hs.265398 | ESTs, Weakly similar to transformation-r | 8.7 |
| | 408771 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 8.5 |
| | 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 8.4 |
| 40 | 442353 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 8.3 |
| | 451561 | N52812 | Hs.177403 | ESTs | 8.2 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 8.2 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | 8.1 |
| | 423887 | AL080207 | Hs.134585 | DKFZP434G232 protein | 8.1 |
| 45 | 405095 | NA | | Target Exon | 8.1 |
| | 419296 | AA236115 | Hs.120785 | ESTs | 8.0 |
| | 447164 | AF026941 | Hs.17518 | Homo sapiens cig5 mRNA, partial sequence | 8.0 |
| | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 8.0 |
| | 416747 | AW876523 | Hs.15929 | hypothetical protein FLJ12910 | 8.0 |
| 50 | 415385 | R17798 | Hs.7535 | COBW-like protein | 7.9 |
| | 434424 | AI811202 | Hs.325335 | Homo sapiens cDNA: FLJ23523 fis, clone L | 7.9 |
| | 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 7.9 |
| | 406687 | M31126 | Hs.272620 | matrix metalloproteinase 11 (MMP11; stro | 7.8 |
| | 400285 | NA | | Eos Control | 7.7 |
| 55 | 437207 | T27503 | Hs.15929 | hypothetical protein FLJ12910 | 7.6 |
| | 427119 | AW880562 | Hs.114574 | ESTs | 7.5 |
| | 429534 | AW976987 | Hs.163327 | ESTs, Weakly similar to 2109260A B cell | 7.5 |
| | 433426 | H69125 | Hs.133525 | ESTs | 7.5 |
| | 411078 | AI222020 | Hs.182364 | CocooCrisp | 7.4 |
| 60 | 426214 | H59846 | Hs.128355 | ESTs, Moderately similar to ALU7_HUMAN A | 7.4 |
| | 447475 | AI380797 | Hs.158992 | ESTs | 7.3 |
| | 415263 | AA948033 | Hs.130853 | ESTs | 7.2 |
| | 439569 | AW602166 | Hs.222399 | CEGP1 protein | 7.2 |
| | 414142 | AW368397 | Hs.150042 | Homo sapiens cDNA FLJ14438 fis, clone HE | 7.1 |
| 65 | 426261 | AW242243 | Hs.168670 | peroxisomal farnesylated protein | 7.0 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 6.9 |
| | 445885 | AI734009 | Hs.127699 | KIAA1603 protein | 6.9 |

| | | | | | |
|----|--------|-----------|------------------------------|--|-----|
| | 429432 | AI678059 | Hs.202676 | synaptonemal complex protein 2 | 6.9 |
| | 410781 | AI375672 | Hs.165028 | ESTs | 6.9 |
| | 443788 | AI732643 | Hs.144151 | ESTs | 6.9 |
| | 421373 | AA808229 | Hs.167771 | ESTs | 6.8 |
| 5 | 451398 | AI793124 | Hs.144479 | ESTs | 6.8 |
| | 404253 | | NM_021058* | Homo sapiens H2B histone fami | 6.8 |
| | 441098 | AI015591 | Hs.131004 | ESTs, Weakly similar to T17227 hypotheti | 6.7 |
| | 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | 6.6 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (CX | 6.6 |
| 10 | 422956 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 6.6 |
| | 411111 | AW818127 | gb:CM1-ST0277-061299-059-b07 | ST0277 Homo | 6.6 |
| | 434988 | AI418055 | Hs.161160 | ESTs | 6.6 |
| | 442580 | AI733682 | Hs.130239 | ESTs | 6.6 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 6.6 |
| 15 | 408000 | L11690 | Hs.620 | bullous pemphigoid antigen 1 (230/240kD) | 6.5 |
| | 420757 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 6.5 |
| | 431089 | BE041395 | Hs.283676 | ESTs, Weakly similar to unknown protein | 6.5 |
| | 400301 | X03635 | Hs.1657 | estrogen receptor 1 | 6.5 |
| | 427356 | AW023482 | Hs.97849 | ESTs | 6.5 |
| 20 | 425704 | U79293 | Hs.159264 | Human clone 23948 mRNA sequence | 6.4 |
| | 441134 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 6.4 |
| | 424902 | NM_003866 | Hs.153687 | inositol polyphosphate-4-phosphatase, ty | 6.4 |
| | 448693 | AW004854 | Hs.228320 | hypothetical protein FLJ23537 | 6.4 |
| | 431448 | AL137517 | Hs.334473 | hypothetical protein DKFZp664O1278 | 6.2 |
| 25 | 444342 | NM_014398 | Hs.10887 | similar to lysosome-associated membrane | 6.1 |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 6.1 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 6.1 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (MMP1; inters | 6.0 |
| | 441233 | AA972965 | Hs.135568 | ESTs | 6.0 |
| 30 | 418092 | R45154 | Hs.106604 | ESTs | 6.0 |
| | 430044 | AA464510 | Hs.152812 | ESTs | 5.9 |
| | 432837 | AA310693 | Hs.87329 | HSPC072 protein | 5.9 |
| | 433285 | AW975944 | Hs.237396 | ESTs | 5.9 |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.9 |
| 35 | 425707 | AF115402 | Hs.11713 | E74-like factor 5 (ets domain transcript | 5.9 |
| | 410785 | AW803341 | gb:IL2-UM0079-090300-050-D03 | UM0079 Homo | 5.9 |
| | 425398 | AL049689 | Hs.156369 | hypothetical protein similar to tenascin | 5.9 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 5.8 |
| | 459371 | R20991 | gb:yg06h01.r1 | Soares infant brain 1N1B H | 5.8 |
| 40 | 411284 | N28519 | Hs.135191 | ESTs, Weakly similar to unnamed protein | 5.8 |
| | 453511 | AL031224 | Hs.33102 | transcription factor AP-2 beta (activati | 5.8 |
| | 451807 | W52854 | Hs.27099 | hypothetical protein FLJ23293 similar to | 5.7 |
| | 430510 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 5.7 |
| | 415539 | AI733881 | Hs.72472 | BMP-R1B | 5.6 |
| 45 | 438199 | AW016531 | Hs.122147 | ESTs | 5.6 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 5.5 |
| | 430019 | AA463893 | Hs.220933 | ESTs | 5.5 |
| | 439809 | R41396 | Hs.101774 | hypothetical protein FLJ23045 | 5.5 |
| | 423811 | AW299598 | Hs.50895 | homeo box C4 | 5.4 |
| 50 | 434539 | AW748078 | Hs.214410 | ESTs, Weakly similar to MUC2_HUMAN MUCIN | 5.4 |
| | 439138 | AI742605 | Hs.193696 | ESTs | 5.4 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 5.4 |
| | 444078 | BE246919 | Hs.10290 | U5 snRNP-specific 40 kDa protein (hPrp8- | 5.4 |
| | 447102 | BE167434 | Hs.98471 | ESTs, Weakly similar to T18712 hypotheti | 5.4 |
| 55 | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 5.4 |
| | 425236 | AW067800 | Hs.155223 | stanniocalcin 2 | 5.3 |
| | 421464 | AA291553 | Hs.190086 | ESTs | 5.3 |
| | 450736 | AW970060 | gb:EST382140 | MAGE resequences, MAGK Homo | 5.3 |
| | 428085 | AA421081 | Hs.12388 | ESTs | 5.3 |
| 60 | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 5.3 |
| | 445424 | AB028945 | Hs.12696 | cortactin SH3 domain-binding protein | 5.3 |
| | 456938 | X52509 | Hs.161640 | tyrosine aminotransferase | 5.3 |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (COM | 5.2 |
| | 438167 | R28363 | Hs.24286 | ESTs | 5.2 |
| 65 | 433330 | AW207084 | Hs.132816 | hypothetical protein MGC14801 | 5.2 |
| | 449765 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN A | 5.2 |
| | 416276 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | 5.2 |

| | | | | |
|----|--------|-----------|--|-----|
| | 400300 | X03363 | HER2 receptor tyrosine kinase (c-erb-b2, | 5.2 |
| | 418004 | U37519 | Hs.87539 aldehyde dehydrogenase 3 family, member | 5.2 |
| | 439840 | AW449211 | Hs.105445 GDNF family receptor alpha 1 | 5.2 |
| | 428771 | AB028992 | Hs.193143 KIAA1069 protein | 5.2 |
| 5 | 455047 | AW852530 | gb:PM1-CT0243-071099-001-g06 CT0243 Homo | 5.2 |
| | 419169 | AW851980 | Hs.262346 ESTs, Weakly similar to S72482 hypotheti | 5.2 |
| | 453197 | AI916269 | Hs.109057 ESTs, Weakly similar to ALU5_HUMAN ALU S | 5.1 |
| | 400298 | AA032279 | Hs.61635 six transmembrane epithelial antigen of | 5.1 |
| | 431023 | AI283133 | Hs.297420 ESTs | 5.1 |
| 10 | 427686 | AI791495 | Hs.180142 calmodulin-like skin protein | 5.1 |
| | 427718 | AI798680 | Hs.25933 ESTs | 5.1 |
| | 434531 | AA642007 | Hs.116369 ESTs | 5.1 |
| | 429220 | AW207206 | Hs.136319 ESTs | 5.1 |
| | 405494 | NA | C2001837*:gil12697903 dbj BAB21770.1 (A | 5.1 |
| 15 | 452930 | AW195285 | Hs.194097 ESTs, Weakly similar to I38022 hypotheti | 5.1 |
| | 444910 | AI201849 | gb:qs76g04.x1 NCL CGAP_Pr28 Homo sapiens | 5.1 |
| | 453310 | X70697 | Hs.553 solute carrier family 6 (neurotransmitte | 5.0 |
| | 444381 | BE387335 | Hs.283713 ESTs, Weakly similar to S64054 hypotheti | 5.0 |
| | 450603 | R43646 | Hs.12422 ESTs | 5.0 |
| 20 | 416575 | W02414 | Hs.38383 ESTs | 5.0 |
| | 438504 | AW665281 | Hs.224625 ESTs | 5.0 |
| | 416209 | AA236776 | Hs.79078 MAD2 (mitotic arrest deficient, yeast, h | 5.0 |
| | 428804 | AK000713 | Hs.193736 hypothetical protein FLJ20706 | 5.0 |
| | 420077 | AW512260 | Hs.87767 ESTs | 4.9 |
| 25 | 450480 | X82125 | Hs.25040 zinc finger protein 239 | 4.9 |
| | 437637 | AJ003029 | Hs.65792 syntrophin, gamma 2 | 4.9 |
| | 431808 | M30703 | Hs.270833 amphiregulin (schwannoma-derived growth | 4.9 |
| | 418836 | AI655499 | Hs.161712 ESTs | 4.8 |
| | 442441 | AI820662 | Hs.129598 ESTs | 4.8 |
| 30 | 435635 | AF220050 | Hs.181385 uncharacterized hematopoietic stem/proge | 4.8 |
| | 400286 | NA | C16000922:gil7499103 pir T20903 hypotheti | 4.8 |
| | 407506 | U71600 | gb:Human zinc finger protein zfp31 (zfp31 | 4.8 |
| | 420026 | AI831190 | Hs.166676 ESTs | 4.8 |
| | 441377 | BE218239 | Hs.202656 ESTs | 4.8 |
| 35 | 457726 | AI217477 | Hs.194591 ESTs | 4.8 |
| | 412785 | AW997556 | Hs.78521 KIAA1717 protein | 4.8 |
| | 428368 | BE440042 | Hs.83326 matrix metalloproteinase 3 (stromelysin | 4.7 |
| | 436026 | AI349764 | Hs.217081 ESTs | 4.7 |
| | 409110 | AA191493 | Hs.48778 niban protein | 4.7 |
| 40 | 400284 | NA | estrogen receptor 1 | 4.7 |
| | 410102 | AW248508 | Hs.279727 Homo sapiens cDNA FLJ14035 fis, clone HE | 4.7 |
| | 407819 | R42185 | Hs.274803 ESTs | 4.7 |
| | 430486 | BE062109 | Hs.241551 chloride channel, calcium activated, fam | 4.7 |
| | 422896 | AW961489 | Hs.154116 ESTs | 4.7 |
| 45 | 453616 | NM_003462 | Hs.33846 dynein, axonemal, light intermediate pol | 4.7 |
| | 427427 | AF077345 | Hs.177936 ESTs | 4.6 |
| | 421751 | AW813731 | Hs.159153 ESTs, Moderately similar to S65657 alpha | 4.6 |
| | 454074 | R63503 | Hs.28419 ESTs | 4.6 |
| | 405718 | | C4000799*:gil6330365 dbj BAA86508.1 (AB | 4.6 |
| 50 | 444649 | AW207523 | Hs.197628 ESTs | 4.6 |
| | 429431 | Z40313 | Hs.106330 Homo sapiens clone IMAGE:23371, mRNA seq | 4.6 |
| | 427811 | M81057 | Hs.180884 carboxypeptidase B1 (tissue) | 4.6 |
| | 447342 | AI199268 | Hs.19322 Homo sapiens, Similar to RIKEN cDNA 2010 | 4.6 |
| | 430345 | AK000282 | Hs.239681 hypothetical protein FLJ20275 | 4.6 |
| 55 | 454307 | AW855717 | gb:RC1-CT0279-081299-013-b01 CT0279 Homo | 4.6 |
| | 400303 | AA242758 | Hs.79136 LIV-1 protein, estrogen regulated | 4.6 |
| | 438180 | AA808189 | Hs.272151 ESTs | 4.6 |
| | 451340 | AW936273 | gb:QV0-DT0020-090200-107-g07 DT0020 Homo | 4.6 |
| | 458711 | AL036877 | Hs.282878 ESTs | 4.6 |
| 60 | 457430 | AA514660 | Hs.128443 ESTs | 4.6 |
| | 416030 | H15261 | Hs.21948 ESTs | 4.6 |
| | 447233 | AW246333 | Hs.17901 Homo sapiens, clone IMAGE:3937015, mRNA, | 4.6 |
| | 445537 | AJ245671 | Hs.12844 EGF-like-domain, multiple 6 (EGFL6) | 4.5 |
| | 424590 | AW966399 | Hs.46821 hypothetical protein FLJ20086 | 4.5 |
| 65 | 432374 | W68815 | Hs.301885 Homo sapiens cDNA FLJ11346 fis, clone PL | 4.5 |
| | 423833 | AW503329 | gb:UI-HF-BND-akx-e-02-0-UI.r1 NIH_MGC_50 | 4.5 |
| | 406747 | AI925153 | Hs.217493 annexin A2 | 4.5 |

| | | | | |
|----|--------|-----------|--|-----|
| | 412102 | H56435 | gb:yq98e09.r1 Soares fetal liver spleen | 4.5 |
| | 431716 | D89053 | Hs.268012 fatty-acid-Coenzyme A ligase, long-chain | 4.5 |
| | 411050 | AW814902 | gb:MR1-ST0206-120400-022-f08 ST0206 Homo | 4.5 |
| | 401418 | NA | C14000338*gi 7459502 pir S74665 outer | 4.5 |
| 5 | 436194 | AK001074 | Hs.333435 Homo sapiens cDNA FLJ10212 fis, clone HE | 4.5 |
| | 436211 | AK001581 | Hs.334828 hypothetical protein FLJ10719; KIAA1794 | 4.4 |
| | 414080 | AA135257 | Hs.47783 B aggressive lymphoma gene | 4.4 |
| | 424115 | AA335497 | Hs.293965 ESTs, Weakly similar to I38022 hypotheti | 4.4 |
| | 415786 | AW419196 | Hs.257924 hypothetical protein FLJ13782 | 4.4 |
| 10 | 442117 | AW664964 | Hs.128899 ESTs | 4.4 |
| | 452784 | BE463857 | Hs.151258 hypothetical protein FLJ21062 | 4.4 |
| | 432731 | R31178 | Hs.287820 fibronectin 1 | 4.4 |
| | 410534 | AW905138 | gb:QV0-NN1071-280400-207-g07 NN1071 Homo | 4.4 |
| | 405196 | NA | C2000662*gi 7512792 pir T12482 hypothe | 4.4 |
| 15 | 430217 | N47863 | Hs.336901 ribosomal protein S24 | 4.4 |
| | 401793 | | C17001545gi 5360127 gb AAD42882.1 AF155 | 4.4 |
| | 415747 | AA381209 | gb:EST94257 Activated T-cells I Homo sap | 4.4 |
| | 423679 | AB007975 | Hs.131454 KIAA0506 protein | 4.4 |
| | 400238 | NA | C19000274*gi 12741327 ref XP_008833.2 | 4.4 |
| 20 | 425627 | AF019612 | Hs.297007 membrane-bound transcription factor prot | 4.4 |
| | 400608 | | C10001899gi 7508633 pir T25392 hypothe | 4.4 |
| | 458634 | AV657310 | Hs.282898 ESTs | 4.3 |
| | 407771 | AL138272 | Hs.62713 ESTs | 4.3 |
| | 405906 | NA | Target Exon | 4.3 |
| 25 | 405925 | NA | Target Exon | 4.3 |
| | 439382 | BE247684 | Hs.103070 ESTs | 4.3 |
| | 445263 | H57646 | Hs.42586 KIAA1560 protein | 4.3 |
| | 407162 | N63855 | Hs.142634 zinc finger protein | 4.3 |
| 30 | 419536 | AA603305 | gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens | 4.3 |
| | 454359 | N71277 | gb:za36e03.s1 Soares fetal liver spleen | 4.3 |
| | 411558 | AA102670 | Hs.70725 gamma-aminobutyric acid (GABA) A recepto | 4.2 |
| | 450715 | AI266484 | Hs.31570 ESTs, Weakly similar to KIAA1324 protein | 4.2 |
| | 421451 | AA291377 | Hs.50831 ESTs | 4.2 |
| | 452864 | AA033714 | Hs.287629 hypothetical protein FLJ14260 | 4.2 |
| 35 | 409757 | NM_001898 | Hs.123114 cystatin SN | 4.2 |
| | 413043 | BE158766 | gb:IL2-HT0397-071299-024-F02 HT0397 Homo | 4.2 |
| | 413499 | BE144884 | gb:CM0-HT0182-041099-065-e11 HT0182 Homo | 4.2 |
| | 444619 | BE538082 | Hs.8172 ESTs, Moderately similar to A46010 X-In | 4.2 |
| | 408380 | AF123050 | Hs.44532 diubiquitin | 4.2 |
| 40 | 406992 | S82472 | gb:beta-pol=DNA polymerase beta (exon a | 4.2 |
| | 404285 | NA | C6001909gi 704441 dbj BAA18909.1 (D298 | 4.2 |
| | 425247 | NM_005940 | Hs.155324 matrix metalloproteinase 11 (MMP11; stro | 4.2 |
| | 428046 | AW812795 | Hs.155381 ESTs, Moderately similar to I38022 hypot | 4.2 |
| | 446163 | AA026880 | Hs.25252 prolactin receptor | 4.2 |
| 45 | 421147 | AW592167 | Hs.293299 ESTs | 4.2 |
| | 426451 | AI908165 | Hs.169946 GATA-binding protein 3 (T-cell receptor | 4.2 |
| | 415227 | AW821113 | Hs.72402 ESTs | 4.2 |
| | 452176 | AA024538 | Hs.282990 Human DNA sequence from clone RP1-28H20 | 4.2 |
| | 452862 | AW378065 | Hs.8687 ESTs | 4.2 |
| 50 | 443646 | AI085198 | Hs.164226 ESTs | 4.2 |
| | 425523 | AB007948 | Hs.158244 KIAA0479 protein | 4.1 |
| | 424687 | J05070 | Hs.151738 matrix metalloproteinase 9 (gelatinase B | 4.1 |
| | 430009 | AA894564 | Hs.22242 ESTs | 4.1 |
| | 434469 | AA634806 | gb:ab28c02.r1 Stratagene lung (937210) H | 4.1 |
| 55 | 451381 | BE241831 | Hs.172330 hypothetical protein MGC2705 | 4.1 |
| | 450229 | R18717 | Hs.8929 hypothetical protein FLJ11362 | 4.1 |
| | 455700 | BE68115 | gb:CM1-BT0368-061299-060-g07 BT0368 Homo | 4.1 |
| | 431924 | AK000850 | Hs.272203 Homo sapiens cDNA FLJ20843 fis, clone AD | 4.1 |
| | 438885 | AI885558 | Hs.184987 ESTs | 4.1 |
| 60 | 401451 | | NM_004496*:Homo sapiens hepatocyte nucle | 4.1 |
| | 431676 | AI685464 | gb:ft88f04.x1 NCL_CGAP_Pr28 Homo sapiens | 4.1 |
| | 409092 | AI735283 | Hs.172608 ESTs | 4.1 |
| | 429270 | W60379 | Hs.57773 ESTs | 4.1 |
| | 443903 | AI220547 | Hs.135223 ESTs | 4.1 |
| 65 | 427122 | AW057736 | Hs.323910 HER2 receptor tyrosine kinase (c-erb-b2, | 4.1 |
| | 410275 | U85658 | Hs.61796 transcription factor AP-2 gamma (activat | 4.1 |
| | 432912 | BE007371 | Hs.200313 ESTs | 4.1 |

| | | | | |
|----|--------|-----------|--|-----|
| | 403585 | | Target Exon | 4.1 |
| | 438295 | AI394151 | Hs.37932 ESTs | 4.1 |
| | 420380 | AA640891 | Hs.102406 ESTs | 4.1 |
| 5 | 431118 | BE264901 | Hs.250502 carbonic anhydrase VIII | 4.1 |
| | 416182 | NM_004354 | Hs.79069 cyclin G2 | 4.1 |
| | 418994 | AA296520 | Hs.89546 selectin E (endothelial adhesion molecu | 4.1 |
| | 400555 | | Target Exon | 4.1 |
| | 410079 | U94362 | Hs.58589 glycogenin 2 | 4.0 |
| | 427674 | NM_003528 | Hs.2178 H2B histone family, member Q | 4.0 |
| 10 | 427131 | AA448460 | Hs.112017 GE36 gene | 4.0 |
| | 439759 | AL359055 | Hs.67709 Homo sapiens mRNA full length insert cDN | 4.0 |
| | 429353 | AL117406 | Hs.200102 ATP-binding cassette transporter MRP8 | 4.0 |
| | 421296 | NM_002666 | Hs.103253 perilipin | 4.0 |
| | 418819 | AA228776 | Hs.191721 ESTs | 4.0 |
| 15 | 424188 | AW954552 | Hs.142634 zinc finger protein | 4.0 |
| | 455431 | AW938484 | gb:CM0-DT0057-290200-253-d06 DT0057 Homo | 4.0 |
| | 404142 | NA | Target Exon | 4.0 |
| | 441143 | AI027604 | Hs.159650 ESTs | 4.0 |
| | 444540 | AI693927 | Hs.265165 ESTs | 4.0 |
| 20 | 415579 | AA165232 | Hs.222069 ESTs | 4.0 |
| | 452891 | N75582 | Hs.212875 ESTs, Weakly similar to DYH9_HUMAN CILIA | 4.0 |
| | 414605 | BE390440 | gb:601283601F1 NIH_MGC_44 Homo sapiens c | 4.0 |
| | 452281 | T93500 | Hs.28792 Homo sapiens cDNA FLJ11041 fis, clone PL | 4.0 |
| | 417801 | AA417383 | Hs.82582 integrin, beta-like 1 (with EGF-like rep | 4.0 |
| 25 | 446232 | AI281848 | Hs.194691 retinol acid induced 3 | 4.0 |
| | 447377 | X77343 | Hs.334334 transcription factor AP-2 alpha (activat | 4.0 |
| | 437854 | AL119723 | gb:DKFZp761A2124_r1 761 (synonym: hamy2) | 4.0 |
| | 446140 | AA356170 | Hs.26750 hypothetical protein FLJ21908 | 4.0 |
| | 452240 | AI591147 | Hs.61232 ESTs | 4.0 |
| 30 | 459574 | AI741122 | Hs.101810 Homo sapiens cDNA FLJ14232 fis, clone NT | 4.0 |
| | 458673 | N99626 | gb:za39d11.r1 Soares fetal liver spleen | 4.0 |
| | 444858 | AI199738 | Hs.208275 ESTs, Weakly similar to ALUA_HUMAN IIII | 4.0 |
| | 452166 | AI948607 | Hs.264680 ESTs | 4.0 |
| | 452681 | AF153330 | Hs.30246 solute carrier family 19 (thiamine trans | 3.9 |
| 35 | 450192 | AA263143 | Hs.24596 RAD51-Interacting protein | 3.9 |
| | 406554 | NA | Target Exon | 3.9 |
| | 416259 | AA573006 | Hs.19173 ESTs | 3.9 |
| | 445813 | Z42023 | Hs.106576 alanine-glyoxylate aminotransferase 2-II | 3.9 |
| | 451024 | AA442176 | gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_ | 3.9 |
| 40 | 413930 | M86153 | Hs.75618 RAB11A, member RAS oncogene family | 3.9 |
| | 401781 | | Target Exon | 3.9 |
| | 415296 | F05086 | Hs.328142 ESTs | 3.9 |
| | 452564 | AA026777 | gb:ze93c11.r1 Soares_fetal_heart_NbHH19W | 3.9 |
| | 442500 | AI819068 | Hs.209122 ESTs | 3.9 |
| 45 | 419759 | Z21336 | Hs.135411 actin related protein | 3.9 |
| | 424638 | AI472106 | Hs.49303 Homo sapiens cDNA FLJ11663 fis, clone HE | 3.9 |
| | 439699 | AF086534 | Hs.187561 ESTs, Moderately similar to ALU1_HUMAN A | 3.9 |
| | 428042 | AA419529 | Hs.76391 myxovirus (influenza) resistance 1, homo | 3.9 |
| | 452501 | AB037791 | Hs.29716 hypothetical protein FLJ10980 | 3.9 |
| 50 | 453049 | BE537217 | Hs.30343 ESTs | 3.9 |
| | 443213 | BE568414 | Hs.145497 Homo sapiens cDNA: FLJ22097 fis, clone H | 3.9 |
| | 443489 | AI073512 | Hs.133916 ESTs | 3.9 |
| | 455092 | BE152428 | gb:CM0-HT0323-151299-126-b04 HT0323 Homo | 3.9 |
| | 401785 | | NM_002275*:Homo sapiens keratin 15 (KRT1 | 3.9 |
| 55 | 426427 | M86699 | Hs.169840 TTK protein kinase | 3.9 |
| | 446009 | AI989885 | Hs.231926 ESTs | 3.9 |
| | 436033 | H75391 | Hs.255748 ESTs | 3.9 |
| | 451067 | BE172186 | gb:MR0-HT0559-110300-005-h11 HT0559 Homo | 3.8 |
| | 419348 | AA236645 | Hs.98274 ESTs | 3.8 |
| 60 | 444635 | AI184268 | Hs.339665 ESTs | 3.8 |
| | 412140 | AA219691 | Hs.73625 RAB6 Interacting, kinesin-like (rabkines | 3.8 |
| | 403593 | NA | Target Exon | 3.8 |
| | 442323 | AW016669 | Hs.29190 ESTs | 3.8 |
| | 419854 | AW664873 | Hs.87836 Homo sapiens PAC clone RP5-1087M19 from | 3.8 |
| 65 | 433871 | W02410 | Hs.205555 ESTs | 3.8 |
| | 445253 | AI217928 | Hs.144762 ESTs | 3.8 |
| | 409542 | AA503020 | Hs.36563 hypothetical protein FLJ22418 | 3.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 3.8 |
| | 458194 | AW383618 | Hs.265459 | ESTs, Moderately similar to ALU2_HUMAN A | 3.8 |
| | 422475 | AL359938 | Hs.117313 | Meis (mouse) homolog 3 | 3.8 |
| | 440705 | AA904244 | Hs.153205 | ESTs | 3.8 |
| 5 | 447290 | AI476732 | Hs.263912 | ESTs | 3.8 |
| | 403426 | | | Target Exon | 3.8 |
| | 427821 | AA470158 | Hs.98202 | ESTs | 3.8 |
| | 454288 | BE222648 | Hs.279458 | ESTs, Highly similar to c380A1.1b [H.sap | 3.8 |
| | 443801 | AW206942 | Hs.253594 | ESTs | 3.8 |
| 10 | 410658 | AW105231 | Hs.192035 | ESTs | 3.8 |
| | 410672 | AW794600 | | gb:RC6-UM0014-170300-022-C05 UM0014 Homo | 3.8 |
| | 428579 | NM_005756 | Hs.184942 | G protein-coupled receptor 64 | 3.8 |
| | 445495 | BE622641 | Hs.38489 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 447995 | AI742618 | Hs.181733 | ESTs, Weakly similar to nitrilase homolo | 3.7 |
| 15 | 401747 | | | Homo sapiens keratin 17 (KRT17) | 3.7 |
| | 420633 | NM_014581 | Hs.274480 | odorant-binding protein 2A | 3.7 |
| | 423545 | AP000692 | Hs.129781 | chromosome 21 open reading frame 5 | 3.7 |
| | 433138 | AB029496 | Hs.59729 | semaphorin sem2 | 3.7 |
| | 434715 | BE005346 | Hs.116410 | ESTs | 3.7 |
| 20 | 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 3.7 |
| | 450951 | AA018534 | Hs.103334 | ESTs | 3.7 |
| | 402696 | NA | | C3002523:g 6686211 sp Q27533 YH2M_CAEEL | 3.7 |
| | 446868 | AV660737 | Hs.135100 | ESTs | 3.7 |
| | 458154 | AW816379 | Hs.335018 | ESTs | 3.7 |
| 25 | 422026 | U80736 | Hs.110826 | trinucleotide repeat containing 9 | 3.7 |
| | 419440 | AB020689 | Hs.90419 | KIAA0882 protein | 3.7 |
| | 421524 | AA312082 | Hs.105445 | GNF family receptor alpha 1 | 3.7 |
| | 417283 | N62840 | Hs.48648 | ESTs | 3.7 |
| | 401508 | NA | | NM_024817:Homo sapiens hypothetical prot | 3.7 |
| 30 | 410303 | AA324597 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 3.7 |
| | 420362 | U79734 | Hs.97206 | huntingtin interacting protein 1 | 3.7 |
| | 433384 | AI021992 | Hs.124244 | ESTs | 3.7 |
| | 434302 | AA629065 | Hs.116301 | ESTs | 3.7 |
| | 443938 | R55373 | Hs.20864 | ESTs | 3.7 |
| 35 | 448420 | BE623004 | | gb:601441282F1 NIH_MGC_72 Homo sapiens c | 3.7 |
| | 458712 | AI347502 | Hs.107872 | hypothetical protein FLJ20761 | 3.7 |
| | 433404 | T32982 | Hs.102720 | ESTs | 3.7 |
| | 405232 | | | NM_015832:Homo sapiens methyl-CpG bindin | 3.7 |
| | 430491 | AL109791 | Hs.241559 | Homo sapiens mRNA full length insert cDN | 3.7 |
| 40 | 455609 | BE011668 | | gb:CM3-BN0223-100500-177-a04 BN0223 Homo | 3.7 |
| | 450164 | AI239923 | Hs.30098 | ESTs | 3.7 |
| | 453948 | AI970797 | Hs.64859 | ESTs | 3.7 |
| | 436061 | AI248584 | Hs.190745 | Homo sapiens cDNA: FLJ21326 fis, clone C | 3.7 |
| | 401049 | NA | | Target Exon | 3.6 |
| 45 | 418867 | D31771 | Hs.89404 | msh (Drosophila) homeo box homolog 2 | 3.6 |
| | 420179 | N74530 | Hs.21168 | ESTs | 3.6 |
| | 458663 | AV658444 | Hs.280776 | tankyrase, TRF1-interacting ankyrin-rela | 3.6 |
| | 437259 | AI377755 | Hs.120695 | ESTs | 3.6 |
| | 428309 | M97815 | Hs.183650 | cellular retinoic acid-binding protein 2 | 3.6 |
| 50 | 450522 | AI698839 | | gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s | 3.6 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 3.6 |
| | 412209 | AW901456 | | gb:RC0-NN1012-270300-031-c07 NN1012 Homo | 3.6 |
| | 425201 | AA352111 | | gb:EST60061 Activated T-cells XX Homo sa | 3.6 |
| | 443830 | AI142095 | Hs.143273 | ESTs | 3.6 |
| 55 | 439255 | BE164500 | | gb:RC4-HT0469-230300-014-e10 HT0469 Homo | 3.6 |
| | 414869 | AA157291 | Hs.21479 | ubiquitin 1 | 3.6 |
| | 409064 | AA062954 | Hs.141883 | ESTs | 3.6 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-(Y)-phosphoryl | 3.6 |
| | 445135 | AK000054 | Hs.12347 | hypothetical protein FLJ20047 | 3.6 |
| 60 | 404091 | NA | | Target Exon | 3.6 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, Identified in neuroblast | 3.6 |
| | 405153 | | | Target Exon | 3.6 |
| | 423248 | AA380177 | Hs.125845 | ribulose-5-phosphate-3-epimerase | 3.6 |
| | 403639 | NA | | ENSP00000233023*:CDNA FLJ12662 fis, clon | 3.6 |
| 65 | 404380 | | | C7001385:g 12082809 gb AAG48618.1 AF315 | 3.6 |
| | 422352 | AA766296 | Hs.99200 | ESTs | 3.6 |
| | 423338 | AB007961 | Hs.127338 | KIAA0492 protein | 3.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 424202 | BE350295 | Hs.15032 | RAN binding protein 17 | 3.6 |
| | 431750 | AA514986 | Hs.283705 | ESTs | 3.6 |
| | 439907 | AA853978 | Hs.124577 | ESTs | 3.6 |
| 5 | 453596 | AA441838 | Hs.62905 | hypothetical protein FLJ14834 | 3.6 |
| | 406446 | NA | | Target Exon | 3.6 |
| | 418454 | AA315308 | Hs.195870 | hypothetical protein FLJ14991 | 3.6 |
| | 434360 | AW015415 | Hs.127780 | ESTs | 3.6 |
| | 409079 | W87707 | Hs.82065 | interleukin 6 signal transducer (gp130, | 3.6 |
| | 440132 | AI697121 | Hs.202466 | ESTs, Weakly similar to S65824 reverse t | 3.6 |
| 10 | 448706 | AW291095 | Hs.21814 | interleukin 20 receptor, alpha | 3.6 |
| | 440671 | AW297920 | Hs.130054 | ESTs | 3.5 |
| | 407647 | AW860158 | | gb:RC0-CT0379-290100-032-b04 CT0379 Homo | 3.5 |
| | 459023 | AW968226 | Hs.60798 | ESTs | 3.5 |
| 15 | 402820 | | | NM_017646*:Homo sapiens tRNA Isopentenyl | 3.5 |
| | 417009 | AA191719 | Hs.314714 | ESTs | 3.5 |
| | 447048 | AW393080 | Hs.228320 | hypothetical protein FLJ23537 | 3.5 |
| | 449978 | AI806335 | Hs.200829 | ESTs, Weakly similar to T30171 ninein - | 3.5 |
| | 428062 | AA420683 | Hs.98321 | hypothetical protein FLJ14103 | 3.5 |
| 20 | 452909 | NM_015368 | Hs.30985 | pannexin 1 | 3.5 |
| | 400610 | NA | | Target Exon | 3.5 |
| | 417843 | W07361 | Hs.22545 | Homo sapiens cDNA FLJ12935 fis, clone NT | 3.5 |
| | 419335 | AW960146 | Hs.284137 | hypothetical protein FLJ12888 | 3.5 |
| | 451592 | AI805416 | Hs.213897 | ESTs | 3.5 |
| 25 | 443270 | NM_004272 | Hs.337737 | Homer, neuronal immediate early gene, 1B | 3.5 |
| | 423948 | AW392342 | Hs.283077 | centrosomal P4.1-associated protein; unc | 3.5 |
| | 449424 | AW448937 | Hs.197030 | ESTs | 3.5 |
| | 423841 | AW753967 | | gb:RC2-CT0304-080100-011-h12 CT0304 Homo | 3.5 |
| | 416806 | NM_000288 | Hs.79993 | peroxisomal biogenesis factor 7 | 3.5 |
| 30 | 422060 | R20893 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 3.5 |
| | 433104 | AL043002 | Hs.128246 | ESTs, Moderately similar to unnamed prot | 3.5 |
| | 415778 | H84847 | Hs.49391 | hypothetical protein LOC54149 | 3.5 |
| | 413054 | AW316843 | Hs.66309 | hypothetical protein MGC11061 | 3.5 |
| | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 3.5 |
| 35 | 424639 | AI917494 | Hs.9812 | Homo sapiens cDNA FLJ14388 fis, clone HE | 3.5 |
| | 424827 | AI057094 | Hs.96867 | Homo sapiens cDNA: FLJ23155 fis, clone L | 3.5 |
| | 437782 | AI370876 | Hs.79090 | exportin 1 (CRM1, yeast, homolog) | 3.5 |
| | 411514 | AW850178 | | gb:IL3-CT0219-271099-022-H12 CT0219 Homo | 3.5 |
| | 413783 | AA314337 | Hs.301547 | ribosomal protein S7 | 3.5 |
| 40 | 421106 | AA877124 | Hs.172844 | ESTs | 3.5 |
| | 431291 | N25521 | Hs.25275 | Kruppel-type zinc finger protein | 3.5 |
| | 440623 | AI935016 | Hs.216639 | ESTs | 3.5 |
| | 455838 | BE145808 | | gb:MR0-HT0208-101299-103-f11 HT0208 Homo | 3.5 |
| | 458771 | AW295151 | Hs.163612 | ESTs | 3.5 |
| 45 | 442942 | AW167087 | Hs.131562 | ESTs | 3.5 |
| | 436550 | Z50158 | Hs.270235 | ESTs, Weakly similar to MMHUB1 laminin b | 3.5 |
| | 418849 | AW474547 | Hs.53565 | Homo sapiens PIG-M mRNA for mannosyltran | 3.5 |
| | 424420 | BE614743 | Hs.146688 | prostaglandin E synthase | 3.5 |
| | 430916 | AW505021 | Hs.88414 | BTB and CNC homology 1, basic leucine zi | 3.5 |
| 50 | 432030 | AI908400 | Hs.143789 | ESTs | 3.5 |
| | 439405 | AF086224 | Hs.55238 | ESTs | 3.5 |
| | 405917 | NA | | C17000675:gil7290703[gb]AAF46150.1 (AE0 | 3.5 |
| | 452727 | AW993582 | Hs.176220 | ESTs | 3.5 |
| | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 3.4 |
| 55 | 421070 | AA283185 | Hs.19327 | ESTs | 3.4 |
| | 424625 | AW904466 | Hs.321197 | PDZ domain protein (Drosophila inaD-like | 3.4 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 3.4 |
| | 455651 | BE064962 | | gb:RC1-BT0313-130400-016-c02 BT0313 Homo | 3.4 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 3.4 |
| 60 | 447754 | AW073310 | Hs.163533 | Homo sapiens cDNA FLJ14142 fis, clone MA | 3.4 |
| | 418636 | AW749855 | | gb:QV4-BT0534-281299-053-c05 BT0534 Homo | 3.4 |
| | 404097 | NA | | C5000242*:gil9369379[gb]AAF87128.1 AC006 | 3.4 |
| | 434205 | AF119861 | Hs.283032 | hypothetical protein PRO2015 | 3.4 |
| | 421072 | AI215069 | Hs.89113 | ESTs | 3.4 |
| 65 | 402421 | NA | | C1001578*:gil6759903[gb]AAF28099.1 (AF1 | 3.4 |
| | 405248 | NA | | Target Exon | 3.4 |
| | 407638 | AJ404672 | Hs.334483 | hypothetical protein FLJ23571 | 3.4 |
| | 403000 | BE247275 | Hs.151787 | U5 snRNP-specific protein, 116 kD | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 433393 | AF038564 | Hs.98074 | itchy (mouse homolog) E3 ublquitin prote | 3.4 |
| | 432239 | X81334 | Hs.2936 | matrix metalloproteinase 13 (collagenase | 3.4 |
| | 458747 | BE618395 | Hs.257391 | hypothetical protein DKFZp761J1523 | 3.4 |
| | 442082 | R41823 | Hs.7413 | ESTs; calyntenin-2 | 3.4 |
| 5 | 417974 | AA210765 | | gb:zr90c06.r1 NCL_CGAP_GCB1 Homo sapiens | 3.4 |
| | 446002 | AI346468 | Hs.145789 | ESTs | 3.4 |
| | 448995 | AI613276 | Hs.5662 | guanine nucleotide binding protein (G pr | 3.4 |
| | 436007 | AI247716 | Hs.232168 | ESTs | 3.4 |
| | 424698 | AA164366 | Hs.151973 | hypothetical protein FLJ23511 | 3.4 |
| 10 | 435202 | AI971313 | Hs.170204 | KIAA0551 protein | 3.4 |
| | 410467 | AF102546 | Hs.63931 | dachshund (Drosophila) homolog | 3.3 |
| | 405460 | NA | | Target Exon | 3.3 |
| | 441826 | AW503603 | Hs.129915 | phosphotriesterase related | 3.3 |
| | 453472 | AL037925 | | gb:DKFZp564M037_r1 564 (synonym: hibr2) | 3.3 |
| 15 | 447078 | AW885727 | Hs.301570 | ESTs | 3.3 |
| | 441690 | R81733 | Hs.33106 | ESTs | 3.3 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 3.3 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 3.3 |
| | 408908 | BE296227 | Hs.250822 | serine/threonine kinase 15 | 3.3 |
| 20 | 414737 | AI160386 | Hs.125087 | ESTs | 3.3 |
| | 449650 | AF055575 | Hs.23838 | calcium channel, voltage-dependent, L ty | 3.3 |
| | 418912 | NM_000685 | Hs.89472 | angiotensin receptor 1 | 3.3 |
| | 436405 | AA160079 | Hs.172932 | Homo sapiens mRNA for partial 3'UTR, seq | 3.3 |
| | 453911 | AW503857 | Hs.4007 | Sarcolemmal-associated protein | 3.3 |
| 25 | 409361 | NM_005982 | Hs.54416 | sine oculis homeobox (Drosophila) homolo | 3.3 |
| | 429548 | AW138872 | Hs.135288 | ESTs | 3.3 |
| | 420807 | AA280627 | Hs.57846 | ESTs | 3.3 |
| | 409695 | AA296961 | | gb:EST112514 Adrenal gland tumor Homo sa | 3.3 |
| | 445189 | AI936450 | Hs.147482 | ESTs | 3.3 |
| 30 | 402892 | NA | | Target Exon | 3.3 |
| | 426681 | AA994896 | Hs.22514 | ESTs | 3.3 |
| | 458722 | AA741545 | Hs.282832 | ESTs, Weakly similar to T24961 hypotheti | 3.3 |
| | 409430 | R21945 | Hs.166975 | splicing factor, arginine/serine-rich 5 | 3.3 |
| | 443194 | AI954968 | Hs.279009 | matrix Gla protein | 3.3 |
| 35 | 445432 | AV653771 | | gb:AV653771 GLC Homo sapiens cDNA clone | 3.3 |
| | 410908 | AA121686 | Hs.10592 | ESTs | 3.3 |
| | 406151 | NA | | Target Exon | 3.3 |
| | 436461 | AW511956 | Hs.293261 | ESTs | 3.3 |
| | 411171 | AW820260 | | gb:QV2-ST0296-150200-040-c10 ST0296 Homo | 3.3 |
| 40 | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 3.3 |
| | 439310 | AF086120 | Hs.102793 | ESTs | 3.3 |
| | 401575 | NA | | Target Exon | 3.3 |
| | 420900 | AL045633 | Hs.44269 | ESTs | 3.3 |
| | 445628 | AI344166 | Hs.155743 | ESTs | 3.3 |
| 45 | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 3.3 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 3.3 |
| | 442118 | AA976718 | Hs.202242 | ESTs | 3.3 |
| | 416783 | AA206186 | Hs.79889 | monocyte to macrophage differentiation-a | 3.3 |
| | 435039 | AW043921 | Hs.130526 | ESTs | 3.3 |
| 50 | 451474 | T70874 | Hs.207636 | ESTs | 3.2 |
| | 442559 | T10213 | Hs.159993 | glycosyltransferase | 3.2 |
| | 453921 | AI824009 | Hs.44577 | ESTs | 3.2 |
| | 420036 | R60336 | Hs.52792 | Homo sapiens mRNA; cDNA DKFZp5861823 (f | 3.2 |
| | 435627 | W88774 | Hs.118370 | ESTs | 3.2 |
| 55 | 411598 | BE336654 | Hs.70937 | H3 histone family, member A | 3.2 |
| | 446733 | AA863360 | Hs.26040 | ESTs, Weakly similar to fatty acid omega | 3.2 |
| | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | 3.2 |
| | 403637 | NA | | C3001106*gi10047201 dbj BAB13394.1 (A | 3.2 |
| | 405547 | | | NM_018833*:Homo sapiens transporter 2, A | 3.2 |
| 60 | 427878 | C05766 | Hs.181022 | CGI-07 protein | 3.2 |
| | 451871 | AI821005 | Hs.118599 | ESTs | 3.2 |
| | 410313 | R10305 | Hs.185683 | ESTs | 3.2 |
| | 416856 | N27833 | Hs.269028 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 449490 | AI652777 | Hs.197069 | ESTs | 3.2 |
| 65 | 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 3.2 |
| | 440684 | AI253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 3.2 |
| | 459055 | N23235 | Hs.30567 | ESTs, Weakly similar to B34087 hypotheti | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 452190 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 3.2 |
| | 430965 | AA489732 | Hs.154918 | ESTs | 3.2 |
| | 405394 | | | Target Exon | 3.2 |
| 5 | 424693 | BE169810 | Hs.47557 | ESTs | 3.2 |
| | 454265 | H03556 | Hs.300949 | ESTs, Weakly similar to thyrold hormone | 3.2 |
| | 437687 | AA765917 | Hs.122840 | ESTs | 3.2 |
| | 428372 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 3.2 |
| | 414083 | AL121282 | Hs.257786 | ESTs | 3.2 |
| 10 | 411670 | AW856552 | | gb:RC1-CT0294-080100-012-a04 CT0294 Homo | 3.2 |
| | 416283 | NM_005429 | Hs.79141 | vascular endothelial growth factor C | 3.2 |
| | 437488 | AA758239 | Hs.180330 | ESTs | 3.2 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 3.2 |
| | 452042 | H38857 | Hs.243901 | Homo sapiens cDNA FLJ20738 fis, clone HE | 3.2 |
| 15 | 421477 | AI904743 | Hs.104650 | hypothetical protein FLJ10292 | 3.2 |
| | 438078 | AI016377 | Hs.131693 | ESTs | 3.2 |
| | 448816 | AB033052 | Hs.22151 | KIAA1226 protein | 3.2 |
| | 419519 | AI198719 | Hs.176376 | ESTs | 3.2 |
| | 404580 | | | NM_014112*:Homo sapiens trichorhinophala | 3.2 |
| 20 | 447046 | AA326187 | Hs.17170 | G protein-coupled receptor 4 | 3.2 |
| | 457473 | AW974903 | Hs.291231 | ESTs | 3.1 |
| | 429838 | AW904907 | Hs.30732 | hypothetical protein FLJ13409; KIAA1711 | 3.1 |
| | 459702 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 3.1 |
| | 400195 | NA | | NM_007057*:Homo sapiens ZW10 Interactor | 3.1 |
| 25 | 417860 | AW408557 | Hs.235498 | hypothetical protein FLJ14075 | 3.1 |
| | 417995 | AW974175 | Hs.188751 | ESTs, Weakly similar to MAPB_HUMAN MICRO | 3.1 |
| | 422589 | AA312735 | Hs.30512 | Homo sapiens mRNA for KIAA0556 protein, | 3.1 |
| | 435870 | AA701327 | Hs.17949 | ESTs | 3.1 |
| | 440801 | AA906366 | Hs.190535 | ESTs | 3.1 |
| 30 | 426274 | D38122 | Hs.2007 | tumor necrosis factor (ligand) superfami | 3.1 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbon | 3.1 |
| | 439677 | R82331 | Hs.164599 | ESTs | 3.1 |
| | 452834 | AI638627 | Hs.105685 | KIAA1688 protein | 3.1 |
| | 431349 | AA503653 | Hs.156942 | ESTs, Moderately similar to ALU2_HUMAN A | 3.1 |
| 35 | 417576 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 3.1 |
| | 430264 | AA470519 | | gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens | 3.1 |
| | 418827 | BE327311 | Hs.47166 | HT021 | 3.1 |
| | 410835 | AW806906 | | gb:QV4-ST0023-160400-172-d12 ST0023 Homo | 3.1 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 3.1 |
| 40 | 405336 | NA | | Target Exon | 3.1 |
| | 437783 | AI683150 | Hs.201550 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.1 |
| | 440931 | AI583052 | Hs.270058 | ESTs | 3.1 |
| | 455945 | BE160636 | | gb:PM1-HT0422-291299-002-c08 HT0422 Homo | 3.1 |
| | 430437 | AI768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fis, clone PL | 3.1 |
| 45 | 405848 | NA | | Target Exon | 3.1 |
| | 455685 | BE066976 | | gb:PM0-BT0340-211299-003-c12 BT0340 Homo | 3.1 |
| | 406970 | M29994 | | gb:Human alpha-I spectrin gene, exon 12. | 3.1 |
| | 409602 | W26713 | Hs.256972 | ESTs | 3.1 |
| | 423518 | D45027 | Hs.129732 | R3H domain (binds single-stranded nuclei | 3.1 |
| 50 | 425653 | AI065104 | Hs.249718 | ESTs, Weakly similar to A46010 X-linked | 3.1 |
| | 426326 | BE165753 | Hs.250528 | Homo sapiens, clone IMAGE:4098694, mRNA, | 3.1 |
| | 433805 | AA706910 | Hs.112742 | ESTs | 3.1 |
| | 437152 | AL050027 | | gb:Homo sapiens mRNA; cDNA DKFZp566C03243.1 | 3.1 |
| | 448602 | AI541305 | Hs.48778 | niban protein | 3.1 |
| 55 | 452844 | AW407181 | Hs.218377 | Homo sapiens cDNA FLJ11927 fis, clone HE | 3.1 |
| | 407366 | AF026942 | | gb:Homo sapiens clg33 mRNA, partial sequ | 3.1 |
| | 408254 | AW807227 | | gb:MR4-ST0062-180200-001-e10 ST0062 Homo | 3.1 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 3.1 |
| | 416790 | R83066 | Hs.7043 | succinate-CoA ligase, GDP-forming, alpha | 3.1 |
| 60 | 420020 | BE295866 | Hs.94382 | adenosine kinase | 3.1 |
| | 426119 | W94997 | Hs.189917 | ESTs | 3.1 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 3.1 |
| | 457421 | AL117431 | Hs.112165 | Homo sapiens cDNA FLJ12198 fis, clone MA | 3.1 |
| | 453403 | BE466639 | Hs.61779 | Homo sapiens cDNA FLJ13591 fis, clone PL | 3.1 |
| 65 | 454141 | AW138413 | Hs.139336 | ATP-binding cassette, sub-family C (CFTR | 3.1 |
| | 426650 | AA382814 | | gb:EST96097 Testis I Homo sapiens cDNA 5 | 3.1 |
| | 450865 | AI248013 | Hs.106532 | ESTs, Weakly similar to I38588 reverse t | 3.1 |
| | 407993 | AW135274 | Hs.12433 | ESTs | 3.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 446466 | H38026 | Hs.308 | arrestin 3, retinal (X-arrestin) | 3.1 |
| | 457888 | BE219794 | Hs.293471 | ESTs | 3.1 |
| | 420058 | AK001423 | Hs.94694 | Homo sapiens cDNA FLJ10561 fis, clone NT | 3.0 |
| | 409248 | AB033035 | Hs.51965 | KIAA1209 protein | 3.0 |
| 5 | 452747 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 3.0 |
| | 418926 | AA232658 | Hs.105794 | UDP-glucose:glycoprotein glucosyltransfe | 3.0 |
| | 419346 | AI830417 | Hs.44143 | polybromo 1 | 3.0 |
| | 429826 | N93266 | Hs.40747 | ESTs | 3.0 |
| | 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (f | 3.0 |
| 10 | 420139 | NM_005357 | Hs.95351 | lipase, hormone-sensitive | 3.0 |
| | 405609 | NA | | ENSP00000241065*:cDNA | 3.0 |
| | 404274 | | | NM_002944*:Homo sapiens v-ros avian UR2 | 3.0 |
| | 449777 | AI971362 | Hs.231945 | ESTs | 3.0 |
| | 415459 | H07118 | Hs.6099 | ESTs | 3.0 |
| 15 | 415245 | N59650 | Hs.27252 | ESTs | 3.0 |
| | 406291 | NA | | Target Exon | 3.0 |
| | 414210 | BE383592 | | gb:601297871F1 NIH_MGC_19 Homo sapiens c | 3.0 |
| | 432055 | AW972359 | Hs.293334 | ESTs | 3.0 |
| | 442246 | AI791988 | Hs.129115 | ESTs | 3.0 |
| 20 | 451353 | N21043 | Hs.42932 | ESTs | 3.0 |
| | 451177 | AI969716 | Hs.13034 | ESTs | 3.0 |
| | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 3.0 |
| | 401326 | NA | | C10000447*:gil1168375 sp P43467 AGA1_PED | 3.0 |
| | 409920 | BE169746 | Hs.12504 | likely ortholog of mouse Arkadia | 3.0 |
| 25 | 432887 | AI926047 | Hs.162859 | ESTs | 3.0 |
| | 411789 | AF245505 | Hs.72157 | DKFZP56411922 protein | 3.0 |
| | 401045 | | | C11001883*:gil6753278 ref NP_033938.1 c | 3.0 |
| | 432162 | AA584062 | Hs.272798 | hypothetical protein FLJ20413 | 3.0 |
| | 434627 | AI221894 | Hs.39311 | ESTs | 3.0 |
| 30 | 442611 | BE077155 | Hs.177537 | hypothetical protein DKFZp761B1514 | 3.0 |
| | 425477 | AW958879 | Hs.270535 | ESTs | 3.0 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 3.0 |
| | 433014 | NM_014711 | Hs.279912 | KIAA0419 gene product | 3.0 |
| | 415542 | R13474 | Hs.290263 | ESTs, Weakly similar to I38022 hypotheti | 3.0 |
| 35 | 416173 | R52782 | | gb:yg99d09.r1 Soares infant brain 1N1B H | 3.0 |
| | 408155 | AB014528 | Hs.43133 | KIAA0628 gene product | 3.0 |
| | 453913 | AW004683 | Hs.78934 | mutS (E. coli) homolog 2 (colon cancer, | 3.0 |
| | 435495 | AI754212 | Hs.21951 | Homo sapiens Xq pseudoautosomal region; | 3.0 |
| | 423629 | AW021173 | Hs.18612 | Homo sapiens cDNA: FLJ21909 fis, clone H | 3.0 |
| 40 | 411836 | AW901879 | Hs.314453 | ESTs | 3.0 |
| | 415030 | D31118 | Hs.191735 | hypothetical protein MGC10520 | 3.0 |
| | 419606 | AW294795 | Hs.198529 | ESTs | 3.0 |
| | 440310 | AA878939 | Hs.125406 | ESTs | 3.0 |
| | 443608 | AI375957 | Hs.289074 | F-box only protein 22 | 3.0 |
| 45 | 414140 | AA281279 | Hs.23317 | hypothetical protein FLJ14681 | 3.0 |
| | 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | 3.0 |
| | 435393 | AA701259 | Hs.189299 | ESTs | 3.0 |
| | 454071 | AI041793 | Hs.42502 | ESTs | 3.0 |
| | 446922 | BE175605 | | gb:RC5-HT0580-100500-022-H07 HT0580 Homo | 3.0 |
| 50 | 448062 | AW295923 | Hs.255472 | KIAA1843 protein | 3.0 |
| | 427711 | M31659 | Hs.180408 | solute carrier family 25 (mitochondrial | 3.0 |
| | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 3.0 |
| | 424866 | W01938 | Hs.337243 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.9 |
| | 433043 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | 2.9 |
| 55 | 420802 | U22376 | Hs.1334 | v-myb avian myeloblastosis viral oncogen | 2.9 |
| | 445625 | BE246743 | Hs.288529 | hypothetical protein FLJ22635 | 2.9 |
| | 403677 | NA | | C4001462:gil4887715 gb AAA79329.2 (L088 | 2.9 |
| | 411093 | BE067650 | | gb:MR4-BT0358-090300-003-e01 BT0358 Homo | 2.9 |
| | 435255 | W87434 | Hs.106015 | ESTs, Moderately similar to ALU1_HUMAN A | 2.9 |
| 60 | 443127 | BE568102 | Hs.180312 | mitochondrial ribosomal protein S16 | 2.9 |
| | 448104 | AI674818 | Hs.316433 | Homo sapiens cDNA FLJ11375 fis, clone HE | 2.9 |
| | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 2.9 |
| | 430414 | AW365665 | Hs.120388 | ESTs | 2.9 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 2.9 |
| 65 | 458562 | N34128 | Hs.145268 | ESTs | 2.9 |
| | 402109 | NA | | Target Exon | 2.9 |
| | 429629 | BE501732 | Hs.30622 | Homo sapiens cDNA FLJ13010 fis, clone NT | 2.9 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 442295 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fis, clone HE | 2.9 |
| | 419752 | AA249573 | Hs.152618 | ESTs, Moderately similar to ZN91_HUMAN Z | 2.9 |
| | 404721 | | | NM_005596*:Homo sapiens nuclear factor I | 2.9 |
| 5 | 445107 | AI208121 | Hs.147313 | ESTs, Weakly similar to I38022 hypotheti | 2.9 |
| | 401987 | | | NM_002737*:Homo sapiens protein kinase C | 2.9 |
| | 430566 | AA481282 | Hs.190149 | ESTs | 2.9 |
| | 444517 | AI939339 | Hs.146883 | ESTs | 2.9 |
| | 445563 | AW873606 | Hs.149006 | ESTs | 2.9 |
| 10 | 427691 | AW194426 | Hs.20726 | ESTs | 2.9 |
| | 456561 | AI868634 | Hs.246358 | ESTs, Weakly similar to T32250 hypotheti | 2.9 |
| | 401458 | | | Target Exon | 2.9 |
| | 421039 | NM_003478 | Hs.101299 | cullin 5 | 2.9 |
| | 459504 | BE514127 | | gb:501315974F1 NIH_MGC_8 Homo sapiens cD | 2.9 |
| 15 | 424962 | NM_012288 | Hs.153954 | TRAM-like protein | 2.9 |
| | 409617 | BE003760 | Hs.55209 | Homo sapiens mRNA; cDNA DKFZp434K0514 (f | 2.9 |
| | 416931 | D45371 | Hs.80485 | adipose most abundant gene transcript 1 | 2.9 |
| | 413221 | BE161151 | | gb:PMO-HT0425-141299-001-F08 HT0425 Homo | 2.9 |
| | 409732 | NM_016122 | Hs.56148 | NY-REN-58 antigen | 2.9 |
| 20 | 433687 | AA743991 | | gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens | 2.9 |
| | 434340 | AI193043 | Hs.128685 | ESTs, Weakly similar to T17226 hypotheti | 2.9 |
| | 454529 | Z45439 | Hs.270425 | ESTs | 2.9 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 2.9 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 2.9 |
| 25 | 457402 | AW452648 | Hs.149342 | activation-induced cytidine deaminase | 2.9 |
| | 449051 | AW961400 | Hs.333526 | HER2 receptor tyrosine kinase (c-erb-b2, | 2.9 |
| | 408761 | AA057264 | Hs.238936 | ESTs, Weakly similar to (define not ava | 2.9 |
| | 401093 | | | C12000586*:gij6330167 dbj BAA86477.1) (A | 2.9 |
| | 435061 | AI651474 | Hs.163944 | ESTs | 2.9 |
| 30 | 447985 | AI681475 | Hs.200949 | ESTs | 2.9 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 2.9 |
| | 426384 | AI472078 | Hs.303662 | ESTs | 2.9 |
| | 411905 | BE265067 | | gb:601193893F1 NIH_MGC_7 Homo sapiens cD | 2.9 |
| | 405953 | NA | | Target Exon | 2.8 |
| 35 | 420854 | AW296927 | | gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCL_CGAP_Su | 2.8 |
| | 434265 | AA846811 | Hs.130554 | Homo sapiens cDNA: FLJ23089 fis, clone L | 2.8 |
| | 428365 | AA295331 | Hs.183861 | Homo sapiens cDNA FLJ20042 fis, clone CO | 2.8 |
| | 442861 | AA243837 | Hs.57787 | ESTs | 2.8 |
| | 448337 | AW206453 | Hs.3782 | ESTs | 2.8 |
| 40 | 452554 | AW452434 | Hs.58006 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.8 |
| | 412248 | BE176480 | | gb:RC3-HT0585-160300-022-c02 HT0585 Homo | 2.8 |
| | 449450 | AL039852 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 2.8 |
| | 434757 | AI038997 | Hs.132921 | ESTs | 2.8 |
| | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 2.8 |
| 45 | 454545 | AW806899 | | gb:QV4-ST0023-160400-172-c12 ST0023 Homo | 2.8 |
| | 439842 | AI910896 | Hs.132413 | ESTs | 2.8 |
| | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 2.8 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 2.8 |
| | 411086 | BE070800 | | gb:RC3-BT0502-251199-011-c07 BT0502 Homo | 2.8 |
| 50 | 400250 | NA | | Eos Control | 2.8 |
| | 449168 | NM_016206 | Hs.23142 | colon carcinoma related protein | 2.8 |
| | 456482 | AA485224 | | gb:aa41b12.s1 NCL_CGAP_GCB1 Homo sapiens | 2.8 |
| | 426044 | AA502490 | Hs.336695 | ESTs | 2.8 |
| | 431854 | AA383550 | Hs.271699 | polymerase (DNA directed) Iota | 2.8 |
| | 405873 | NA | | Target Exon | 2.8 |
| 55 | 440400 | AA994364 | Hs.125594 | ESTs, Weakly similar to T25472 hypotheti | 2.8 |
| | 458265 | AI075375 | Hs.128193 | ESTs, Weakly similar to IRX2_HUMAN IROQU | 2.8 |
| | 413708 | BE158791 | | gb:IL2-HT0397-091299-025-D02 HT0397 Homo | 2.8 |
| | 423739 | AA398155 | Hs.97600 | ESTs | 2.8 |
| 60 | 424408 | AI754813 | Hs.146428 | collagen, type V, alpha 1 | 2.8 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 2.8 |
| | 421825 | AA298758 | Hs.183747 | ESTs, Moderately similar to CALB_HUMAN C | 2.8 |
| | 417742 | R64719 | | gb:EST22d11 WATM1 Homo sapiens cDNA clon | 2.8 |
| | 402765 | | | C1003621*:gij12407405 gb AAG53491.1 AF22 | 2.8 |
| 65 | 444378 | R41339 | Hs.12569 | ESTs | 2.8 |
| | 419172 | AW338625 | Hs.22120 | ESTs | 2.8 |
| | 401497 | | | Target Exon | 2.8 |
| | 402376 | | | C19000763*:gij1363912 pir JC4296 ring f | 2.8 |

| | | | | |
|----|--------|-----------|--|-----|
| | 405041 | NA | C3001706*:gi1345652[sp]P15989[CA36_CHIC | 2.8 |
| | 408758 | NM_003686 | Hs.47504 exonuclease 1 | 2.8 |
| | 431917 | D16181 | Hs.2868 peripheral myelin protein 2 | 2.8 |
| | 437583 | AA761190 | Hs.244627 ESTs | 2.8 |
| 5 | 453737 | AA744862 | Hs.194293 ESTs, Weakly similar to I54374 gene NF2 | 2.8 |
| | 458094 | AF086325 | gb:Homo sapiens full length insert cDNA | 2.8 |
| | 401283 | NA | Target Exon | 2.8 |
| | 410784 | AW803201 | gb:IL2-UM0077-070500-080-E06 UM0077 Homo | 2.8 |
| 10 | 417601 | NM_014735 | Hs.82292 KIAA0215 gene product | 2.8 |
| | 418236 | AW994005 | Hs.337534 ESTs | 2.8 |
| | 435532 | AW291488 | Hs.117305 Homo sapiens, clone IMAGE:3682908, mRNA | 2.8 |
| | 454714 | AW815098 | gb:QV4-ST0212-091199-023-f10 ST0212 Homo | 2.8 |
| | 418629 | BE247550 | Hs.86859 growth factor receptor-bound protein 7 | 2.8 |
| 15 | 442101 | AI651930 | Hs.135684 ESTs | 2.8 |
| | 405080 | AK000375 | Hs.88820 HDCMC28P protein | 2.8 |
| | 414661 | T97401 | Hs.21929 ESTs | 2.8 |
| | 425589 | AI650633 | Hs.143688 Homo sapiens cDNA: FLJ23031 fis, clone L | 2.8 |
| | 429638 | AI916662 | Hs.211577 kinectin 1 (kinesin receptor) | 2.7 |
| 20 | 428824 | W23624 | Hs.173059 ESTs | 2.7 |
| | 421566 | NM_000399 | Hs.1395 early growth response 2 (Krox-20 (Drosop | 2.7 |
| | 414596 | BE386870 | gb:601275271F1 NIH_MGC_20 Homo sapiens c | 2.7 |
| | 440868 | R79707 | Hs.263339 ESTs, Moderately similar to I38022 hypot | 2.7 |
| | 452943 | BE247449 | Hs.31082 hypothetical protein FLJ10525 | 2.7 |
| 25 | 443772 | AV646449 | Hs.282872 ESTs | 2.7 |
| | 432361 | AI378562 | Hs.159585 ESTs | 2.7 |
| | 430375 | AW371048 | Hs.93758 H4 histone family, member H | 2.7 |
| | 406504 | NA | C5000558:gi14504675[ref]NP_002175.1 int | 2.7 |
| | 423279 | AW959861 | Hs.290943 ESTs | 2.7 |
| 30 | 424871 | NM_004525 | Hs.153595 low density lipoprotein-related protein | 2.7 |
| | 453619 | H87648 | Hs.33922 Homo sapiens, clone MGC:9084, mRNA, comp | 2.7 |
| | 423961 | D13666 | Hs.136348 osteoblast specific factor 2 (fasciclin | 2.7 |
| | 422156 | N34524 | gb:yy56d10.s1 Soares_multiple_sclerosis_ | 2.7 |
| | 415752 | BE314524 | Hs.78776 putative transmembrane protein | 2.7 |
| 35 | 419987 | NM_005014 | Hs.94070 osteomodulin | 2.7 |
| | 406182 | NA | Target Exon | 2.7 |
| | 416495 | X69970 | Hs.79350 RYK receptor-like tyrosine kinase | 2.7 |
| | 444701 | AI916512 | Hs.198394 ESTs | 2.7 |
| | 408171 | AA301228 | Hs.43299 hypothetical protein FLJ12890 | 2.7 |
| 40 | 430153 | AW968128 | Hs.336679 ESTs | 2.7 |
| | 413383 | AA128978 | Hs.154706 hypothetical protein FLJ14917 | 2.7 |
| | 414831 | M31158 | Hs.77439 protein kinase, cAMP-dependent, regulato | 2.7 |
| | 413278 | BE563085 | Hs.833 interferon-stimulated protein, 15 kDa | 2.7 |
| | 433132 | AB026264 | Hs.284245 hypothetical protein IMPACT | 2.7 |
| 45 | 437030 | AA742577 | Hs.303781 EST | 2.7 |
| | 439031 | AF075079 | gb:Homo sapiens full length insert cDNA | 2.7 |
| | 449532 | W74653 | Hs.271593 ESTs, Moderately similar to A47582 B-cel | 2.7 |
| | 406153 | | Target Exon | 2.7 |
| | 406625 | Y13647 | Hs.119597 stearoyl-CoA desaturase (delta-9-desatur | 2.7 |
| 50 | 444698 | AI188139 | Hs.147050 ESTs | 2.7 |
| | 432328 | AI572739 | Hs.195471 6-phosphofructo-2-kinase/fructose-2,6-bi | 2.7 |
| | 429628 | H09604 | Hs.13268 ESTs | 2.7 |
| | 420149 | AA255920 | Hs.88095 ESTs | 2.7 |
| | 431207 | AA495925 | Hs.9394 ESTs | 2.7 |
| 55 | 438394 | BE379623 | Hs.27693 peptidylprolyl isomerase (cyclophilin)-I | 2.7 |
| | 443304 | AI050073 | Hs.135338 ESTs | 2.7 |
| | 427660 | AI741320 | Hs.114121 Homo sapiens cDNA: FLJ23228 fis, clone C | 2.7 |
| | 408460 | AA054726 | Hs.285574 ESTs | 2.7 |
| | 416515 | N91716 | Hs.194140 ESTs, Weakly similar to I38022 hypotheti | 2.7 |
| 60 | 429922 | Z97630 | Hs.226117 H1 histone family, member 0 | 2.7 |
| | 418203 | X54942 | Hs.83758 CDC28 protein kinase 2 | 2.7 |
| | 439509 | AF086332 | Hs.58314 ESTs | 2.7 |
| | 402184 | NA | ENSP00000245238*:CDNA FLJ10922 fis, clon | 2.7 |
| | 450496 | AW449251 | Hs.257131 ESTs | 2.7 |
| 65 | 451963 | AI825440 | Hs.224952 ESTs | 2.7 |
| | 457938 | AI373638 | Hs.133900 ESTs | 2.7 |
| | 441541 | AA938663 | Hs.199828 ESTs | 2.7 |
| | 441111 | AI806867 | Hs.126594 ESTs | 2.7 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 2.7 |
| | 445354 | AV653485 | Hs.6390 | Homo sapiens clone FLB3344 PRO0845 mRNA | 2.7 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 2.7 |
| 5 | 410889 | X91662 | Hs.66744 | twist (Drosophila) homolog (acrocephalos | 2.7 |
| | 445234 | AW137636 | Hs.146059 | ESTs | 2.7 |
| | 413903 | AA496493 | Hs.23136 | ESTs | 2.7 |
| | 406069 | NA | | Target Exon | 2.7 |
| | 447410 | AI470235 | Hs.172698 | EST | 2.7 |
| | 401256 | NA | | NM_024089*:Homo sapiens hypothetical pro | 2.7 |
| 10 | 415139 | AW975942 | Hs.48524 | ESTs | 2.7 |
| | 420218 | AW958037 | Hs.286 | ribosomal protein L4 | 2.7 |
| | 455511 | BE144762 | | gb:CM0-HT0180-041099-065-b04 HT0180 Homo | 2.7 |
| | 438825 | BE327427 | Hs.79953 | ESTs | 2.6 |
| 15 | 409564 | AA045857 | Hs.54943 | fracture callus 1 (rat) homolog | 2.6 |
| | 452837 | AL121053 | Hs.5534 | Homo sapiens cDNA FLJ12961 fis, clone NT | 2.6 |
| | 434876 | AF160477 | Hs.61460 | Ig superfamily receptor LNIR | 2.6 |
| | 421565 | AK001122 | Hs.105859 | hypothetical protein FLJ10260 | 2.6 |
| | 453279 | AW893940 | Hs.59698 | ESTs | 2.6 |
| | 430785 | Z30201 | | gb:HHEA22G Atrium cDNA library Human hea | 2.6 |
| 20 | 456986 | D38299 | Hs.170917 | prostaglandin E receptor 3 (subtype EP3) | 2.6 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 2.6 |
| | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 1 H | 2.6 |
| | 429208 | AA447990 | Hs.190478 | ESTs | 2.6 |
| | 430733 | AW975920 | Hs.283361 | ESTs | 2.6 |
| 25 | 441720 | AI346487 | Hs.28739 | ESTs | 2.6 |
| | 418986 | AI123555 | Hs.81796 | ESTs | 2.6 |
| | 432481 | AW451645 | Hs.151504 | Homo sapiens cDNA FLJ11973 fis, clone HE | 2.6 |
| | 434338 | AW754311 | | gb:CM1-CT0337-141299-068-f07 CT0337 Homo | 2.6 |
| 30 | 417061 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 2.6 |
| | 410530 | M25809 | Hs.64173 | ATPase, H transporting, lysosomal (vacuo | 2.6 |
| | 456672 | AK002016 | Hs.114727 | Homo sapiens, clone MGC:16327, mRNA, com | 2.6 |
| | 425071 | NM_013989 | Hs.154424 | deiodinase, lodothyronine, type II | 2.6 |
| | 408868 | AW292286 | Hs.255058 | ESTs | 2.6 |
| 35 | 451531 | AA018311 | Hs.114762 | ESTs | 2.6 |
| | 405822 | | | Target Exon | 2.6 |
| | 418301 | AW976201 | Hs.53913 | hypothetical protein FLJ10252 | 2.6 |
| | 417315 | AI080042 | Hs.336901 | ribosomal protein S24 | 2.6 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 2.6 |
| 40 | 443204 | AW205878 | Hs.29643 | Homo sapiens cDNA FLJ13103 fis, clone NT | 2.6 |
| | 405638 | | | Target Exon | 2.6 |
| | 452542 | AW812256 | | gb:RC0-ST0174-191099-031-a07 ST0174 Homo | 2.6 |
| | 403943 | | | C5000355:g 4503225[ref]NP_000765.1 cyt | 2.6 |
| | 404535 | Z25884 | Hs.121483 | chloride channel 1, skeletal muscle (Th | 2.6 |
| 45 | 402800 | NA | | Target Exon | 2.6 |
| | 449144 | AI989503 | Hs.233405 | ESTs | 2.6 |
| | 454934 | AW846080 | Hs.314324 | ESTs | 2.6 |
| | 424717 | H03754 | Hs.152213 | wingless-type MMTV integration site fami | 2.6 |
| | 428303 | AW974476 | Hs.183601 | regulator of G-protein signalling 16 | 2.6 |
| 50 | 427970 | AA418187 | Hs.330515 | ESTs | 2.6 |
| | 450638 | AK001826 | Hs.25245 | hypothetical protein FLJ11269 | 2.6 |
| | 453034 | BE246010 | Hs.271468 | Homo sapiens mRNA for FLJ00038 protein, | 2.6 |
| | 455097 | AW855802 | | gb:RC1-CT0279-170200-023-d08 CT0279 Homo | 2.6 |
| | 427317 | AB028955 | Hs.175780 | KIAA1032 protein | 2.6 |
| 55 | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.6 |
| | 427510 | Z47542 | Hs.179312 | small nuclear RNA activating complex, po | 2.6 |
| | 423201 | NM_000163 | Hs.125180 | growth hormone receptor | 2.6 |
| | 406271 | | | Target Exon | 2.6 |
| | 442696 | BE566962 | Hs.7063 | Homo sapiens cDNA: FLJ20913 fis, clone A | 2.6 |
| 60 | 454018 | AW016892 | Hs.100855 | ESTs | 2.6 |
| | 435420 | AI928513 | Hs.59203 | ESTs | 2.6 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase | 2.6 |
| | 455708 | BE069326 | | gb:QV3-BT0381-170100-060-g03 BT0381 Homo | 2.6 |
| | 439347 | W24320 | Hs.102941 | Homo sapiens cDNA: FLJ21531 fis, clone C | 2.6 |
| | 407523 | X64984 | | gb:H.sapiens mRNA HTPCRX10 for olfactory | 2.6 |
| 65 | 425101 | AA830431 | Hs.180811 | ESTs | 2.6 |
| | 435153 | AA668763 | Hs.291939 | ESTs | 2.6 |
| | 409139 | AI681917 | Hs.3321 | ESTs, Highly similar to IRX1_HUMAN IROQU | 2.6 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 455100 | BE160198 | | gb:QV1-HT0413-010200-059-h03 HT0413 Homo | 2.6 |
| | 414612 | BE274552 | Hs.76578 | protein inhibitor of activated STAT3 | 2.6 |
| | 440283 | AI732892 | Hs.190489 | ESTs | 2.6 |
| | 423025 | AA831267 | Hs.12244 | hypothetical protein FLJ20097 | 2.6 |
| 5 | 431473 | AA825686 | Hs.321176 | ESTs, Weakly similar to S65824 reverse t | 2.6 |
| | 404440 | | | NM_021048:Homo sapiens melanoma antigen, | 2.6 |
| | 403388 | NA | | C3001398*gi 12248917 tbl BAB20375.1 (A | 2.6 |
| | 403775 | NA | | Target Exon | 2.6 |
| | 405037 | NA | | NM_021628*:Homo sapiens arachidonate lip | 2.6 |
| 10 | 407447 | AF290544 | | gb:Homo sapiens aminopeptidase mRNA, par | 2.6 |
| | 420952 | AA282067 | Hs.88972 | ESTs, Moderately similar to A46010 X-In | 2.6 |
| | 435447 | AI872932 | | gb:wm72e03.x1 NCLCGAP_U12 Homo sapiens | 2.6 |
| | 440202 | AW516211 | Hs.125300 | ring finger protein 21, Interferon-respo | 2.6 |
| | 445854 | AI702885 | Hs.145568 | ESTs | 2.6 |
| 15 | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 2.6 |
| | 414870 | N72264 | Hs.300670 | KIAA1204 protein | 2.6 |
| | 457411 | AW085961 | Hs.130093 | ESTs | 2.6 |
| | 424676 | Y08565 | Hs.151678 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 2.6 |
| | 404443 | | | C8001428*gi 6572242 emb CAB62951.1 (Z9 | 2.6 |
| 20 | 452268 | NM_003512 | Hs.28777 | H2A histone family, member L | 2.6 |
| | 430832 | AI073913 | Hs.100686 | ESTs, Weakly similar to JE0350 Anterior | 2.6 |
| | 444779 | AI192105 | Hs.147170 | ESTs | 2.6 |
| | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 2.6 |
| | 459089 | F13036 | Hs.27373 | Homo sapiens mRNA; cDNA DKFZp564O1763 (f2.6 | 2.6 |
| 25 | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 2.6 |
| | 454111 | AW081681 | Hs.269064 | ESTs, Weakly similar to T42689 hypotheti | 2.6 |
| | 411165 | NM_000169 | Hs.69089 | galactosidase, alpha | 2.6 |
| | 406922 | S70284 | | gb:stearoyl-CoA desaturase [human, adipo | 2.6 |
| | 456045 | H62943 | Hs.154188 | ESTs | 2.6 |
| 30 | 413111 | BE065837 | | gb:RC2-BT0318-110100-012-g12 BT0318 Homo | 2.6 |
| | 423123 | NM_012247 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selen | 2.6 |
| | 432201 | AI538613 | Hs.298241 | Transmembrane protease, serine 3 | 2.5 |
| | 427032 | AF012023 | Hs.173274 | integrin cytoplasmic domain-associated p | 2.5 |
| | 445417 | AK001058 | Hs.12680 | Homo sapiens cDNA FLJ10196 fis, clone HE | 2.5 |
| 35 | 422225 | BE245652 | Hs.118281 | zinc finger protein 266 | 2.5 |
| | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (MMP7; uterin | 2.5 |
| | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 2.5 |
| | 426310 | NM_000909 | Hs.169266 | neuropeptide Y receptor Y1 | 2.5 |
| | 419589 | AW973708 | Hs.201925 | Homo sapiens cDNA FLJ13446 fis, clone PL | 2.5 |
| 40 | 437770 | AA767881 | Hs.122897 | ESTs | 2.5 |
| | 442818 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 2.5 |
| | 414251 | AL042306 | Hs.97689 | VASA protein | 2.5 |
| | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 431956 | AK002032 | Hs.272245 | Homo sapiens cDNA FLJ11170 fis, clone PL | 2.5 |
| 45 | 455732 | BE080908 | | gb:QV1-BT0631-280200-084-h07 BT0631 Homo | 2.5 |
| | 458624 | AI362790 | Hs.278639 | KIAA1684 protein; likely homolog of mous | 2.5 |
| | 428257 | BE394723 | Hs.275243 | S100 calcium-binding protein A6 (calcycl | 2.5 |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 2.5 |
| | 458652 | AW375610 | Hs.117102 | hypothetical protein FLJ13046 similar to | 2.5 |
| 50 | 458012 | AI424899 | Hs.188211 | ESTs | 2.5 |
| | 422996 | BE091089 | | gb:PM4-BT0724-130400-006-c07 BT0724 Homo | 2.5 |
| | 410804 | U64820 | Hs.66521 | Machado-Joseph disease (spinocerebellar | 2.5 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 2.5 |
| | 440029 | AW089705 | Hs.293711 | ESTs, Weakly similar to S64329 probable | 2.5 |
| 55 | 448141 | AI471598 | Hs.197531 | ESTs | 2.5 |
| | 409163 | AA065081 | | gb:zm13a03.s1 Stratagene pancreas (93720 | 2.5 |
| | 431385 | BE178536 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 2.5 |
| | 414569 | AF109298 | Hs.118258 | prostate cancer associated protein 1 | 2.5 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.5 |
| 60 | 455935 | BE158687 | | gb:CM0-HT0395-280100-169-b09 HT0395 Homo | 2.5 |
| | 425025 | AW953168 | Hs.12407 | ESTs | 2.5 |
| | 416589 | AA652687 | Hs.96151 | Human DNA sequence from clone RP5-1103G7 | 2.5 |
| | 404826 | | | Target Exon | 2.5 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 2.5 |
| 65 | 421991 | NM_014918 | Hs.110488 | KIAA0990 protein | 2.5 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 2.5 |
| | 448516 | AW898595 | | gb:RC1-NN0073-260400-011-g09 NN0073 Homo | 2.5 |

| | | | | |
|----|--------|-----------|--|-----|
| | 403356 | NA | ENSP00000251525*:Hypothetical protein KI | 2.5 |
| | 404983 | | ENSP00000252242*:Keratin, type II cytosk | 2.5 |
| | 418282 | AA215535 | Hs.98133 ESTs | 2.5 |
| 5 | 427409 | AW467143 | Hs.135411 actin related protein | 2.5 |
| | 431806 | AF186114 | Hs.270737 tumor necrosis factor (ligand) superfam | 2.5 |
| | 443367 | AW071349 | Hs.215937 ESTs | 2.5 |
| | 421246 | AW582962 | Hs.102897 CGI-47 protein | 2.5 |
| | 439217 | AF086041 | Hs.42975 ESTs | 2.5 |
| | 400925 | | Target Exon | 2.5 |
| 10 | 404552 | NA | ENSP00000220888*:ZINC FINGER TRANSCRIPT2.5 | 2.5 |
| | 417168 | AL133117 | Hs.81376 Homo sapiens mRNA; cDNA DKFZp586L1121 (f | 2.5 |
| | 418841 | NM_002332 | Hs.89137 low density lipoprotein-related protein | 2.5 |
| | 426853 | U32974 | Hs.172777 baculoviral IAP repeat-containing 4 | 2.5 |
| 15 | 427738 | NM_000318 | Hs.180612 peroxisomal membrane protein 3 (35kD, Ze | 2.5 |
| | 457384 | AA501760 | Hs.15806 Homo sapiens mRNA; cDNA DKFZp434H2019 (f | 2.5 |
| | 447128 | AI271898 | Hs.164866 cyclin K | 2.5 |
| | 454693 | AW813428 | gb:MR3-ST0192-010200-210-c05 ST0192 Homo | 2.5 |
| | 434657 | AA641876 | Hs.191840 ESTs | 2.5 |
| | 402077 | NA | Target Exon | 2.5 |
| 20 | 400289 | X07820 | Hs.2258 matrix metalloproteinase 10 (MMP10; str | 2.5 |
| | 409723 | AW885757 | Hs.257862 ESTs | 2.5 |
| | 447020 | T27308 | Hs.16986 hypothetical protein FLJ11046 | 2.5 |
| | 455068 | AI807894 | Hs.47274 Homo sapiens mRNA; cDNA DKFZp564B176 (fr | 2.5 |
| | 431232 | AI024353 | Hs.131755 hypothetical protein FLJ14298 | 2.5 |
| 25 | 408938 | AA059013 | Hs.22607 ESTs | 2.5 |
| | 411571 | AA122393 | Hs.70811 hypothetical protein FLJ20516 | 2.5 |
| | 426504 | AW162919 | Hs.170160 RAB2, member RAS oncogene family-like | 2.5 |
| | 428248 | AI126772 | Hs.40479 ESTs | 2.5 |
| 30 | 408813 | AI580090 | Hs.48295 RNA helicase family | 2.5 |
| | 423504 | N80077 | Hs.24792 chromosome 12 open reading frame 5 | 2.5 |
| | 425441 | AA449644 | Hs.193063 Homo sapiens cDNA FLJ14201 fis, clone NT | 2.5 |
| | 443066 | AW297921 | Hs.255703 ESTs | 2.5 |
| | 443556 | AA256769 | Hs.94949 methylmalonyl-CoA epimerase | 2.5 |
| 35 | 428943 | AW086180 | Hs.37636 ESTs, Weakly similar to KIAA1392 protein | 2.5 |
| | 425320 | U29344 | Hs.83190 fatty acid synthase | 2.5 |
| | 430388 | AA356923 | Hs.240770 nuclear cap binding protein subunit 2, 2 | 2.5 |
| | 423242 | AL039402 | Hs.125783 DEME-6 protein | 2.5 |
| | 416241 | N52639 | Hs.32683 ESTs | 2.5 |
| | 440244 | AI743977 | Hs.205144 ESTs | 2.5 |
| 40 | 409239 | AA740875 | Hs.44307 ESTs, Moderately similar to I38022 hypot | 2.5 |
| | 452464 | AW500507 | Hs.192619 KIAA1600 protein | 2.5 |
| | 410718 | AI920783 | Hs.191435 ESTs | 2.5 |
| | 408877 | AA479033 | Hs.130315 ESTs, Weakly similar to A47582 B-cell gr | 2.5 |
| 45 | 445150 | AI446747 | Hs.338704 olfactory receptor, family 7, subfamily | 2.5 |
| | 407756 | AA116021 | Hs.38260 ubiquitin specific protease 18 | 2.5 |
| | 407633 | NM_007069 | Hs.37189 similar to rat HREV107 | 2.5 |
| | 449754 | H00820 | Hs.30977 ESTs, Weakly similar to B34087 hypotheti | 2.5 |
| | 419316 | AA236255 | Hs.298419 ESTs | 2.5 |
| 50 | 429118 | H20669 | Hs.35406 ESTs, Highly similar to unnamed protein | 2.5 |
| | 440331 | AL046412 | Hs.202151 ESTs | 2.5 |
| | 449344 | AI640355 | Hs.312691 ESTs | 2.5 |
| | 459006 | AW298631 | Hs.27721 Wolf-Hirschhorn syndrome candidate 1-lik | 2.5 |
| | 423165 | AI937547 | Hs.124915 hypothetical protein MGC2601 | 2.5 |
| 55 | 411337 | AW837349 | gb:QV2-LT0038-270300-108-d12 LT0038 Homo | 2.5 |
| | 438290 | AA843719 | Hs.122341 ESTs | 2.5 |
| | 406414 | | C5000506*:gij124941 sp P18614 ITA1_RAT | 2.5 |
| | 424498 | AB033043 | Hs.149377 hypothetical protein DKFZp761L0424 | 2.5 |
| | 443464 | BE548446 | Hs.5167 Homo sapiens mRNA; cDNA DKFZp434F152 (fr | 2.5 |
| 60 | 424856 | AA347746 | Hs.9521 ESTs, Weakly similar to ZN43_HUMAN ZINC | 2.5 |
| | 440304 | BE159984 | Hs.125395 ESTs | 2.5 |
| | 409045 | AA635062 | Hs.50094 Homo sapiens mRNA; cDNA DKFZp434O0515 (f2.5 | 2.5 |
| | 422648 | D86983 | Hs.118893 Melanoma associated gene | 2.5 |
| | 428819 | AL135623 | Hs.193914 KIAA0575 gene product | 2.5 |
| 65 | 412520 | AA442324 | Hs.795 H2A histone family, member O | 2.5 |
| | 430602 | D13752 | Hs.184927 cytochrome P450, subfamily X1B (steroid | 2.5 |
| | 408031 | AA081395 | Hs.42173 Homo sapiens cDNA FLJ10366 fis, clone NT | 2.5 |
| | 403133 | | Target Exon | 2.5 |

| | | | | |
|--------|----------|-----------|--|-----|
| 413189 | BE070231 | | gb:QV4-BT0407-260100-087-f12 BT0407 Homo | 2.5 |
| 400346 | AB041269 | Hs.272263 | Homo sapiens mRNA for keratin 19, partia | 2.5 |
| 435509 | AI458679 | Hs.181915 | ESTs | 2.5 |
| 458145 | AI239457 | Hs.130794 | ESTs | 2.5 |

5

TABLE 19A

Table 19A shows the accession numbers for those pkeys lacking unigeneID's for Table 19. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15

| Pkey | CAT number | Accessions |
|--------|------------|---|
| 407647 | 1007366_1 | AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656 |
| 407980 | 103087_1 | AA046309 AI263500 AA046397 |
| 408254 | 1049346_1 | AW807227 AW807576 AW807137 AW807157 AW807495 AW807494 AW807417 AW807083 AW845786 AW845801 AW807130 AW807335 AW807081 AW807349 AW807339 AW807164 AW807341 AW807224 AW845903 AW177424 AW807159 AW807123 BE141576 AW807340 AW807334 AW807520 AW807205 AW807505 BE141574 AW807390 AW807395 AW845789 AW807101 AW807089 AW807519 AW807239 AW807509 AW807356 AW807526 AW807098 AW807307 AW807153 AW807295 AW807313 AW807322 AW807265 AW807513 AW807516 AW807166 AW807501 AW807120 AW807168 AW807121 AW807527 AW807151 AW807203 AW807489 AW807511 AW807158 AW845800 AW807507 AW845793 AW845796 AW807296 AW845781 AW807444 AW845871 AW807512 AW807242 AW807141 AW807522 AW807487 AW807514 AW807142 AW807232 AW807379 AW807114 AW807518 AW807199 AW807211 AW807498 AW807086 AW807492 AW807218 AW807082 AW807525 AW807493 AW807523 AW807087 AW845784 AW807037 AW807128 AW807080 AW807118 AW845807 AW807524 AW845803 AW807249 AW845795 AW807160 AW807343 AW807515 AW807233 AW807289 AW177102 AW807352 AW807394 AW177105 AW807176 AW177103 AW845870 AW177099 AW177101 AW807528 AW807336 AW807038 AW177100 AW807411 AW807088 AW845865 AW807226 AW807517 AW807397 AW807303 AW807177 AW807154 AW807136 AW807146 AW807085 AW807521 AW807488 AW807385 AW807355 AW807223 AW807155 |
| 409163 | 110418_1 | AA065081 AA075017 AA084791 AA071015 AA081560 AA071459 AA545727 AA083100 AA085366 AA115845 AA075457 AA064704 AA082878 AA075742 AA069162 |
| 409695 | 114876_1 | AA296961 AA296889 AA076945 AA077528 AA077497 |
| 410534 | 1207247_1 | AW905138 AW753008 R13818 Z43519 |
| 410672 | 1214882_1 | AW794600 AW794730 |
| 410784 | 1221005_1 | AW803201 BE079700 BE062940 |
| 410785 | 1221055_1 | AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355 |
| 410835 | 1223785_1 | AW806906 AW806915 AW866460 AW866475 AW866462 AW866448 AW866372 AW866604 |
| 411050 | 1230330_1 | AW814902 BE156656 BE156667 BE156590 BE156441 BE156447 |
| 411086 | 1231500_1 | BE070800 AW875226 BE149115 |
| 411093 | 1231970_1 | BE067650 AW817053 |
| 411111 | 1232669_1 | AW818127 AW818161 R09719 |
| 411171 | 1234393_1 | AW820260 AW820332 R94406 |
| 411337 | 1239217_1 | AW837349 AW837355 AW882717 |
| 411514 | 1248638_1 | AW850178 AW850233 AW850445 AW850446 |
| 411670 | 1253680_1 | AW856552 AW861101 AW856574 AW861099 AW861100 AW856573 AW856576 AW856562 |
| 411905 | 1265181_1 | BE265067 BE264978 AW875420 |
| 412102 | 1277395_1 | H56435 H56572 AW892929 |
| 412209 | 1283610_1 | AW901456 AW901450 AW901441 |
| 412248 | 1285000_1 | BE176480 AW903298 AW903313 |
| 413043 | 1346556_1 | BE158766 BE061699 BE147360 BE147362 BE061666 BE061697 BE061647 BE061678 |
| 413111 | 1349546_1 | BE065837 BE065805 BE065799 BE065818 BE065839 BE065831 BE065894 BE065789 BE065792 |
| 413189 | 1352723_1 | BE070231 BE070229 BE070255 |
| 413221 | 1353887_1 | BE161151 BE162495 BE161002 BE072205 BE160989 BE162482 |
| 413499 | 1373910_1 | BE144884 H97942 |
| 413708 | 1384140_1 | BE158791 BE158806 BE158748 BE158744 BE158740 BE158739 BE158811 BE158700 BE158741 BE158683 BE158685 |
| 414210 | 1426051_1 | BE383592 BE261671 |
| 414596 | 1465004_1 | BE386870 Z41986 H08501 |

| | | | |
|----|--------|-----------|--|
| | 414605 | 1465790_1 | BE390440 |
| | 415747 | 155189_1 | AA381209 AA381245 AA167683 |
| | 416173 | 1574973_1 | R52782 R17313 H24192 R19876 |
| 5 | 417742 | 1696282_1 | R64719 Z44680 R12451 |
| | 417974 | 171237_1 | AA210765 T95700 H94407 |
| | 418636 | 177402_1 | AW749855 AA225995 AW750208 AW750206 |
| | 419536 | 185688_1 | AA603305 AA244095 AA244183 |
| | 420854 | 197072_1 | AW296927 AI684514 AI263168 AA281079 |
| 10 | 422156 | 212379_1 | N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 |
| | | | AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732 |
| | 422996 | 223666_1 | BE091089 BE091123 AA319959 |
| | 423833 | 232451_1 | AW503329 N46610 AA331571 |
| | 423841 | 232507_1 | AW753967 AA370795 AA331630 AW962550 |
| 15 | 423945 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| | 425201 | 247933_1 | AA352111 AW962247 AA429695 |
| | 426650 | 270283_1 | AA382814 AA402411 AA412355 |
| | 426878 | 273265_1 | BE069341 AW748403 AL044891 AI908240 AA393080 |
| | 430264 | 315008_1 | AA470519 BE303010 BE302954 BE384120 |
| | 430785 | 323486_1 | Z30201 AA486132 T72025 |
| 20 | 431676 | 336411_1 | AI685464 AW971336 AA513587 AA525142 |
| | 433687 | 373061_1 | AA743991 AA604852 AW272737 |
| | 434338 | 383982_1 | AW754311 AA630185 AW803285 |
| | 434469 | 387447_1 | AA634806 C18732 AA729161 AA729860 |
| | 435447 | 406400_1 | AI872932 AA682306 BE220163 W88695 T81307 H91447 |
| 25 | 437152 | 43386_1 | AL050027 BE089051 |
| | 437854 | 44418_1 | AL119723 AL119874 AI909018 U50537 |
| | 439031 | 46798_1 | AF075079 H48601 H48795 |
| | 439255 | 470321_1 | BE164500 AA832198 BE164502 |
| | 444910 | 624951_1 | AI201849 BE069007 AW946544 |
| 30 | 445432 | 63943_1 | AV653771 BE089370 |
| | 446922 | 69865_1 | BE175605 Z43529 F06610 BE175602 AV661027 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| | 448420 | 76273_1 | BE623004 AA380669 BE263627 BE246433 |
| | 448516 | 766241_1 | AW898595 AW898588 AW898590 AW898663 AW898592 AI525093 |
| 35 | 450522 | 837264_1 | AI698839 AI909260 AI909259 |
| | 450736 | 844652_1 | AW970060 AI732366 AI792313 AW839644 |
| | 451024 | 85565_1 | AA442176 AA259181 |
| | 451067 | 85759_1 | BE172186 AA059279 AA020815 AA013437 |
| | 451340 | 86640_1 | AW936273 AW340350 AA017208 |
| 40 | 452542 | 921410_1 | AW812256 AW812257 AI906423 AI906422 |
| | 452564 | 92227_1 | AA026777 N50065 R09961 N54721 |
| | 453472 | 968371_1 | AL037925 AL037931 AL037957 |
| | 454307 | 1106070_1 | AW855717 AW362452 AW362443 |
| | 454359 | 1130674_1 | N71277 AW390764 |
| 45 | 454545 | 1223779_1 | AW806899 AW866451 AW866393 AW866297 AW817869 |
| | 454693 | 1229132_1 | AW813428 AW813444 AW813367 AW813368 AW813429 AW813424 |
| | 454714 | 1230493_1 | AW815098 BE154843 BE154831 |
| | 455047 | 1250536_1 | AW852530 AW852527 AW852526 |
| | 455092 | 1252971_1 | BE152428 AW855572 AW855607 |
| 50 | 455097 | 1253130_1 | AW855802 AW855794 AW855797 AW855806 AW855796 AW855808 AW855793 AW855807 |
| | 455100 | 1253334_1 | BE160198 AW935898 T11520 AW935930 AW856073 AW861034 |
| | 455431 | 1289854_1 | AW938484 BE001245 BE001190 |
| | 455511 | 1321229_1 | BE144762 AW979091 |
| | 455609 | 1337548_1 | BE011668 BE011689 BE011627 BE011679 BE011699 BE011678 BE011696 BE011675 BE011622 BE011635 |
| 55 | 455651 | 1348732_1 | BE064962 BE064979 BE064853 BE064857 BE064856 BE064977 BE064960 BE064860 BE064815 BE064957 BE064804 |
| | | | BE064816 BE064850 BE064806 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059 |
| | 455685 | 1350393_1 | BE066976 BE066928 BE066927 |
| | 455700 | 1351264_1 | BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198 |
| | 455708 | 1352232_1 | BE069326 BE069290 BE069352 |
| 60 | 455732 | 1353874_1 | BE080908 BE072258 BE072190 BE072236 |
| | 455838 | 1374605_1 | BE145808 BE145807 BE181883 |
| | 455935 | 1384144_1 | BE158687 BE158688 |
| | 455945 | 1385588_1 | BE160636 BE160606 BE160703 |
| | 456207 | 165078_1 | AA193450 |
| 65 | 456482 | 192289_1 | AA485224 AA287308 AA258121 |
| | 458094 | 47311_1 | AF086325 W72956 W73221 AA219112 |
| | 458673 | 679507_1 | N99626 AI302701 |

TABLE 19B

5 **Table 19B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 19. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 15 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|---|
| 400555 | 9801191 | Minus | 134694-134817 |
| 400608 | 9887666 | Minus | 96756-97558 |
| 400610 | 9887671 | Minus | 117606-117928,124040-124147 |
| 400925 | 7651921 | Plus | 38183-38391,43900-44086 |
| 401045 | 8117619 | Plus | 90044-90184,91111-91345 |
| 401049 | 7232177 | Plus | 149157-150692 |
| 401093 | 8516137 | Minus | 22335-23166 |
| 401256 | 9796573 | Minus | 45482-45620 |
| 401283 | 9800093 | Minus | 47256-47456 |
| 401326 | 9212516 | Minus | 226246-227505 |
| 401418 | 7452889 | Minus | 124865-125075 |
| 401451 | 6634068 | Minus | 119926-121272 |
| 401458 | 9187886 | Plus | 76485-77597 |
| 401497 | 7381770 | Plus | 92607-92813 |
| 401508 | 7534110 | Minus | 110779-110983 |
| 401575 | 7229804 | Minus | 76253-76364 |
| 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011 |
| 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814 |
| 401785 | 7249190 | Minus | 165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942 |
| 401793 | 7263888 | Minus | 102945-103083 |
| 401987 | 4406829 | Minus | 72893-73021,76938-77049 |
| 402077 | 8117414 | Plus | 65014-65195 |
| 402109 | 8131678 | Minus | 171722-171859,173197-173303 |
| 402184 | 8576001 | Minus | 112844-112986,113505-113636 |
| 402376 | 9625329 | Minus | 21753-22385 |
| 402421 | 9796341 | Minus | 46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924 |
| 402578 | 9884928 | Plus | 66350-66496 |
| 402606 | 9909429 | Minus | 81747-82094 |
| 402696 | 7328818 | Minus | 23600-23731 |
| 402765 | 9367757 | Plus | 109588-109726 |
| 402800 | 6010175 | Plus | 43921-44049,46181-46273 |
| 402820 | 6456853 | Minus | 82274-82443 |
| 402892 | 8086844 | Minus | 194384-194645 |
| 403133 | 7331427 | Plus | 38314-38634 |
| 403356 | 8569930 | Plus | 92839-93036 |
| 403388 | 9438331 | Plus | 112733-113001,114599-114735 |
| 403426 | 9719529 | Minus | 157156-158183 |
| 403585 | 8101208 | Minus | 131266-131769 |
| 403593 | 6862650 | Minus | 62554-62712,69449-69602 |
| 403637 | 8671936 | Minus | 142647-142771,145531-145762 |
| 403639 | 8671948 | Plus | 113234-113326,115186-115287,119649-119786 |
| 403677 | 7331517 | Minus | 55008-55083,62860-63051 |
| 403775 | 7770580 | Minus | 102247-102326,103095-103148 |
| 403943 | 7711864 | Plus | 100742-100904,101322-101503 |

| | | | | |
|----|--------|---------|-------|---|
| | 404091 | 7684554 | Minus | 82121-83229 |
| | 404097 | 7770701 | Plus | 55512-55781 |
| | 404142 | 9856692 | Minus | 80316-80459 |
| | 404253 | 9367202 | Minus | 55675-56055 |
| 5 | 404274 | 9885189 | Plus | 104127-104318 |
| | 404285 | 2326514 | Plus | 32282-32416 |
| | 404360 | 9858450 | Minus | 122873-122966,151324-151469,153093-153253 |
| | 404440 | 7528051 | Plus | 80430-81581 |
| | 404443 | 7579073 | Minus | 87198-87441 |
| 10 | 404552 | 7243881 | Plus | 19854-20010 |
| | 404561 | 9795980 | Minus | 69039-70100 |
| | 404580 | 6539738 | Minus | 240588-241589 |
| | 404721 | 9856648 | Minus | 173763-174294 |
| | 404826 | 6572184 | Plus | 47726-48046 |
| 15 | 404983 | 4432779 | Minus | 51178-51374,52000-52173 |
| | 405037 | 7543748 | Minus | 127374-127578 |
| | 405041 | 7547195 | Plus | 121230-121714 |
| | 405095 | 8072599 | Plus | 138877-139066 |
| | 405153 | 9965565 | Minus | 175317-175500 |
| 20 | 405196 | 7230083 | Minus | 135716-135851 |
| | 405232 | 7249042 | Plus | 125904-126063 |
| | 405248 | 7259728 | Plus | 637-777 |
| | 405336 | 6094635 | Plus | 33267-33563 |
| | 405394 | 6624123 | Minus | 31900-32373 |
| 25 | 405460 | 7684569 | Minus | 52223-52389 |
| | 405494 | 8050952 | Minus | 70284-70518 |
| | 405547 | 1054740 | Plus | 124361-124520,124914-125050 |
| | 405609 | 5757553 | Minus | 42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727 |
| 30 | 405638 | 6289229 | Plus | 199260-199372,199826-199929 |
| | 405654 | 4895155 | Minus | 53624-53759 |
| | 405718 | 9795467 | Plus | 113080-113266 |
| | 405822 | 6273498 | Minus | 154660-154974,155203-155379 |
| | 405848 | 7651809 | Minus | 28135-28244 |
| 35 | 405873 | 6758747 | Minus | 32129-32764 |
| | 405906 | 7705124 | Minus | 10835-11059 |
| | 405917 | 7712162 | Minus | 106829-107213 |
| | 405925 | 6758795 | Plus | 129935-130282 |
| | 405953 | 7960374 | Minus | 65101-65574 |
| 40 | 406069 | 9117732 | Plus | 68880-69374 |
| | 406151 | 7144806 | Minus | 94087-94285 |
| | 406153 | 9929734 | Minus | 12902-13069 |
| | 406182 | 5923650 | Minus | 28256-28935 |
| | 406271 | 7534217 | Plus | 36179-36692 |
| 45 | 406291 | 5686274 | Plus | 9562-9867 |
| | 406348 | 9255985 | Minus | 71754-71944 |
| | 406414 | 9256407 | Plus | 49593-49850 |
| | 406446 | 9454509 | Minus | 116424-116527,118721-118859,121187-121364 |
| | 406504 | 7711360 | Minus | 107068-107277 |
| 50 | 406554 | 7711566 | Plus | 106956-107121 |

**TABLE 20: 544 GENES UP-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT TISSUES THAT ARE
LIKELY TO ENCODE EXTRACELLULAR OR CELL-
SURFACE PROTEINS**

Table 20 shows 544 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85th percentile value amongst 144 non-malignant tissues, and the 96th percentile value amongst the 73 breast cancer specimens was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Pred.Prot.Domains: Predicted Protein Domains
Unigene Title: Unigene gene title
R1: Ratio of 93rd percentile of tumor to 85th percentile of normal body tissue

| | Pkey | ExAccn | UnigeneID | Pred.Prot.Domains | UnigeneTitle | R1 |
|----|--------|-----------|-----------|--|---|-------|
| | 408591 | AF015224 | Hs.46452 | SS,Uterogloblin,SS,Uterogloblin | mammaglobin 1 | 168.6 |
| | 400291 | AA401369 | Hs.190721 | TM | ESTs | 73.2 |
| | 449746 | AI668594 | Hs.176588 | ,SS,p450 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 65.7 |
| 30 | 407277 | AW170035 | Hs.326736 | TM | Homo sapiens breast cancer antigen NY-BR | 57.6 |
| | 400292 | AA250737 | Hs.72472 | death,ZU5,TM,Activin_rec,pkinase, | BMP-R1B | 55.9 |
| | 424735 | U31875 | Hs.272499 | ,SS,TM | short-chain alcohol dehydrogenase family | 53.8 |
| | 426878 | BE069341 | | TM | gb:QV3-BT0381-270100-073-c08 BT0381 Homo | 50.3 |
| | 428848 | NM_000230 | Hs.194236 | SS,Leptin,SS,Leptin, | leptin (murine obesity homolog) | 40.8 |
| 35 | 407178 | AA195651 | Hs.104106 | ,SS,Dihydroorotase, | ESTs | 39.3 |
| | 408000 | L11690 | Hs.620 | Plectin_repeat,SH3,spectrin,SS,Plectin_r | bullous pemphigoid antigen 1 (230/240kD) | 37.3 |
| | 427585 | D31152 | Hs.179729 | SS,C1q,Collagen,SS,C1q,Collagen, | collagen, type X, alpha 1 (Schmid metaph | 35.2 |
| | 429441 | AJ224172 | Hs.204096 | ,SS,Uterogloblin, | lipophilin B (uterogloblin family member) | 30.0 |
| | 450375 | AA009647 | Hs.8850 | ,SS,TM,disintegrin,Pep_M12B_propep,Repro | a disintegrin and metalloproteinase doma | 25.7 |
| 40 | 420931 | AF044197 | Hs.100431 | SS,IL8,SS | small inducible cytokine B subfamily (Cy | 25.2 |
| | 422109 | S73265 | Hs.1473 | SS,Bombesin,SS | gastrin-releasing peptide | 24.8 |
| | 445730 | AI624342 | Hs.170042 | ,SS,TM,Cation_efflux | ESTs | 24.1 |
| | 451110 | AI955040 | Hs.265398 | SS | ESTs, Weakly similar to transformation-r | 24.0 |
| | 400297 | AI127076 | Hs.334473 | TM | hypothetical protein DKFZp564O1278 | 23.8 |
| 45 | 420813 | X51501 | Hs.99949 | SS,SS | prolactin-induced protein | 22.8 |
| | 452744 | AI267652 | Hs.30504 | ,SS,TM,GNS1_SUR4,cNMP_binding,Rlla | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 22.6 |
| | 424634 | NM_003613 | Hs.151407 | ig,tsp_1,SS,AAA | cartilage intermediate layer protein, nu | 21.7 |
| | 420757 | X78592 | Hs.99915 | hormone_rec,Androgen_recep,zf-C4, | androgen receptor (dihydrotestosterone r | 21.7 |
| | 424399 | AI905687 | Hs.2533 | SS | aldehyde dehydrogenase 9 family, member | 20.3 |
| 50 | 447350 | AI375572 | Hs.172634 | ,pkinase, | ESTs | 19.2 |
| | 456207 | AA193450 | | ,SS,TM,p450,p450 | gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi | 18.3 |
| | 431448 | AL137517 | Hs.334473 | TM | hypothetical protein DKFZp564O1278 | 18.2 |
| | 427217 | AA399272 | Hs.144341 | SS | ESTs | 18.2 |
| | 456938 | X52509 | Hs.161640 | ,SS,TM,aminotran_1_2,Cadherin_C_term,cad | tyrosine aminotransferase | 18.1 |
| 55 | 435496 | AW840171 | Hs.265398 | SS | ESTs, Weakly similar to transformation-r | 17.9 |
| | 402578 | | | SS,p450,SS,TM,p450 | C1001134:gll2117372 pir l65981 fatty ac | 17.8 |
| | 453160 | AI263307 | Hs.239884 | SS | H2B histone family, member L | 17.8 |
| | 422505 | AL120862 | Hs.124165 | SS | programmed cell death 9 (PDCD9) | 17.7 |
| | 444342 | NM_014398 | Hs.10887 | Lamp,SS,TM,Lamp, | similar to lysosome-associated membrane | 17.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|---|------|
| | 449765 | N92293 | Hs.206832 | SS | ESTs, Moderately similar to ALU8_HUMAN A | 17.3 |
| | 428227 | AA321649 | Hs.2248 | SS,IL8, | small inducible cytokine subfamily B (CX | 17.0 |
| | 425692 | D90041 | Hs.155956 | ,SS,Acetyltransf2, | N-acetyltransferase 1 (arylamine N-acetyl | 16.7 |
| | 424001 | W67883 | Hs.137476 | ,pklnase, | paternally expressed 10 | 16.5 |
| 5 | 448595 | AB014544 | Hs.21572 | LRRCT,LRR,SS,LRRCT,serine_carbpept | KIAA0644 gene product | 16.3 |
| | 449448 | D60730 | Hs.57471 | SS | ESTs | 16.2 |
| | 418007 | M13509 | Hs.83169 | SS,hemopexin,Peptidase_M10,SS,Peptidase | matrix metalloproteinase 1 (MMP1; inters | 15.7 |
| | 418994 | AA296520 | Hs.89546 | SS,lectin_c,sushi,EGF,SS,EGF,lectin_c,su | selectin E (endothelial adhesion molecu | 15.5 |
| | 453596 | AA441838 | Hs.62905 | SS | hypothetical protein FLJ14834 | 15.5 |
| 10 | 452401 | NM_007115 | Hs.29352 | ,SS,CUB,Xlink, | tumor necrosis factor, alpha-induced pro | 15.0 |
| | 446591 | H44186 | Hs.15456 | PDZ,SS | PDZ domain containing 1 | 14.9 |
| | 419296 | AA236115 | Hs.120785 | SS | ESTs | 14.8 |
| | 452838 | U65011 | Hs.30743 | SS,SS | preferentially expressed antigen in mela | 14.7 |
| | 422805 | AA436989 | Hs.121017 | histone,SS,histone,histone | H2A histone family, member A | 14.3 |
| 15 | 448390 | AL035414 | Hs.21068 | SS | hypothetical protein | 14.2 |
| | 447342 | AI199268 | Hs.19322 | ,SS,lipocalin | Homo sapiens, Similar to RIKEN cDNA 2010 | 14.2 |
| | 411869 | W20027 | Hs.23439 | ,SS,Peptidase_M1, | ESTs | 13.9 |
| | 443709 | AI082692 | Hs.134662 | ,SS,TM,SNF | ESTs | 13.7 |
| | 459587 | AA031956 | | ,SS,LIM, | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 13.7 |
| 20 | 442580 | AI733682 | Hs.130239 | SS | ESTs | 13.5 |
| | 400289 | X07820 | Hs.2258 | hemopexin,Peptidase_M10,SS,Peptidase_M10 | matrix metalloproteinase 10 (MMP10; str | 13.5 |
| | 411598 | BE336654 | Hs.70937 | histone,SS,histone,histone | H3 histone family, member A | 13.3 |
| | 415263 | AA948033 | Hs.130853 | ,SS,histone,histone,linker_histone | ESTs | 13.2 |
| | 433805 | AA706910 | Hs.112742 | ,SS,Ribosomal_L7Ae, | ESTs | 13.1 |
| 25 | 407276 | AI951118 | Hs.326736 | TM | Homo sapiens breast cancer antigen NY-BR | 13.1 |
| | 443348 | AW873596 | Hs.182278 | ,SS,DENN | calmodulin 2 (phosphorylase kinase, delt | 13.0 |
| | 421037 | AI684808 | Hs.197653 | SS | programmed cell death 9 (PDCD9) | 12.9 |
| | 424086 | AI351010 | Hs.102267 | ,SS,Lysyl_oxidase | lysyl oxidase | 12.8 |
| | 400295 | W72838 | Hs.2533 | SS | aldehyde dehydrogenase 9 family, member | 12.7 |
| 30 | 452461 | N78223 | Hs.108106 | ,SS,G9a,PHD, | transcription factor | 12.5 |
| | 427365 | AI873274 | Hs.190721 | TM | ESTs | 12.4 |
| | 433365 | AF026944 | Hs.293797 | ,SS,TPR | ESTs | 12.3 |
| | 409269 | AA576953 | Hs.22972 | SS,TM,UPF0016,SS,TM,UPF0016 | hypothetical protein FLJ13352 | 12.0 |
| | 432596 | AJ224741 | Hs.278461 | SS,EGF,vwa,SS,TM,vwa, | matrilin 3 | 11.9 |
| 35 | 408771 | AW732573 | Hs.47584 | TM,K_tetra,ion_trans,SS,TM,K_tetra,ion_t | potassium voltage-gated channel, delayed | 11.9 |
| | 432912 | BE007371 | Hs.200313 | ,SS,TM,Folate_carrer | ESTs | 11.9 |
| | 447033 | AI357412 | Hs.157601 | SS | ESTs | 11.8 |
| | 421155 | H87879 | Hs.102267 | SS,Lysyl_oxidase,Aldose_epim,Epimerase,S | lysyl oxidase | 11.8 |
| | 424905 | NM_002497 | Hs.153704 | pklnase,SS,TM,pklnase,polyprenyl_synt, | NIMA (never in mitosis gene a)-related k | 11.7 |
| 40 | 425398 | AL049689 | Hs.156369 | SS | hypothetical protein similar to tenascin | 11.6 |
| | 438167 | R28363 | Hs.24286 | ,SS,TM,7tm_1,p450,rm | ESTs | 11.5 |
| | 459583 | AI907673 | | ,pklnase, | gb:IL-BT152-080399-004 BT152 Homo sapien | 11.5 |
| | 423945 | AA410943 | | death,ZU5,TM,Activin_recip,pklnase, | gb:zt32h03.r1 Soares ovary tumor NbHOT H | 11.4 |
| 45 | 439820 | AL360204 | Hs.283853 | SS | Homo sapiens mRNA full length insert cDN | 11.4 |
| | 402606 | | | SS | NM_024626:Homo sapiens hypothetical prot | 11.3 |
| | 445263 | H57646 | Hs.42586 | ,SS,Acyltransferase, | KIAA1560 protein | 11.2 |
| | 430217 | N47863 | Hs.336901 | ,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24e, | ribosomal protein S24 | 11.1 |
| | 447164 | AF026941 | Hs.17518 | ,TM,IBR | Homo sapiens clg5 mRNA, partial sequence | 11.1 |
| | 431385 | BE178536 | Hs.11090 | ,SS,TM | membrane-spanning 4-domains, subfamily A | 11.1 |
| 50 | 423887 | AL080207 | Hs.134585 | ,SS,TM,BRCT,ank,ABC_tran,ABC_tran | DKFZP434G232 protein | 10.9 |
| | 415385 | R17798 | Hs.7535 | ,SS,Fork_head, | COBW-like protein | 10.9 |
| | 425704 | U79293 | Hs.159264 | SS | Human clone Z3948 mRNA sequence | 10.7 |
| | 429859 | NM_007050 | Hs.225952 | ,SS,TM,Y_phosphatase,MAM,fn3, | protein tyrosine phosphatase, receptor t | 10.4 |
| | 425523 | AB007948 | Hs.158244 | ,SS,laminin_B,laminin_EGF,laminin_Nterm | KIAA0479 protein | 10.3 |
| 55 | 428368 | BE440042 | Hs.83326 | SS,Peptidase_M10,hemopexin,SS,Peptidase | matrix metalloproteinase 3 (stromelysin | 10.3 |
| | 418912 | NM_000685 | Hs.89472 | SS,TM,7tm_1,SS,TM,7tm_1, | angiotensin receptor 1 | 10.3 |
| | 422026 | U80736 | Hs.110826 | SS | trinucleotide repeat containing 9 | 10.3 |
| | 451952 | AL120173 | Hs.301663 | ,SS,pklnase, | ESTs | 10.3 |
| | 438199 | AW016531 | Hs.122147 | ,SS,ArfGap, | ESTs | 10.2 |
| 60 | 400608 | | | SS,TM,SS,TM | C10001899:gi 7508633 pir T25392 hypothe | 10.1 |
| | 413472 | BE242870 | Hs.75379 | SS | solute carrier family 1 (glial high affi | 10.0 |
| | 432374 | W68815 | Hs.301885 | SS | Homo sapiens cDNA FLJ11346 fis, clone PL | 9.9 |
| | 402408 | NA | | ,SS,carb_anhydrase | NM_030920:Homo sapiens hypothetical pro | 9.8 |
| 65 | 445537 | AJ245671 | Hs.12844 | ,SS,TM,ras | EGF-like-domain, multiple 6 (EGFL6) | 9.7 |
| | 451621 | AI879148 | Hs.26770 | SS,lipocalin,lipocalin, | fatty acid binding protein 7, brain | 9.6 |
| | 405654 | NA | | BTB,SS | C12001521:gi 7513934 pir T31081 cca3 pr | 9.6 |
| | 434988 | AI418055 | Hs.161160 | SS | ESTs | 9.6 |

| | | | | | | |
|----|--------|-----------|-----------|--|--|-----|
| | 416220 | N49776 | Hs.170994 | ,SS,TM | hypothetical protein MGC10946 | 9.5 |
| | 431808 | M30703 | Hs.270833 | SS,TM,EGF,SS | amphiregulin (schwannoma-derived growth | 9.5 |
| | 414142 | AW368397 | Hs.150042 | ,SS,UDPGT | Homo sapiens cDNA FLJ14438 fis, clone HE | 9.4 |
| 5 | 400298 | AA032279 | Hs.61635 | TM | six transmembrane epithelial antigen of | 9.4 |
| | 418601 | AA279490 | Hs.86368 | SS,TM,calreticulin,SS,TM,calreticulin, | calmegin | 9.4 |
| | 415539 | AI733881 | Hs.72472 | death,ZU5,TM,Activin_rec,pkinase, | BMP-R1B | 9.4 |
| | 421451 | AA291377 | Hs.50831 | TM | ESTs | 9.3 |
| | 429432 | AI678059 | Hs.202676 | SS | synaptonemal complex protein 2 | 9.3 |
| | 442441 | AI820662 | Hs.129598 | SS | ESTs | 9.1 |
| 10 | 426429 | X73114 | Hs.169849 | ,SS,TM,fn3,Ig, | myosin-binding protein C, slow-type | 9.1 |
| | 406687 | M31126 | Hs.272620 | SS,Peptidase_M10,hemopexin,SS,Peptidase | matrix metalloproteinase 11 (MMP11; stro | 9.1 |
| | 448693 | AW004854 | Hs.228320 | SS | hypothetical protein FLJ23537 | 9.1 |
| | 419948 | AB041035 | Hs.93847 | Ferric_reduct,TM,Ferric_reduct, | NM_016931:Homo sapiens NADPH oxidase 4 (| 9.1 |
| 15 | 426214 | H59846 | Hs.128355 | SS | ESTs, Moderately similar to ALU7_HUMAN A | 9.0 |
| | 427718 | AI798680 | Hs.25933 | ,SS,TM,histone,Sec1,histone,sugar_tr | ESTs | 8.9 |
| | 414812 | X72755 | Hs.77367 | SS,IL8,SS,IL8 | monokine induced by gamma interferon | 8.8 |
| | 400285 | NA | | ,TM,ABC_tran,ABC_membrane, | Eos Control | 8.8 |
| | 422330 | D30783 | Hs.115263 | SS,TM,EGF,SS,TM | epiregulin | 8.8 |
| 20 | 416182 | NM_004354 | Hs.79069 | cyclin,SS | cyclin G2 | 8.8 |
| | 420077 | AW512260 | Hs.87767 | SS | ESTs | 8.7 |
| | 452281 | T93500 | Hs.28792 | ,SS,TGF-beta,TGFb_propeptide, | Homo sapiens cDNA FLJ11041 fis, clone PL | 8.7 |
| | 434531 | AA642007 | Hs.116369 | SS | ESTs | 8.6 |
| | 408380 | AF123050 | Hs.44532 | ,SS,TM,ubiquitin,7tm_3,ANF_receptor,sush | diubiquitin | 8.6 |
| 25 | 443788 | AI732643 | Hs.144151 | TM | ESTs | 8.6 |
| | 411078 | AI222020 | Hs.182364 | SS,SS | CocoaCrisp | 8.5 |
| | 445495 | BE622641 | Hs.38489 | SS,SS,ENTH,I_LWEQ,ENTH,I_LWEQ,DNA_mis | reESTs, Weakly similar to I38022 hypotheti | 8.5 |
| | 433426 | H69125 | Hs.133525 | ,SS,TM | ESTs | 8.5 |
| | 424871 | NM_004525 | Hs.153595 | SS,EGF,kd_recept_a,kd_recept_b,SS,TM,E | low density lipoprotein-related protein | 8.4 |
| 30 | 426215 | AW963419 | Hs.155223 | SS | stanniocalcin 2 | 8.4 |
| | 409045 | AA635062 | Hs.50094 | TM | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 8.4 |
| | 435525 | AI831297 | Hs.123310 | TM | ESTs | 8.3 |
| | 409203 | AA780473 | Hs.687 | SS,p450,SS,p450 | cytochrome P450, subfamily IVB, polypept | 8.3 |
| | 424902 | NM_003866 | Hs.153687 | SS,SS | inositol polyphosphate-4-phosphatase, ty | 8.3 |
| 35 | 431725 | X65724 | Hs.2839 | SS,Cys_knot,SS | Norrie disease (pseudoglioma) | 8.3 |
| | 418092 | R45154 | Hs.106604 | ,death,ZU5,pkinase,Activin_rec, | ESTs | 8.3 |
| | 439840 | AW449211 | Hs.105445 | SS | GDNF family receptor alpha 1 | 8.2 |
| | 427811 | M81057 | Hs.180884 | SS,Zn_carbOpept,Propep_M14,SS,Propep_M14 | carboxypeptidase B1 (tissue) | 8.2 |
| | 420807 | AA280627 | Hs.57846 | SS,cpn10 | ESTs | 8.2 |
| 40 | 426320 | W47595 | Hs.169300 | SS,TGF-beta,TGFb_propeptide,SS | transforming growth factor, beta 2 | 8.2 |
| | 447078 | AW885727 | Hs.301570 | ,SS,kazal, | ESTs | 8.1 |
| | 415786 | AW419196 | Hs.257924 | SS | hypothetical protein FLJ13782 | 8.1 |
| | 410102 | AW248508 | Hs.279727 | SS | Homo sapiens cDNA FLJ14035 fis, clone HE | 8.0 |
| | 404347 | | | SS | Target Exon | 8.0 |
| 45 | 433687 | AA743991 | | TM | gbny57g01.s1 NCI_CGAP_Pr18 Homo sapiens | 8.0 |
| | 421373 | AA808229 | Hs.167771 | ,SS,IMPDH_C,IMPDH_N,CBS | ESTs | 8.0 |
| | 422634 | NM_016010 | Hs.118821 | SS | CGI-62 protein | 7.9 |
| | 453310 | X70697 | Hs.553 | TM,SNF,SS,TM,SNF, | solute carrier family 6 (neurotransmitte | 7.9 |
| | 435957 | N39015 | Hs.190368 | ,SS,TM | ESTs | 7.8 |
| 50 | 407771 | AL138272 | Hs.62713 | ,TM,cpn60_TCP1,Sema, | ESTs | 7.8 |
| | 443646 | AI085198 | Hs.164226 | ,TSPN,vwc,tsp_1,EGF,thlored, | ESTs | 7.8 |
| | 446142 | AI754693 | Hs.145968 | ,TM,cadherin,Cadherin_C_term, | ESTs | 7.7 |
| | 444649 | AW207523 | Hs.197628 | ,SS,rm, | ESTs | 7.6 |
| | 435147 | AL133731 | Hs.4774 | ,TM,SDF,UPAR_LY6, | Homo sapiens mRNA; cDNA DKFZp761C1712 (f | 7.6 |
| 55 | 439138 | AI742605 | Hs.193696 | TM | ESTs | 7.6 |
| | 429220 | AW207206 | Hs.136319 | SS | ESTs | 7.6 |
| | 428804 | AK000713 | Hs.193736 | ,SS,UDPGT | hypothetical protein FLJ20706 | 7.5 |
| | 453511 | AL031224 | Hs.33102 | SS,SS | transcription factor AP-2 beta (activati | 7.5 |
| | 439809 | R41396 | Hs.101774 | SS | hypothetical protein FLJ23045 | 7.5 |
| 60 | 414869 | AA157291 | Hs.21479 | SS | ubiquitin 1 | 7.5 |
| | 416276 | U41060 | Hs.79136 | SS,TM,TM | LIV-1 protein, estrogen regulated | 7.5 |
| | 452862 | AW378065 | Hs.8687 | ,SS,Pep_M12B_propep,Repolysin,tsp_1, | ESTs | 7.4 |
| | 452926 | AI742170 | Hs.31297 | ,SS,TM | duodenal cytochrome b | 7.4 |
| | 453331 | AI240665 | Hs.8895 | ,SS,TM,disintegrin,Pep_M12B_propep,Repro | ESTs | 7.3 |
| 65 | 420802 | U22376 | Hs.1334 | SS,NA,myb_DNA-binding | v-myb avian myeloblastosis viral oncogen | 7.3 |
| | 450603 | R43646 | Hs.12422 | SS | ESTs | 7.2 |
| | 422867 | L32137 | Hs.1584 | SS,EGF,tsp_3,SS,E2F_TDP, | cartilage oligomeric matrix protein (COM | 7.2 |
| | 418004 | U37519 | Hs.87539 | SS,aldehyd,SS,aldehyd, | aldehyde dehydrogenase 3 family, member | 7.2 |

| | | | | | | |
|----|--------|------------|------------------------------|--|--|-----|
| | 426451 | AI908165 | Hs.169946 | SS,GATA, | GATA-binding protein 3 (T-cell receptor | 7.1 |
| | 450701 | H39960 | Hs.288467 | ,SS,LRR | Homo sapiens cDNA FLJ12280 fis, clone MA | 7.1 |
| | 419519 | AI198719 | Hs.176376 | SS | ESTs | 7.1 |
| | 410555 | U92649 | Hs.64311 | ,TM,disintegrin,Repolyisin, | a disintegrin and metalloproteinase doma | 7.1 |
| 5 | 433138 | AB029496 | Hs.59729 | SS,ig,Sema,SS,Sema,efhand | semaphorin sem2 | 7.0 |
| | 411558 | AA102670 | Hs.70725 | SS,TM,SS,TM | gamma-aminobutyric acid (GABA) A recepto | 7.0 |
| | 409079 | W87707 | Hs.82065 | ,TM,fn3, | interleukin 6 signal transducer (gp130, | 7.0 |
| | 417275 | X63578 | Hs.295449 | SS,efhand,SS,efhand,ras | parvalbumin | 7.0 |
| | 432731 | R31178 | Hs.287820 | ,SS,fn3,fn1,fn2,fn1 | fibronectin 1 | 6.9 |
| 10 | 442818 | AK001741 | Hs.8739 | WD40,SS | hypothetical protein FLJ10879 | 6.9 |
| | 407366 | AF026942 | | ,TM,IBR | gb:Homo sapiens cig33 mRNA, partial sequ | 6.8 |
| | 427427 | AF077345 | Hs.177936 | SS,lectin_c,SS | ESTs | 6.8 |
| | 410785 | AW803341 | | SS | gb:IL2-UM0079-090300-050-D03 UM0079 Homo | 6.7 |
| | 401045 | | | ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p | | |
| 15 | | C11001883* | gij6753278 ref NP_033938.1 c | | 6.7 | |
| | 418986 | AI123555 | Hs.81796 | ,SS,Repolyisin,isp_1, | ESTs | 6.7 |
| | 442082 | R41823 | Hs.7413 | ,TM,EPH_lbd,pkinase,SAM,fn3, | ESTs; calsynenin-2 | 6.7 |
| | 442861 | AA243837 | Hs.57787 | SS | ESTs | 6.6 |
| | 418836 | AI655499 | Hs.161712 | ,TM,Activin_rec,pkinase,death,ZU5, | ESTs | 6.6 |
| 20 | 422060 | R20893 | Hs.325823 | ,SS,TM,CD36 | ESTs, Moderately similar to ALU5_HUMAN A | 6.6 |
| | 444381 | BE387335 | Hs.283713 | ,SS,mito_carr | ESTs, Weakly similar to S64054 hypothe | 6.6 |
| | 404091 | NA | | ,TM,7tm_3,ANF_receptor, | Target Exon | 6.6 |
| | 417866 | AW067903 | Hs.82772 | SS,Collagen,COLFI,TSPN,SS,TSPN | collagen, type XI, alpha 1 | 6.6 |
| | 428819 | AL135623 | Hs.193914 | SS,SS | KIAA0575 gene product | 6.5 |
| 25 | 410275 | U85658 | Hs.61796 | ,SS,Ribosomal_S4e | transcription factor AP-2 gamma (activat | 6.4 |
| | 425236 | AW067800 | Hs.155223 | SS | stanniocalcin 2 | 6.2 |
| | 415669 | NM_005025 | Hs.78589 | ,SS,serpin, | serine (or cysteine) proteinase inhibito | 6.2 |
| | 416319 | AI815601 | Hs.79197 | SS,TM,ig,SS,TM | CD83 antigen (activated B lymphocytes, I | 6.2 |
| | 412140 | AA219691 | Hs.73625 | ,SS,kinesin, | RAB6 interacting, kinesin-like (rabkines | 6.2 |
| 30 | 442942 | AW167087 | Hs.131562 | ,SS,ig,Sema,pkinase, | ESTs | 6.2 |
| | 446163 | AA026880 | Hs.25252 | ,SS,TM,fn3, | prolactin receptor | 6.1 |
| | 443162 | T49951 | Hs.9029 | filament,SS,filament,filament | DKFZP434G032 protein | 6.1 |
| | 409602 | W26713 | Hs.256972 | ,SS,TM,DAGKa,DAGKc, | ESTs | 6.1 |
| | 428479 | Y00272 | Hs.184572 | ,SS,pkinase,pkinase | cell division cycle 2, G1 to S and G2 to | 6.1 |
| 35 | 400300 | X03363 | | ,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur | HER2 receptor tyrosine kinase (c-erb-b2, | 6.1 |
| | 433404 | T32982 | Hs.102720 | SS | ESTs | 6.1 |
| | 410079 | U94362 | Hs.58589 | Glyco_transf_8,SS | glycogenin 2 | 6.1 |
| | 401781 | | | ,SS,filament,Pribosyltran,filament,Armad | Target Exon | 6.1 |
| | 447359 | NM_012093 | Hs.18268 | SS,adenylatekinase, | adenylate kinase 5 | 6.1 |
| 40 | 402230 | NA | | ,SS,TM,p450, | Target Exon | 6.1 |
| | 427674 | NM_003528 | Hs.2178 | histone,SS,histone, | H2B histone family, member Q | 6.1 |
| | 428398 | AI249368 | Hs.98558 | ,SS,TM | ESTs | 6.0 |
| | 458098 | BE550224 | Hs.74170 | SS | metallothionein 1E (functional) | 6.0 |
| | 419968 | X04430 | Hs.93913 | SS,IL6,IL6, | interleukin 6 (interferon, beta 2) | 6.0 |
| 45 | 416636 | N32536 | Hs.42645 | ,SS,TM | solute carrier family 16 (monocarboxylic | 6.0 |
| | 419703 | AI793257 | Hs.128151 | ,SS,zf-C2H2, | ESTs | 5.8 |
| | 424687 | J05070 | Hs.151738 | SS,Peptidase_M10,fn2,hemopexin,SS,TM,Pep | matrix metalloproteinase 9 (gelatinase B | 5.8 |
| | 449679 | AI823951 | Hs.129700 | SS | tolloid-like 1 | 5.8 |
| | 421296 | NM_002666 | Hs.103253 | SS | perilipin | 5.8 |
| 50 | 442117 | AW664964 | Hs.128899 | ,SS,TM | ESTs | 5.7 |
| | 400303 | AA242758 | Hs.79136 | ,SS,TM | LIV-1 protein, estrogen regulated | 5.7 |
| | 419440 | AB020689 | Hs.90419 | SS | KIAA0882 protein | 5.7 |
| | 444858 | AI199738 | Hs.208275 | SS | ESTs, Weakly similar to ALUA_HUMAN !!!! | 5.7 |
| | 432239 | X81334 | Hs.2936 | SS,Peptidase_M10,hemopexin,SS,Peptidase_ | matrix metalloproteinase 13 (collagenase | 5.6 |
| 55 | 440705 | AA904244 | Hs.153205 | TM | ESTs | 5.6 |
| | 400286 | NA | | SS,TM,ABC_tran,ABC_membrane,SS | C16000922:gij7499103 pir T20903 hypothe | 5.6 |
| | 446466 | H38026 | Hs.308 | arrestin,SS | arrestin 3, retinal (X-arrestin) | 5.5 |
| | 423201 | NM_000163 | Hs.125180 | SS,TM,fn3,SS | growth hormone receptor | 5.5 |
| | 433043 | W57554 | Hs.125019 | SS | lymphoid nuclear protein (LAF-4) mRNA | 5.5 |
| 60 | 439509 | AF086332 | Hs.58314 | ,SS,TM,Syntaxin | ESTs | 5.4 |
| | 425247 | NM_005940 | Hs.155324 | SS,Peptidase_M10,hemopexin,SS | matrix metalloproteinase 11 (MMP11; stro | 5.4 |
| | 409757 | NM_001898 | Hs.123114 | ,SS,cystatin, | cystatin SN | 5.4 |
| | 425292 | NM_005824 | Hs.155545 | SS | 37 kDa leucine-rich repeat (LRR) protein | 5.4 |
| | 448045 | AJ297436 | Hs.20166 | ,SS,TM | prostate stem cell antigen | 5.4 |
| 65 | 452681 | AF153330 | Hs.30246 | ,SS,TM | solute carrier family 19 (thiamine trans | 5.3 |
| | 452243 | AL355715 | Hs.28555 | SS | programmed cell death 9 | 5.3 |
| | 439310 | AF086120 | Hs.102793 | ,SS,TM,UDPGT,casein_kappa | ESTs | 5.2 |

| | | | | | | |
|----|--------|-----------|-----------|--|--|-----|
| | 441111 | AI806867 | Hs.126594 | ,SS,TM,Phosphodiesterase | ESTs | 5.2 |
| | 452355 | N54926 | Hs.29202 | TM,7tm_1,TM | G protein-coupled receptor 34 | 5.2 |
| | 427711 | M31659 | Hs.180408 | SS | solute carrier family 25 (mitochondrial) | 5.2 |
| 5 | 418636 | AW749855 | | ,SS,TM,HECT | gb:QV4-BT0534-281299-053-c05 BT0534 Homo | 5.2 |
| | 429353 | AL117406 | Hs.200102 | ,SS,TM,ABC_tran,ABC_membrane, | ATP-binding cassette transporter MRP8 | 5.1 |
| | 441690 | R81733 | Hs.33106 | ,SS,HECT,zf-UBR1,PABP,14-3-3, | ESTs | 5.1 |
| | 430447 | W17064 | Hs.332848 | SS | SW/SNF related, matrix associated, actin | 5.1 |
| | 429698 | AI685086 | Hs.26339 | ,SS,ras, | ESTs, Weakly similar to S21348 probable | 5.1 |
| 10 | 425325 | X52730 | Hs.1892 | SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,STAR | | |
| | | | | phenylethanolamine N-methyltransferase | 5.1 | |
| | 423600 | AI633559 | Hs.310359 | SS | ESTs | 5.1 |
| | 414737 | AI160386 | Hs.125087 | SS | ESTs | 5.1 |
| | 403593 | NA | | ,CIDE-N,pkinase | Target Exon | 5.1 |
| 15 | 407758 | D50915 | Hs.38365 | SS,SS | KIAA0125 gene product | 5.0 |
| | 445234 | AW137636 | Hs.146059 | ,SS,TM | ESTs | 5.0 |
| | 411165 | NM_000169 | Hs.69089 | SS,Melibiase,BTK,PH,pkinase,SH2,SH3,Ribo | galactosidase, alpha | 4.9 |
| | 420633 | NM_014581 | Hs.274480 | SS,lipocalin,SS,lipocalin | odorant-binding protein 2A | 4.9 |
| | 414117 | W88559 | Hs.1787 | ,TM,ion_trans,K_tetra, | proteolipid protein 1 (Pelizaeus-Merzbach) | 4.9 |
| 20 | 416783 | AA206186 | Hs.79889 | SS,TM,TM | monocyte to macrophage differentiation-a | 4.9 |
| | 401093 | | | TM,LRRCT,TM,LRRCT, | C12000586*:gij6330167[dbj]BAA86477.1] (A | 4.9 |
| | 411096 | U80034 | Hs.68583 | Peptidase_M3, | mitochondrial intermediate peptidase | 4.9 |
| | 457411 | AW085961 | Hs.130093 | SS | ESTs | 4.9 |
| | 436007 | AI247716 | Hs.232168 | ,SS,adh_zinc, | ESTs | 4.9 |
| 25 | 450506 | NM_004460 | Hs.418 | SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV_N | fibroblast activation protein, alpha | 4.9 |
| | 417975 | AA641836 | Hs.30085 | ,SS,trypsin | hypothetical protein FLJ23186 | 4.9 |
| | 421072 | AI215069 | Hs.89113 | SS | ESTs | 4.8 |
| | 427032 | AF012023 | Hs.173274 | ,SS,14-3-3 | integrin cytoplasmic domain-associated p | 4.8 |
| | 447752 | M73700 | Hs.105938 | SS,transferrin,7tm_1,transferrin, | lactotransferrin | 4.8 |
| 30 | 403199 | NA | | SS,TM,Folate_carrier,SS,TM,Folate_carrier | NM_025243*:Homo sapiens solute carrier f | 4.8 |
| | 427122 | AW057736 | Hs.323910 | ,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur | HER2 receptor tyrosine kinase (c-erb-b2, | 4.8 |
| | 445900 | AF070526 | Hs.13429 | ,SS,Ca_channel_B, | Homo sapiens clone 24787 mRNA sequence | 4.7 |
| | 413048 | M93221 | Hs.75182 | SS,TM,lectin_c,ln2,Ricin_B_lectin,SS,TM | mannose receptor, C type 1 | 4.7 |
| | 419563 | AA526235 | Hs.193162 | SS | Homo sapiens cDNA FLJ11983 fis, clone HE | 4.7 |
| 35 | 442432 | BE093589 | Hs.38178 | SS | hypothetical protein FLJ23468 | 4.6 |
| | 452093 | AA447453 | Hs.27860 | ,SS,TM,7tm_1, | Homo sapiens mRNA; cDNA DKFZp568M0723 (f | 4.6 |
| | 442323 | AW016669 | Hs.29190 | ,SS,TM,CBS,voltage_CLC | ESTs | 4.6 |
| | 450606 | AI668605 | Hs.60380 | ,TM,Glyco_hydro_1 | ESTs, Moderately similar to ALU6_HUMAN A | 4.6 |
| | 435542 | AA687376 | Hs.269533 | ,SS,pkinase,RhoGEF,lg,PH,SH3, | ESTs | 4.6 |
| 40 | 417576 | AA339449 | Hs.82285 | AIRS,formyl_L_transf,GARS,SS,GARS,AIRS,for | phosphoribosylglycinamide formyltransfer | 4.6 |
| | 446089 | AI860021 | Hs.270651 | ,pkinase | ESTs, Moderately similar to A47582 B-cel | 4.6 |
| | 445413 | AA151342 | Hs.12677 | SS,UPF0099,SS,UPF0099, | CGI-147 protein | 4.6 |
| | 424420 | BE614743 | Hs.146688 | ,SS,TM,MAPEG, | prostaglandin E synthase | 4.5 |
| | 432378 | AI493046 | Hs.146133 | ,SS,TM,UDPGT | ESTs | 4.5 |
| 45 | 452190 | H26735 | Hs.91668 | ,SS,TM,PH,SH2,Furin-like,pkinase,Recep_L | Homo sapiens clone PP1498 unknown mRNA | 4.5 |
| | 434674 | AA831879 | Hs.136985 | ,SS,Hist_deacetyl, | ESTs | 4.5 |
| | 419986 | AI345455 | Hs.78915 | pkinase,OPR, | GA-binding protein transcription factor, | 4.5 |
| | 421582 | AI910275 | Hs.1406 | SS,trefoil,SS,TM,ldL_recept_a,SRCR,tryps | trefoil factor 1 (pS2) | 4.5 |
| | 410361 | BE391804 | Hs.62661 | SS,TM,GBP,TM,GBP | guanylate binding protein 1, Interferon- | 4.5 |
| 50 | 426327 | W03242 | Hs.44898 | SS | Homo sapiens clone TCCCTA00151 mRNA sequ | 4.5 |
| | 406639 | M97711 | | SS,SS,lg, | gb:Human T-cell receptor (V beta 18.1, J | 4.5 |
| | 452834 | AI638627 | Hs.105685 | ,SS,DEAD,Fork_head | KIAA1688 protein | 4.5 |
| | 427315 | AA179949 | Hs.175563 | SS | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 4.4 |
| | 446733 | AA863360 | Hs.26040 | ,SS,TM,p450, | ESTs, Weakly similar to fatty acid omega | 4.4 |
| 55 | 442118 | AA976718 | Hs.202242 | ,lg,Sema, | ESTs | 4.4 |
| | 421524 | AA312082 | Hs.105445 | SS | GDNF family receptor alpha 1 | 4.4 |
| | 453060 | AW294092 | Hs.21594 | ,SS,ras,Y_phosphatase,ras | hypothetical protein MGC15754 | 4.4 |
| | 453403 | BE466639 | Hs.61779 | ,SS,HMG_box,filament, | Homo sapiens cDNA FLJ13591 fis, clone PL | 4.4 |
| | 444301 | AK000136 | Hs.10760 | SS,LRR,SS | asporin (LRR class 1) | 4.4 |
| 60 | 453619 | H87648 | Hs.33922 | SS | Homo sapiens, clone MGC:9084, mRNA, comp | 4.3 |
| | 432656 | NM_000246 | Hs.3076 | SS,LRR, | MHC class II transactivator | 4.3 |
| | 426384 | AI472078 | Hs.303662 | ,SS,ArlGap, | ESTs | 4.3 |
| | 431701 | AW935490 | Hs.14658 | ,SS,BIR | Human chromosome 5q13.1 clone 5G8 mRNA | 4.3 |
| | 416931 | D45371 | Hs.80485 | SS,C1q,Collagen,SS,C1q, | adipose most abundant gene transcript 1 | 4.3 |
| 65 | 420854 | AW296927 | | ,SS,TM,Peptidase_M1, | gb:U1H-BW0-ajc-c-07-0-U1.s1 NCI_CGAP_Su | 4.3 |
| | 418867 | D31771 | Hs.89404 | SS,homeobox,homeobox, | msh (Drosophila) homeo box homolog 2 | 4.3 |
| | 443514 | BE464288 | Hs.141937 | ,SS,TM,MIP, | ESTs | 4.3 |
| | 447499 | AW262580 | Hs.147674 | ,SS,TM,cadherin,cadherin | protocadherin beta 16 | 4.3 |

| | | | | | | |
|----|--------|-----------|-----------|--|--|-----|
| | 441560 | F13386 | Hs.7888 | ,pkinase, | Homo sapiens clone 23736 mRNA sequence | 4.3 |
| | 409064 | AA062954 | Hs.141883 | ,SS,CUB, | ESTs | 4.3 |
| | 422667 | H25642 | Hs.133471 | ,SS,TM,FMO-like | ESTs | 4.3 |
| 5 | 454032 | W31790 | Hs.194293 | ,SS,TM | ESTs, Weakly similar to I54374 gene NF2 | 4.3 |
| | 432663 | AI984317 | Hs.122589 | TM | ESTs | 4.3 |
| | 401747 | | | ,SS,filament,filament | Homo sapiens keratin 17 (KRT17) | 4.3 |
| | 432882 | NM_013257 | Hs.279696 | pkinase,pkinase_C, | serum/glucocorticoid regulated kinase-II | 4.2 |
| | 437036 | AI571514 | Hs.133022 | ,SS,TM | ESTs | 4.2 |
| 10 | 447754 | AW073310 | Hs.163533 | ,pkinase, | Homo sapiens cDNA FLJ14142 fis, clone MA | 4.2 |
| | 443194 | AI954968 | Hs.279009 | ,SS,TM | matrix Gla protein | 4.2 |
| | 451871 | AI821005 | Hs.118599 | ,SS,GDNF, | ESTs | 4.2 |
| | 457211 | AW972565 | Hs.32399 | WH1,WH1 | ESTs, Weakly similar to S51797 vasodilat | 4.2 |
| | 421566 | NM_000399 | Hs.1395 | zf-C2H2,SS | early growth response 2 (Krox-20 (Drosop | 4.2 |
| 15 | 431657 | AI345227 | Hs.105448 | ,SS,TM,pkinase | ESTs, Weakly similar to B34087 hypotheti | 4.1 |
| | 427899 | AA829286 | Hs.332053 | ,SS,SAA_proteins,ABC_membrane,ABC_tran, | serum amyloid A1 | 4.1 |
| | 444779 | AI192105 | Hs.147170 | SS | ESTs | 4.1 |
| | 442295 | AI827248 | Hs.224398 | ,COLFI,vwc,Collagen, | Homo sapiens cDNA FLJ11469 fis, clone HE | 4.1 |
| | 436396 | AI683487 | Hs.152213 | ,wnt, | wingless-type MMTV integration site fami | 4.1 |
| 20 | 446039 | AI150491 | Hs.90756 | ,TM,Glyco_hydro_1 | ESTs | 4.1 |
| | 422938 | NM_001809 | Hs.1594 | ,SS,TM,thiolase, | centromere protein A (17kD) | 4.1 |
| | 406922 | S70284 | | SS,TM,Desaturase,SS | gb:stearoyl-CoA desaturase [human, adipo | 4.1 |
| | 439285 | AL133916 | Hs.172572 | ,SS,ig,pkinase,LRRNT,LRRCT, | hypothetical protein FLJ20093 | 4.1 |
| | 424800 | AL035588 | Hs.153203 | HLH,SS | MyoD family inhibitor | 4.1 |
| 25 | 429922 | Z97630 | Hs.226117 | ,SS,TM,linker_histone,7tm_1 | H1 histone family, member 0 | 4.1 |
| | 447178 | AW594641 | Hs.192417 | ,SS,TM | ESTs | 4.0 |
| | 409038 | T97490 | Hs.50002 | SS,IL8,SS,IL8 | small inducible cytokine subfamily A (Cy | 4.0 |
| | 452747 | BE153855 | Hs.61460 | ,SS,HLH | Ig superfamily receptor LNIR | 4.0 |
| | 420139 | NM_005357 | Hs.95351 | ,SS,TM,p450, | lipase, hormone-sensitive | 4.0 |
| 30 | 408877 | AA479033 | Hs.130315 | ,SS,TM | ESTs, Weakly similar to A47582 B-cell gr | 4.0 |
| | 403329 | NA | | SS,SS | Target Exon | 4.0 |
| | 439926 | AW014875 | Hs.137007 | SS | ESTs | 4.0 |
| | 430832 | AI073913 | Hs.100686 | SS | ESTs, Weakly similar to JE0350 Anterior | 4.0 |
| | 432481 | AW451645 | Hs.151504 | ,SS,Collagen,COLFI,TSPN, | Homo sapiens cDNA FLJ11973 fis, clone HE | 4.0 |
| 35 | 452410 | AL133619 | Hs.29383 | ,SS,TM,ras | Homo sapiens mRNA; cDNA DKFZp434E2321 (f | 4.0 |
| | 418661 | NM_001949 | Hs.1189 | SS | E2F transcription factor 3 | 4.0 |
| | 431958 | X63629 | Hs.2877 | SS,TM,Cadherin_C_term,cadherin,SS,TM,cad | cadherin 3, type 1, P-cadherin (placenta | 4.0 |
| | 425071 | NM_013989 | Hs.154424 | SS,T4_delodnase,T4_delodnase, | delodnase, iodothyronine, type II | 4.0 |
| | 447197 | R36075 | | ,TM,SDF, | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 4.0 |
| 40 | 428722 | U76456 | Hs.190787 | ,SS,TIMP, | tissue inhibitor of metalloproteinase 4 | 3.9 |
| | 428330 | L22524 | Hs.2256 | SS,Peptidase_M10,SS,Peptidase_M10,hemo | hemopematrix metalloproteinase 7 (MMP7; uterin | 3.9 |
| | 423242 | AL039402 | Hs.125783 | SS | DEME-6 protein | 3.9 |
| | 449048 | Z45051 | Hs.22920 | SS,SS,TM | similar to S68401 (cattle) glucose induc | 3.9 |
| | 414831 | M31158 | Hs.77439 | ,SS,cNMP_binding,R11a,HMG_box | protein kinase, cAMP-dependent, regulato | 3.9 |
| 45 | 413589 | AW452631 | Hs.313803 | ,SS,abhydrolase | ESTs, Highly similar to AF157833 1 noncl | 3.8 |
| | 408875 | NM_015434 | Hs.48604 | SS | DKFZP434B168 protein | 3.8 |
| | 418629 | BE247550 | Hs.86859 | SS,SH2,PH,SS,TM,PH,SH2,Furin-like,pkinas | growth factor receptor-bound protein 7 | 3.8 |
| | 450787 | AB006190 | Hs.25475 | SS,TM,MIP,SS,TM,MIP, | aquaporin 7 | 3.8 |
| | 414870 | N72264 | Hs.300670 | SS | KIAA1204 protein | 3.8 |
| | 450325 | AI935962 | Hs.26289 | SS | ESTs | 3.8 |
| 50 | 407633 | NM_007069 | Hs.37189 | TM,TM | similar to rat HREV107 | 3.8 |
| | 426172 | AA371307 | Hs.125056 | ,SS,DENN | ESTs | 3.8 |
| | 442262 | BE170651 | Hs.8700 | ,SS,START, | deleted in liver cancer 1 | 3.8 |
| | 427961 | AW293165 | Hs.143134 | SS | ESTs | 3.8 |
| 55 | 445563 | AW873606 | Hs.149006 | ,SS,WH1,WH1 | ESTs | 3.8 |
| | 403943 | | | p450,SS,p450 | C5000355:gi 4503225 ref NP_000765.1 cyt | 3.8 |
| | 408761 | AA057264 | Hs.238936 | ,SS,TM,7tm_1, | ESTs, Weakly similar to (define not ava | 3.8 |
| | 423279 | AW959861 | Hs.290943 | SS | ESTs | 3.8 |
| | 420440 | NM_002407 | Hs.97644 | ,SS,SRRCR,Uterogloblin | mammaglobin 2 (MGB2; mammaglobin B; lip | 3.8 |
| 60 | 445107 | AI208121 | Hs.147313 | ,SS,TM | ESTs, Weakly similar to I38022 hypotheti | 3.7 |
| | 428303 | AW974476 | Hs.183601 | SS,RGS,RGS,RGS | regulator of G-protein signalling 16 | 3.7 |
| | 411667 | BE160198 | | TM | gb:QV1-HT0413-010200-059-h03 HT0413 Homo | 3.7 |
| | 427809 | M26380 | Hs.180878 | ,SS,lipase,PLAT,Sec7,PH, | lipoprotein lipase | 3.7 |
| | 418203 | X54942 | Hs.83758 | CKS,SS,CKS, | CDC28 protein kinase 2 | 3.7 |
| | 430376 | AW292053 | Hs.12532 | SS | chromosome 1 open reading frame 21 | 3.7 |
| 65 | 444190 | AI878918 | Hs.10526 | SS | cysteine and glycine-rich protein 2 | 3.7 |
| | 433495 | AW373784 | Hs.71 | SS,Ig,MHC_I,connexin,SCAN,SS,TM | alpha-2-glycoprotein 1, zinc | 3.7 |
| | 429638 | AI916662 | Hs.211577 | SS,TM,SS | kinectin 1 (kinesin receptor) | 3.7 |

| | | | | | | |
|----|--------|-----------|-----------|---|--|-----|
| | 454071 | AI041793 | Hs.42502 | ,TM,7tm_1, | ESTs | 3.7 |
| | 451859 | H44491 | Hs.252938 | ,SS,TM,EGF,Idl_recept_a,Idl_recept_b,EGF | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.7 |
| | 420281 | AI623693 | Hs.191533 | ,SS,AAA, | ESTs | 3.7 |
| 5 | 427691 | AW194426 | Hs.20726 | ,SS,Glycos_transf_2, | ESTs | 3.7 |
| | 428824 | W23624 | Hs.173059 | SS | ESTs | 3.7 |
| | 424676 | Y08565 | Hs.151678 | Glycos_transf_2,Ricin_B_lectin,SS,Glycos | UDP-N-acetyl-alpha-D-galactosamine:polyp | 3.7 |
| | 418026 | BE379727 | Hs.83213 | lipocalin,SS,lipocalin,lipocalin,ferritin | fatty acid binding protein 4, adipocyte | 3.7 |
| | 457465 | AW301344 | Hs.122908 | ,SS,Pribosyltran,Sulfatase | DNA replication factor | 3.7 |
| | 417601 | NM_014735 | Hs.82292 | PHD,pkinase,SS | KIAA0215 gene product | 3.7 |
| 10 | 407999 | AI126271 | Hs.49433 | SS | ESTs, Weakly similar to YZ28_HUMAN HYPOT | 3.7 |
| | 425548 | AA890023 | Hs.1906 | SS,TM,fn3,SS,TM,fn3, | prolactin receptor | 3.7 |
| | 446619 | AU076643 | Hs.313 | ,SS,TM,efhand,ion_trans | secreted phosphoprotein 1 (osteopontin, | 3.7 |
| | 411213 | AA676939 | Hs.69285 | SS,TM,CUB,F5_F8_type_C,MAM,SS,TM,CUB,F5 | ,neuropilin 1 | 3.6 |
| | 406625 | Y13647 | Hs.119597 | SS,TM,Desaturase,SS | stearoyl-CoA desaturase (delta-9-desatur | 3.6 |
| 15 | 417511 | AL049176 | Hs.82223 | SS | chordin-like | 3.6 |
| | 428769 | AW207175 | Hs.106771 | ,SS,7tm_1,SPRY, | ESTs | 3.6 |
| | 407137 | T97307 | | ,SS,TM,GDA1_CD39 | gb:ye53h05.s1 Soares fetal liver spleen | 3.6 |
| | 401866 | | | ,SS,filament, | Target Exon | 3.6 |
| | 451195 | U10492 | Hs.438 | SS,homeobox,Ets,SS,homeobox, | mesenchyme homeo box 1 | 3.6 |
| 20 | 426044 | AA502490 | Hs.336695 | SS | ESTs | 3.6 |
| | 426310 | NM_000909 | Hs.169266 | SS,TM,7tm_1, | neuropeptide Y receptor Y1 | 3.6 |
| | 440029 | AW089705 | Hs.293711 | SS | ESTs, Weakly similar to S64329 probable | 3.6 |
| | 408573 | AA284775 | Hs.43148 | ,SS,TM,PMP22_Claudin, | ESTs | 3.6 |
| | 431830 | Y16645 | Hs.271387 | ,SS,TM,IL8 | small inducible cytokine subfamily A (Cy | 3.6 |
| 25 | 444781 | NM_014400 | Hs.11950 | ,SS,PH,lactamase_B | GPI-anchored metastasis-associated prote | 3.6 |
| | 431493 | AI791493 | Hs.129873 | ,SS,p450,p450 | ESTs, Weakly similar to A36036 cytochrom | 3.6 |
| | 414175 | AI308876 | Hs.103849 | ,TM,hemopexin,Peptidase_M10,hemopexin, | Pehypothetical protein DKFZp761D112 | 3.6 |
| | 411789 | AF245505 | Hs.72157 | ig,LRRCT, | DKFZP564I1922 protein | 3.6 |
| | 418851 | AI417828 | Hs.192435 | ,SS,TM | ESTs | 3.5 |
| 30 | 453968 | AA847843 | Hs.62711 | ,SS,HMG_box, | Homo sapiens, clone IMAGE:3351295, mRNA | 3.5 |
| | 407104 | S57296 | Hs.323910 | ,SS,TM,SH2,PH,pkinase,Recep_L_domain,Fur | v-erb-b2 avian erythroblastic leukemia v | 3.5 |
| | 449051 | AW961400 | Hs.333526 | SS | HER2 receptor tyrosine kinase (c-erb-b2, | 3.5 |
| | 434398 | AA121098 | Hs.3838 | pkinase,POLO_box,SS,pkinase,POLO_box, | serum-inducible kinase | 3.5 |
| | 454042 | H22570 | Hs.172572 | ,SS,ig,pkinase,LRRNT,LRRCT, | hypothetical protein FLJ20093 | 3.5 |
| 35 | 459496 | AA808940 | Hs.274450 | ,SS,TM,KRAB,SCAN,zf-C2H2,ig | EST | 3.5 |
| | 414998 | NM_002543 | Hs.77729 | ,SS,TM | oxidised low density lipoprotein (lectin | 3.5 |
| | 407756 | AA116021 | Hs.38260 | SS,UCH-1,UCH-2,SS,TM,G_glu_transpept | ubiquitin specific protease 18 | 3.5 |
| | 442101 | AI651930 | Hs.135684 | SS | ESTs | 3.5 |
| | 449722 | BE280074 | Hs.23960 | cyclin,SS,TM,cyclin, | cyclin B1 | 3.5 |
| 40 | 452554 | AW452434 | Hs.58006 | SS | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.5 |
| | 421991 | NM_014918 | Hs.110488 | SS | KIAA0990 protein | 3.4 |
| | 420058 | AK001423 | Hs.94694 | SS | Homo sapiens cDNA FLJ10561 fis, clone NT | 3.4 |
| | 425776 | U25128 | Hs.159499 | SS,TM,7tm_2,SS,TM,7tm_2 | parathyroid hormone receptor 2 | 3.4 |
| 45 | 407846 | AA426202 | Hs.40403 | ,TM,ABC_membrane,ABC_tran,Ribosomal_S4eCbp | p300-interacting transactivator, wit | 3.4 |
| | 406925 | L34041 | Hs.9739 | ,SS,TM,transport_prot,SWIB,RhoGAP,DAG_P | glycerol-3-phosphate dehydrogenase 1 (so | 3.4 |
| | 445873 | AA250970 | Hs.251946 | ,SS,rm,PABP,pkinase,14-3-3,rm | poly(A)-binding protein, cytoplasmic 1-l | 3.4 |
| | 418054 | NM_002318 | Hs.83354 | ,SS,TM,mito_carr,Lysyl_oxidase | lysyl oxidase-like 2 | 3.4 |
| | 414921 | BE390551 | Hs.77628 | SS,START,SS,START,NNMT_PNMT_TEMT, | steroidogenic acute regulatory protein r | 3.4 |
| 50 | 452268 | NM_003512 | Hs.28777 | SS,histone,Calc_CGRP_IAPP,ig,MHC_I,SPRY,H2A | histone family, member L | 3.4 |
| | 428862 | NM_000346 | Hs.2316 | SS,HMG_box, | SRY (sex determining region Y)-box 9 (ca | 3.4 |
| | 412520 | AA442324 | Hs.795 | histone,SS,histone,Bola | H2A histone family, member O | 3.4 |
| | 410530 | M25809 | Hs.64173 | ATP-synt_ab,SS,7tm_1,ATP-synt_ab | ATPase, H transporting, lysosomal (vacuo | 3.4 |
| | 401780 | | | filament,SS,filament,filament | NM_005557*Homo sapiens keratin 16 (foca | 3.4 |
| | 447131 | NM_004585 | Hs.17466 | TM | retinoic acid receptor responder (tazaro | 3.4 |
| 55 | 418334 | AA319233 | Hs.5521 | ,SS,TM,Ribosomal_L27e, | ESTs | 3.4 |
| | 415138 | C18356 | Hs.295944 | ,Kunitz_BPTI, | tissue factor pathway inhibitor 2 | 3.4 |
| | 421168 | AF182277 | Hs.330780 | SS,p450,SS | cytochrome P450, subfamily IIB (phenobar | 3.4 |
| | 431473 | AA825686 | Hs.321176 | SS | ESTs, Weakly similar to S65824 reverse t | 3.4 |
| | 421379 | Y15221 | Hs.103982 | SS,IL8, | small inducible cytokine subfamily B (Cy | 3.4 |
| 60 | 411984 | NM_005419 | Hs.72988 | SH2,STAT,SS,STAT | signal transducer and activator of trans | 3.4 |
| | 408101 | AW968504 | Hs.123073 | ,pkinase, | CDC2-related protein kinase 7 | 3.4 |
| | 405366 | | | RhoGEF,PH,SS,RhoGEF,PH, | NM_003371*Homo sapiens vav 2 oncogene (| 3.4 |
| | 414612 | BE274552 | Hs.76578 | SAP,SS,FG-GAP,vwa | protein inhibitor of activated STAT3 | 3.4 |
| | 411393 | AW797437 | Hs.69771 | SS,sushi,trypsin,vwa,rm,fibrinogen_C,fn | B-factor, properdin | 3.3 |
| 65 | 435767 | H73505 | Hs.117874 | ,SS,Peptidase_S8,P,Peptidase_S8,P | ESTs | 3.3 |
| | 416406 | D86961 | Hs.79299 | ,SS,TM | lipoma HMGIC fusion partner-like 2 | 3.3 |
| | 433068 | NM_006456 | Hs.288215 | ,SS,Pribosyltran, | siatyltransferase | 3.3 |

| | | | | | | |
|----|--------|-----------|-----------|--|---|-----|
| | 445462 | AA378776 | Hs.288649 | SS,SS | hypothetical protein MGC3077 | 3.3 |
| | 439452 | AA918317 | Hs.57987 | SS,SS | B-cell CLL/lymphoma 11B (zinc finger pro | 3.3 |
| | 452017 | AF109302 | Hs.27495 | SS | prostate cancer associated protein 7 | 3.3 |
| | 409099 | AK000725 | Hs.50579 | SS | hypothetical protein FLJ20718 | 3.3 |
| 5 | 452106 | AI141031 | Hs.21342 | SS | ESTs | 3.3 |
| | 447519 | U46258 | Hs.339665 | SS | ESTs | 3.3 |
| | 426928 | AF037062 | Hs.172914 | ,SS,adh_short,TGF-beta,TGFb_propeptide | retinol dehydrogenase 5 (11-cis and 9-ci | 3.3 |
| | 438825 | BE327427 | Hs.79953 | ,SS,TM,histone,ANF_receptor,guanylate_cy | ESTs | 3.3 |
| | 414575 | H11257 | Hs.22968 | ,SS,pkinase,ig, | Homo sapiens clone IMAGE:451939, mRNA se | 3.3 |
| 10 | 417837 | AL079905 | Hs.1103 | SS,TGFb_propeptide,TGF-beta,SS | transforming growth factor, beta 1 | 3.3 |
| | 422128 | AW881145 | | SS | gb:QV0-OT0033-010400-182-a07 OT0033 Homo | 3.3 |
| | 445941 | AI267371 | Hs.172636 | SS,SS,lipoxygenase,PLAT | ESTs | 3.3 |
| | 429973 | AI423317 | Hs.164680 | ,SS,T-box,UDPGT | ESTs | 3.3 |
| | 444542 | AI161293 | Hs.280380 | SS,SS,Peptidase_M1,EGF,ig,lectin_c,sushi | aminopeptidase | 3.3 |
| 15 | 459561 | AI547306 | Hs.134981 | SS | ESTs | 3.3 |
| | 425741 | AF052152 | Hs.159412 | ,pkinase, | Homo sapiens clone 24628 mRNA sequence | 3.3 |
| | 426501 | AW043782 | Hs.293616 | SS | ESTs | 3.3 |
| | 456508 | AA502764 | Hs.123469 | SS | ESTs, Weakly similar to AF208855 1 BM-01 | 3.3 |
| | 434228 | Z42047 | Hs.283978 | ,SS,TM,7tm_1 | Homo sapiens PRO2751 mRNA, complete cds | 3.3 |
| 20 | 415752 | BE314524 | Hs.78776 | TM | putative transmembrane protein | 3.3 |
| | 400419 | AF084545 | | ,SS,Peptidase_M1, | Target | 3.3 |
| | 439750 | AL359053 | Hs.57664 | ,TM,Integrin_B,Ricln_B_lectin,rm | Homo sapiens mRNA full length insert cDN | 3.3 |
| | 423858 | AL137326 | Hs.133483 | ,SS,TM | Homo sapiens mRNA; cDNA DKFZp434B0650 (f | 3.3 |
| | 428514 | AW236861 | Hs.193139 | ,SS,START,NNMT_PNMT_TEMT, | ESTs | 3.3 |
| 25 | 428698 | AA852773 | Hs.334838 | SS | KIAA1866 protein | 3.3 |
| | 448988 | Y09763 | Hs.22785 | SS,TM,TM | gamma-aminobutyric acid (GABA) A recepto | 3.3 |
| | 432072 | N62937 | Hs.269109 | ,Sema,ig, | ESTs | 3.3 |
| | 417433 | BE270266 | Hs.82128 | SS,TM,LRRCT,LRRNT,LRR,TM,LRRCT, | ST4 oncofetal trophoblast glycoprotein | 3.3 |
| | 452194 | AI694413 | Hs.332649 | ,SS,TM,7tm_3,ANF_receptor,sushi | olfactory receptor, family 2, subfamily | 3.2 |
| 30 | 444051 | N48373 | Hs.10247 | ,SS,ig, | activated leucocyte cell adhesion molecu | 3.2 |
| | 420042 | AW015140 | Hs.161723 | ,SS,CUB, | ESTs | 3.2 |
| | 457292 | AI921270 | Hs.334882 | SS,TM,SS,TM,G-patch | hypothetical protein FLJ14251 | 3.2 |
| | 421458 | NM_003654 | Hs.104576 | SS | carbohydrate (keratan sulfate Gal-6) sul | 3.2 |
| | 431104 | AW970859 | Hs.313503 | ,Sema,ig, | ESTs | 3.2 |
| 35 | 443767 | BE562136 | Hs.9736 | ,SS,PC1,RasGEF,hormone_rec,zf-C4, | proteasome (prosome, macropain) 26S subu | 3.2 |
| | 419589 | AW973708 | Hs.201925 | ,FGF, | Homo sapiens cDNA FLJ13446 fis, clone PL | 3.2 |
| | 415447 | Z97171 | Hs.78454 | SS,OLF,OLF,OLF,Ribosomal_L4 | myoclin, trabecular meshwork Inducible | 3.2 |
| | 443464 | BE548446 | Hs.5167 | SS,TM,SSF,SS,TM | Homo sapiens mRNA; cDNA DKFZp434F152 (fr | 3.2 |
| | 423431 | AA326062 | | ,SS,p450,p450 | gb:EST29171 Cerebellum II Homo sapiens c | 3.2 |
| 40 | 413278 | BE563085 | Hs.833 | ,SS,TM,ubiquitin,laminin_G,laminin_EGF,k | interferon-stimulated protein, 15 kDa | 3.2 |
| | 458451 | AW297181 | Hs.195922 | ,SS,Ribosomal_L14 | ESTs | 3.2 |
| | 440449 | AA885430 | Hs.201925 | ,FGF, | Homo sapiens cDNA FLJ13446 fis, clone PL | 3.2 |
| | 413753 | U17760 | Hs.75517 | SS,laminin_EGF,laminin_Nterm,adh_short,S | laminin, beta 3 (niclin (125kD), kalinin | 3.2 |
| | 434876 | AF160477 | Hs.61460 | ,SS,HLH | Ig superfamily receptor LNIR | 3.2 |
| 45 | 435575 | AF213457 | Hs.44234 | SS,ig,SS,TM | triggering receptor expressed on myeloid | 3.2 |
| | 415773 | R21651 | Hs.324725 | ,SS,TM,Ribosomal_S3Ae,G-gamma | ESTs, Moderately similar to A47582 B-cel | 3.2 |
| | 446440 | AV658411 | Hs.42656 | SS | KIAA1681 protein | 3.2 |
| | 450847 | NM_003155 | Hs.25590 | ,SS,homeobox, | stanniocalcin 1 | 3.2 |
| | 426075 | AW513691 | Hs.270149 | ,SS,fn3, | ESTs, Weakly similar to 2109260A B cell | 3.2 |
| 50 | 452110 | T47667 | Hs.28005 | ,SS,TM,Activin_rec,pkinase | Homo sapiens cDNA FLJ11309 fis, clone PL | 3.2 |
| | 439963 | AW247529 | Hs.6793 | ,TM,p450,Ets | platelet-activating factor acetylhydrola | 3.2 |
| | 402837 | NA | | SS | ENSP00000241312*:DJ947L8.1.8 (novel Sush | 3.2 |
| | 439451 | AF086270 | Hs.278554 | ,SS,Chromo_shadow,chromo, | heterochromatin-like protein 1 | 3.1 |
| | 406664 | L34041 | Hs.9739 | ,SS,TM,transport_prot,SWIB,RhoGAP,DAG_P | Eglycerol-3-phosphate dehydrogenase 1 (so | 3.1 |
| 55 | 417315 | AI080042 | Hs.336901 | ,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24e, | ribosomal protein S24 | 3.1 |
| | 413011 | AW068115 | Hs.821 | SS,LRR,LRRNT,SS,LRRNT,LRR, | biglycan | 3.1 |
| | 414987 | AA524394 | Hs.294022 | ,SS,connexin,hormone_rec,zf-C4,connexin | hypothetical protein FLJ14950 | 3.1 |
| | 429197 | H24471 | Hs.26930 | ,SS,Gelsolin, | ESTs, Weakly similar to T20272 hypotheti | 3.1 |
| | 448030 | N30714 | Hs.325960 | ,SS,TM | membrane-spanning 4-domains, subfamily A | 3.1 |
| 60 | 407604 | AW191962 | Hs.249239 | ,SS,TM,C1q, | collagen, type VIII, alpha 2 | 3.1 |
| | 419092 | J05581 | Hs.89603 | SS,TM,SEA, | mucin 1, transmembrane | 3.1 |
| | 456672 | AK002016 | Hs.114727 | ,SS,PK,PK | Homo sapiens, clone MGC:16327, mRNA, com | 3.1 |
| | 443171 | BE281128 | Hs.9030 | SS,TM,7tm_1,rm,SS | TONDU | 3.1 |
| | 452256 | AK000933 | Hs.28661 | ,TM,GDI,7tm_1, | Homo sapiens cDNA FLJ10071 fis, clone HE | 3.1 |
| 65 | 432201 | AI538613 | Hs.298241 | SS,TM,trypsin,SS,TM,trefol,trypsin,tref | Transmembrane protease, serine 3 | 3.1 |
| | 406642 | AJ245210 | | SS | gb:Homo sapiens mRNA for immunoglobulin | 3.1 |
| | 400903 | NA | | SS | Target Exon | 3.1 |

| | | | | | | |
|----|--------|----------|-----------|--|--|-----|
| | 434408 | AI031771 | Hs.132586 | ,SS,Glyco_hydro_2 | ESTs | 3.1 |
| | 452994 | AW962597 | Hs.31305 | SS,WD40,SS,WD40, | KIAA1547 protein | 3.1 |
| | 445903 | AI347487 | Hs.132781 | fn3,SS,TM,EF1BD | class I cytokine receptor | 3.1 |
| 5 | 424364 | AW383226 | Hs.201189 | SS | ESTs, Weakly similar to G01763 atrophin- | 3.1 |
| | 410196 | AI936442 | Hs.59838 | UBACT_repeat,SS,UBACT_repeat,ThiF_family | hypothetical protein FLJ10808 | 3.1 |
| | 419150 | T29618 | Hs.89640 | ,TM,pkinase,fn3, | TEK tyrosine kinase, endothelial (venous | 3.1 |
| | 433417 | AA587773 | Hs.8859 | ,SS,SRCR, | Homo sapiens, Similar to RIKEN cDNA 5830 | 3.1 |
| | 418624 | AI734080 | Hs.104211 | ,Sema,lg, | ESTs | 3.1 |
| | 436291 | BE568452 | Hs.5101 | ,SS,abhydrolase, | protein regulator of cytokinesis 1 | 3.1 |
| 10 | 411000 | N40449 | Hs.201619 | SS | ESTs, Weakly similar to S38383 SEB4B pro | 3.1 |
| | 412519 | AA196241 | Hs.73980 | SS,Troponin,Hemagglutinin,SS,TM,C2,Tropo | troponin T1, skeletal, slow | 3.1 |
| | 450223 | AA418204 | Hs.241493 | ,SS,pro_isomerase, | natural killer-tumor recognition sequenc | 3.1 |
| | 422790 | AA809875 | Hs.25933 | ,TM,histone,Sec1,histone,sugar_tr | ESTs | 3.1 |
| | 424269 | AW137691 | Hs.199754 | ,SS,TM,7tm_2,GPS | ESTs | 3.1 |
| 15 | 435854 | AJ278120 | Hs.4996 | ,SS,WD40 | putative ankyrin-repeat containing prote | 3.1 |
| | 447388 | AW630534 | Hs.76277 | ,SS,TM,rm,oxidored_q6,oxidored_q6 | Homo sapiens, clone MGC:9381, mRNA, comp | 3.1 |
| | 451631 | R00866 | | SS | gb:ye79c02.s1 Soares fetal liver spleen | 3.0 |
| | 448105 | AW591433 | Hs.298241 | ,SS,TM,trefol,trypsin,trefol | Transmembrane protease, serine 3 | 3.0 |
| | 438637 | BE500941 | Hs.126730 | ,TM,PH, | ESTs, Weakly similar to KIAA1214 protein | 3.0 |
| 20 | 423024 | AA593731 | Hs.325823 | ,SS,TM,CD36 | ESTs, Moderately similar to ALU5_HUMAN A | 3.0 |
| | 456592 | R91600 | | ,SS,Ran_BP1,LIM,Ran_BP1,GRIP,TPR,LIM | gb:yq10c02.r1 Soares fetal liver spleen | 3.0 |
| | 425920 | AL049977 | Hs.162209 | SS,TM,SS,TM,PMP22_Claudin,PMP22_Claudin | claudin 8 | 3.0 |
| | 444670 | H58373 | Hs.332938 | ,SS,TM | hypothetical protein MGC5370 | 3.0 |
| | 401197 | | | arf,arf, | ENSP00000229263*:HSPC213. | 3.0 |
| 25 | 437755 | AW204256 | Hs.291887 | ,wnt, | ESTs | 3.0 |
| | 452560 | BE077084 | Hs.336432 | ,SS,rm,zf-RanBP,pkinase,C2,pkinase_C,DA | ESTs | 3.0 |
| | 410274 | AA381807 | Hs.61762 | SS,SS | hypoxia-inducible protein 2 | 3.0 |
| | 450098 | W27249 | Hs.8109 | SS | hypothetical protein FLJ21080 | 3.0 |
| | 404826 | | | ,SS,TM | Target Exon | 3.0 |
| 30 | 458389 | H70284 | Hs.160152 | ,SS,RA | ESTs, Weakly similar to FPHU alpha-fetop | 3.0 |
| | 408196 | AL034548 | Hs.43627 | HMG_box,pkinase,zf-CCHC,SS,TM,HMG_box | SRY (sex determining region Y)-box 22 | 3.0 |
| | 433675 | AW977653 | Hs.75319 | ,SS,ribonuc_red_sm, | ribonucleotide reductase M2 polypeptide | 3.0 |
| | 418848 | AI820961 | Hs.193465 | ,death,ZU5,pkinase,Activin_rec, | ESTs | 3.0 |
| 35 | 422095 | AI868872 | Hs.282804 | SS,Cu-oxidase,SS,Cu-oxidase,Cu-oxidase | hypothetical protein FLJ22704 | 3.0 |
| | 415992 | C05837 | Hs.145807 | ,SS,TM | hypothetical protein FLJ13593 | 3.0 |
| | 424631 | AA688021 | Hs.179808 | SS | ESTs | 3.0 |
| | 409956 | AW103364 | Hs.727 | SS,TGF-beta,TGFb_propeptide,SS,TGF-beta, | inhibin, beta A (activin A, activin AB a | 3.0 |
| | 419667 | AU077005 | Hs.92208 | SS,disintegrin,Repolysin,Pep_M12B_prope | a disintegrin and metalloproteinase doma | 3.0 |
| | 450946 | AA374569 | Hs.127698 | SS | ESTs, Moderately similar to 2109260A B c | 3.0 |
| 40 | 447770 | AB032417 | Hs.19545 | Frizzled,Fz,SS,TM,Frizzled,Fz, | frizzled (Drosophila) homolog 4 | 3.0 |
| | 423826 | U20325 | Hs.1707 | SS,SS | cocaine- and amphetamine-regulated trans | 3.0 |
| | 418838 | AW385224 | Hs.35198 | ,SS,TM,Phosphodiest, | ectonucleotide pyrophosphatase/phosphodi | 3.0 |
| | 442804 | AW300118 | Hs.131257 | ,SS,TM,G-gamma | ESTs | 3.0 |
| | 432284 | AA532807 | Hs.105822 | ,SS,TM,pkinase, | ESTs | 3.0 |

TABLE 20A

Table 20A shows the accession numbers for those pkeys lacking unigeneID's for Table 20. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| | Pkey | CAT number | Accessions |
|----|--------|------------|---|
| 20 | 410785 | 1221055_1 | AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355 |
| | 411667 | 1253334_1 | BE160198 AW935898 T11520 AW935930 AW856073 AW861034 |
| | 418636 | 177402_1 | AW749855 AA225995 AW750208 AW750206 |
| | 420854 | 197072_1 | AW296927 AI684514 AI263168 AA281079 |
| | 422128 | 211994_1 | AW881145 AA490718 M85637 AA304575 T06067 AA331991 |
| 25 | 423431 | 228162_1 | AA326062 AA325758 AW962182 |
| | 423945 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| | 426878 | 273265_1 | BE069341 AW748403 AL044891 AI908240 AA393080 |
| | 433687 | 373061_1 | AA743991 AA604852 AW272737 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| 30 | 451631 | 878098_1 | R00866 R01523 AI806815 |
| | 456207 | 165078_-1 | AA193450 |
| | 456592 | 202684_1 | R91600 T87079 AA291455 |

TABLE 20B

5 **Table 20B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

| Pkey | Ref | Strand | Nt_position |
|-----------|---------|--------|---|
| 400608 | 9887666 | Minus | 96756-97558 |
| 400903 | 2911732 | Plus | 59112-59228 |
| 20 401045 | 8117619 | Plus | 90044-90184,91111-91345 |
| 401093 | 8516137 | Minus | 22335-23166 |
| 401197 | 9719705 | Plus | 176341-176452 |
| 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011 |
| 25 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573 |
| 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814 |
| 401866 | 8018106 | Plus | 73126-73623 |
| 402230 | 9966312 | Minus | 29782-29932 |
| 402408 | 9796239 | Minus | 110326-110491 |
| 30 402578 | 9884928 | Plus | 66350-66496 |
| 402606 | 9909429 | Minus | 81747-82094 |
| 402837 | 9369121 | Minus | 2013-2186,9570-9758,11136-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320 |
| 403199 | 9958183 | Minus | 58895-59036,66618-66789 |
| 403329 | 8516120 | Plus | 96450-96598 |
| 35 403593 | 6862650 | Minus | 62554-62712,69449-69602 |
| 403943 | 7711864 | Plus | 100742-100904,101322-101503 |
| 404091 | 7684554 | Minus | 82121-83229 |
| 404347 | 9838195 | Plus | 74493-74829 |
| 404826 | 6572184 | Plus | 47726-48046 |
| 40 405366 | 2182280 | Plus | 22478-22632 |
| 405654 | 4895155 | Minus | 53624-53759 |

**TABLE 21: 210 GENES UP-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT TISSUES THAT ARE
LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS
AMENABLE TO MODULATION BY SMALL MOLECULES**

Table 21 shows 210 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85th percentile value amongst 144 non-malignant tissues, and the 96th percentile value amongst 73 breast cancers was greater than or equal 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 93rd percentile tumor to 85th percentile of normal body tissue

| Pkey | ExAccn | UnigenelD | Predicted Protein Domains | UnigeneTitle | R1 |
|--------|-----------|-----------|--|--|------|
| 449746 | AI668594 | Hs.176588 | SS,p450 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | 65.7 |
| 400292 | AA250737 | Hs.72472 | death,ZU5,TM,Activin_rec,pkinase, | BMP-R1B | 55.9 |
| 424735 | U31875 | Hs.272499 | SS,TM | short-chain alcohol dehydrogenase family | 53.8 |
| 407178 | AA195651 | Hs.104106 | SS,Dihydroorotase, | ESTs | 39.3 |
| 408045 | AW138959 | Hs.245123 | Phosphodiester,Somatostatin_B, | ESTs | 34.9 |
| 450375 | AA009647 | Hs.8850 | SS,TM,disintegrin,Pep_M12B_propep,Reprol | a disintegrin and metalloproteinase doma | 25.7 |
| 429170 | NM_001394 | Hs.2359 | DSPc,Rhodanese, | dual specificity phosphatase 4 | 24.9 |
| 445730 | AI624342 | Hs.170042 | SS,TM,Cation_efflux | ESTs | 24.1 |
| 424634 | NM_003613 | Hs.151407 | lg,tsp_1,SS,AAA | cartilage intermediate layer protein, nu | 21.7 |
| 420757 | X78592 | Hs.99915 | hormone_rec,Androgen_recep,zf-C4, | androgen receptor (dihydrotestosterone r | 21.7 |
| 424399 | AI905687 | Hs.2533 | SS | aldehyde dehydrogenase 9 family, member | 20.3 |
| 447350 | AI375572 | Hs.172634 | pkinase, | ESTs | 19.2 |
| 456207 | AA193450 | | SS,TM,p450,p450 | gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi | 18.3 |
| 456938 | X52509 | Hs.161640 | SS,TM,aminotran_1_2,Cadherin_C_term,cadhyrosine aminotransferase | | 18.1 |
| 402578 | | | SS,p450,SS,TM,p450 | C1001134:gil2117372[pil]65981 fatty ac | 17.8 |
| 425692 | D90041 | Hs.155956 | SS,Acetyltransf2, | N-acetyltransferase 1 (arylamine N-acety | 16.7 |
| 424001 | W67883 | Hs.137476 | pkinase, | paternally expressed 10 | 16.5 |
| 418007 | M13509 | Hs.83169 | SS,hemopexin,Peptidase_M10,SS,Peptidase_matrix metalloproteinase 1 (MMP1; Inters | | 15.7 |
| 421727 | Y13153 | Hs.107318 | | kynurenine 3-monooxygenase (kynurenine 3 | 15.3 |
| 411869 | W20027 | Hs.23439 | SS,Peptidase_M1, | ESTs | 13.9 |
| 400289 | X07820 | Hs.2258 | hemopexin,Peptidase_M10,SS,Peptidase_M10matrix metalloproteinase 10 (MMP10; str | | 13.5 |
| 443348 | AW873596 | Hs.182278 | SS,DENN | calmodulin 2 (phosphorylase kinase, del | 13.0 |
| 424086 | AI351010 | Hs.102267 | SS,Lysyl_oxidase | lysyl oxidase | 12.8 |
| 400295 | W72838 | Hs.2533 | SS | aldehyde dehydrogenase 9 family, member | 12.7 |
| 408771 | AW732573 | Hs.47584 | TM,K_tetra,ion_trans,SS,TM,K_tetra,ion_t | potassium voltage-gated channel, delayed | 11.9 |
| 421155 | H87879 | Hs.102267 | SS,Lysyl_oxidase,Aldose_epim,Epimerase,S | lysyl oxidase | 11.8 |
| 424905 | NM_002497 | Hs.153704 | pkinase,SS,TM,pkinase,polyprenyl_synt, | NIMA (never in mitosis gene a)-related k | 11.7 |
| 438167 | R28363 | Hs.24286 | SS,TM,7tm_1,p450,rm | ESTs | 11.5 |
| 459583 | AI907673 | | pkinase, | gb:IL-BT152-080399-004 BT152 Homo saplen | 11.5 |
| 423945 | AA410943 | | death,ZU5,TM,Activin_rec,pkinase, | gb:z32h03.r1 Soares ovary tumor NbHOT H | 11.4 |
| 445263 | H57646 | Hs.42586 | SS,Acyltransferase, | KIAA1560 protein | 11.2 |

| | | | | | | |
|----|--------|---|-----------|---|--|------|
| | 423887 | AL080207 | Hs.134585 | SS,TM,BRCT,ank,ABC_tran,ABC_tran | DKFZP434G232 protein | 10.9 |
| | 429859 | NM_007050 | Hs.225952 | SS,TM,Y_phosphatase,MAM,fn3, | protein tyrosine phosphatase, receptor t | 10.4 |
| | 428368 | BE440042 | Hs.83326 | SS,Peptidase_M10,hemopexin,SS,Peptidase, | matrix metalloproteinase 3 (stromelysin | 10.3 |
| | 418912 | NM_000685 | Hs.89472 | SS,TM,7tm_1,SS,TM,7tm_1, | angiotensin receptor 1 | 10.3 |
| 5 | 451952 | AL120173 | Hs.301663 | SS,kinase, | ESTs | 10.3 |
| | 402408 | NA | | SS,carb_anhydrase | NM_030920*:Homo sapiens hypothetical pro | 9.8 |
| | 415539 | AJ733881 | Hs.72472 | death,ZU5,TM,Activin_recp,kinase, | BMP-R1B | 9.4 |
| | 406687 | M31126 | Hs.272620 | SS,Peptidase_M10,hemopexin,SS,Peptidase, | matrix metalloproteinase 11 (MMP11; stro | 9.1 |
| | 419948 | AB041035 | Hs.93847 | Ferric_reduct,TM,Ferric_reduct, | NM_016931:Homo sapiens NADPH oxidase 4 (| 9.1 |
| 10 | 400285 | NA | | TM,ABC_tran,ABC_membrane, | Eos Control | 8.8 |
| | 408380 | AF123050 | Hs.44532 | SS,TM,ubiquitin,7tm_3,ANF_receptor,sushi | diubiquitin | 8.6 |
| | 409203 | AA780473 | Hs.687 | SS,p450,SS,p450 | cytochrome P450, subfamily IVB, polypept | 8.3 |
| | 424902 | NM_003866 | Hs.153687 | SS,SS | inositol polyphosphate-4-phosphatase, ty | 8.3 |
| | 431725 | X65724 | Hs.2839 | SS,Cys_knot,SS | Norrie disease (pseudoglioma) | 8.3 |
| 15 | 418092 | R45154 | Hs.106604 | death,ZU5,pkinase,Activin_recp, | ESTs | 8.3 |
| | 427811 | M81057 | Hs.180884 | SS,Zn_carbOpept,Propep_M14,SS,Propep_M14 | carboxypeptidase B1 (tissue) | 8.2 |
| | 423554 | M90516 | Hs.1674 | GATase_2,SIS, | glutamine-fructose-6-phosphate transamin | 8.1 |
| | 426261 | AW242243 | Hs.168670 | SS,TM,WD40,ubiquitin,E1-E2_ATPase,Cation | peroxisomal farnesylated protein | 7.8 |
| | 413374 | NM_001034 | Hs.75319 | SS | ribonucleotide reductase M2 polypeptide | 7.6 |
| 20 | 432677 | NM_004482 | Hs.278611 | SS,TM,Glycos_transf_2,Ricin_B_lectin,DPP | UDP-N-acetyl-alpha-D-galactosamine:polyp | 7.6 |
| | 456986 | D38299 | Hs.170917 | SS,TM,7tm_1, | prostaglandin E receptor 3 (subtype EP3) | 7.5 |
| | 453331 | A1240665 | Hs.8895 | SS,TM,disintegrin,Pep_M12B_propep,Reprol | ESTs | 7.3 |
| | 407721 | Y12735 | Hs.38018 | kinase, | dual-specificity tyrosine-(Y)-phosphoryl | 7.2 |
| | 418004 | U37519 | Hs.87539 | SS,aldedh,SS,aldedh, | aldehyde dehydrogenase 3 family, member | 7.2 |
| 25 | 410555 | U92649 | Hs.64311 | TM,disintegrin,Reprolysin, | a disintegrin and metalloproteinase doma | 7.1 |
| | 443695 | AW204099 | Hs.337720 | | ESTs, Weakly similar to AF126780 1 retin | 6.9 |
| | 423545 | AP000692 | Hs.129781 | GAF,PDEase | chromosome 21 open reading frame 5 | 6.8 |
| | 401045 | | | ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p | | |
| 30 | | C11001883:gi 6753278 ref NP_033938.1 c | | | 6.7 | |
| | 442082 | R41823 | Hs.7413 | TM,EPH_lbd,kinase,SAM,fn3, | ESTs; calyntenin-2 | 6.7 |
| | 418836 | AI655499 | Hs.161712 | TM,Activin_recp,kinase,death,ZU5, | ESTs | 6.6 |
| | 404091 | NA | | TM,7tm_3,ANF_receptor, | Target Exon | 6.6 |
| | 450865 | A1248013 | Hs.106532 | zf-C2H2 | ESTs, Weakly similar to I38588 reverse t | 6.5 |
| 35 | 424085 | NM_002914 | Hs.139226 | SS,AAA,Viral_helicase1,rm, | replication factor C (activator 1) 2 (40 | 6.5 |
| | 449650 | AF055575 | Hs.23838 | TM,ion_trans,SS,TM,ion_trans, | calcium channel, voltage-dependent, L ty | 6.4 |
| | 432304 | AA932186 | Hs.69297 | TM,7tm_1, | ESTs | 6.2 |
| | 415669 | NM_005025 | Hs.78589 | SS,serpin, | serine (or cysteine) proteinase inhibito | 6.2 |
| | 442942 | AW167087 | Hs.131562 | SS,Ig,Sema,kinase, | ESTs | 6.2 |
| 40 | 428795 | R45503 | Hs.97469 | SS,TM | ESTs, Highly similar to A39769 N-acetyl | 6.1 |
| | 428479 | Y00272 | Hs.184572 | SS,kinase,kinase | cell division cycle 2, G1 to S and G2 to | 6.1 |
| | 400300 | X03363 | | SS,TM,kinase,Recep_L_domain,SH2,PH,FunHER2 | receptor tyrosine kinase (c-erb-b2, | 6.1 |
| | 447359 | NM_012093 | Hs.18268 | SS,adenylatekinase, | adenylate kinase 5 | 6.1 |
| | 402230 | NA | | SS,TM,p450, | Target Exon | 6.1 |
| 45 | 424687 | J05070 | Hs.151738 | SS,Peptidase_M10,m2,hemopexin,SS,TM,Pep | matrix metalloproteinase 9 (gelatinase B | 5.8 |
| | 432328 | AI572739 | Hs.195471 | 6PF2K,PGAM, | 6-phosphofructo-2-kinase/fructose-2,6-bi | 5.8 |
| | 432239 | X81334 | Hs.2936 | SS,Peptidase_M10,hemopexin,SS,Peptidase, | matrix metalloproteinase 13 (collagenase | 5.6 |
| | 400286 | NA | | SS,TM,ABC_tran,ABC_membrane,SS | C16000922:gi 7499103 pir T20903 hypothe | 5.6 |
| | 425247 | NM_005940 | Hs.155324 | SS,Peptidase_M10,hemopexin,SS | matrix metalloproteinase 11 (MMP11; stro | 5.4 |
| 50 | 434737 | AA828246 | Hs.291884 | UCH-1,kinase,OPR,Rhodanese,AMP-binding,ESTs | | 5.4 |
| | 439310 | AF086120 | Hs.102793 | SS,TM,UDPGT,casein_kappa | ESTs | 5.2 |
| | 441111 | AI806867 | Hs.126594 | SS,TM,Phosphodiast, | ESTs | 5.2 |
| | 452355 | N54926 | Hs.29202 | TM,7tm_1,TM | G protein-coupled receptor 34 | 5.2 |
| | 427711 | M31659 | Hs.180408 | SS | solute carrier family 25 (mitochondrial | 5.2 |
| 55 | 429353 | AL117406 | Hs.200102 | SS,TM,ABC_tran,ABC_membrane, | ATP-binding cassette transporter MRP8 | 5.1 |
| | 425325 | X52730 | Hs.1892 | SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,STAR | | |
| | | phenylethanolamine N-methyltransferase | | | 5.1 | |
| | 448706 | AW291095 | Hs.21814 | SS,TM,kinase, | Interleukin 20 receptor, alpha | 5.1 |
| | 403593 | NA | | CIDE-N,kinase | Target Exon | 5.1 |
| 60 | 432777 | AA564991 | Hs.269477 | alpha-amylase, | ESTs | 5.0 |
| | 446232 | AI281848 | Hs.194691 | SS,TM,7tm_3,Ribosomal_L13 | retinolic acid induced 3 | 4.9 |
| | 411165 | NM_000169 | Hs.69089 | SS,Melibiose,BTK,PH,kinase,SH2,SH3,Ribo | galactosidase, alpha | 4.9 |
| | 414117 | W88559 | Hs.1787 | TM,ion_trans,K_tetra, | proteolipid protein 1 (Pelizaeus-Merzbac | 4.9 |
| | 411096 | U80034 | Hs.68583 | Peptidase_M3, | mitochondrial intermediate peptidase | 4.9 |
| 65 | 450506 | NM_004460 | Hs.418 | SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV_N | fibroblast activation protein, alpha | 4.9 |
| | 417975 | AA641836 | Hs.30085 | SS,trypsin | hypothetical protein FLJ23186 | 4.9 |
| | 447752 | M73700 | Hs.105938 | SS,transferrin,7tm_1,transferrin, | lactotransferrin | 4.8 |
| | 427122 | AW057736 | Hs.323910 | SS,TM,kinase,Recep_L_domain,SH2,PH,FunHER2 | receptor tyrosine kinase (c-erb-b2, | 4.8 |

| | | | | |
|--------|---------------------------|--|--|-----|
| 400181 | NA | SS,TM,3Bela_HSD, | ENSP00000171555:CDNA FLJ10727 fis, clone | 4.6 |
| 452093 | AA447453 Hs.27860 | SS,TM,7tm_1, | Homo sapiens mRNA; cDNA DKFZp586M0723 (f | 4.6 |
| 435542 | AA687376 Hs.269533 | SS,pkinase,RhoGEF,Ig,PH,SH3, | ESTs | 4.6 |
| 417576 | AA339449 Hs.82285 | AIRS,formyl_transf,GARS,SS,GARS,AIRS,for | phosphoribosylglycinamide formyltransfer | 4.6 |
| 5 | 446089 AI860021 Hs.270651 | pkinase | ESTs, Moderately similar to A47582 B-cel | 4.6 |
| 424420 | BE614743 Hs.146688 | SS,TM,MAPEG, | prostaglandin E synthase | 4.5 |
| 452190 | H26735 Hs.91668 | SS,TM,PH,SH2,Furin-like,pkinase,Recep_L_ | Homo sapiens clone PP1498 unknown mRNA | 4.5 |
| 419986 | AI345455 Hs.78915 | pkinase,OPR, | GA-binding protein transcription factor, | 4.5 |
| 421582 | AI910275 Hs.1406 | SS,trefoil,SS,TM,Idl_recept_a,SrcR,typs | trefoil factor 1 (pS2) | 4.5 |
| 10 | 446733 AA863360 Hs.26040 | SS,TM,p450, | ESTs, Weakly similar to fatty acid omega | 4.4 |
| 453060 | AW294092 Hs.21594 | SS,ras,Y_phosphatase,ras | hypothetical protein MGC15754 | 4.4 |
| 400205 | NA | | NM_006265*:Homo sapiens RAD21 (S. pombe) | 4.4 |
| 420854 | AW296927 | SS,TM,Peptidase_M1, | gb:U1-H-BW0-ajc-c-07-0-UI.s1 NC1_CGAP_Su | 4.3 |
| 432690 | AF181490 Hs.278627 | SS,pyr_redox,SS,Ribosomal_L39 | prenylcysteine lyase | 4.3 |
| 15 | 441560 F13386 Hs.7888 | pkinase, | Homo sapiens clone 23736 mRNA sequence | 4.3 |
| 416445 | AL043004 Hs.79337 | SS,pkinase, | KIAA0135 protein | 4.3 |
| 439024 | R96696 Hs.35598 | SS,TM,trypsin,vwd,Ig | ESTs | 4.3 |
| 432882 | NM_013257Hs.279696 | pkinase,pkinase_C, | serum/glucocorticoid regulated kinase-II | 4.2 |
| 20 | 447754 AW073310 Hs.163533 | pkinase, | Homo sapiens cDNA FLJ14142 fis, clone MA | 4.2 |
| 453775 | NM_002916Hs.35120 | SS,AAA,PI3_P4_kinase,PI3Ka,PI3K_rbd,PI3 | replication factor C (activator 1) 4 (37 | 4.2 |
| 431657 | AI345227 Hs.105448 | SS,TM,pkinase | ESTs, Weakly similar to B34087 hypotheti | 4.1 |
| 427899 | AA829286 Hs.332053 | SS,SAA_proteins,ABC_membrane,ABC_tran, | serum amyloid A1 | 4.1 |
| 422938 | NM_001809Hs.1594 | SS,TM,thiolase, | centromere protein A (17kD) | 4.1 |
| 25 | 418478 U38945 Hs.1174 | ank,ank | cyclin-dependent kinase inhibitor 2A (me | 4.1 |
| 406922 | S70284 | SS,TM,Desaturase,SS | gb:stearoyl-CoA desaturase [human, adipo | 4.1 |
| 439285 | AL133916 Hs.172572 | SS,Ig,pkinase,LRRNT,LRRCT, | hypothetical protein FLJ20093 | 4.1 |
| 429922 | Z97630 Hs.226117 | SS,TM,linker_histone,7tm_1 | H1 histone family, member 0 | 4.1 |
| 420139 | NM_005357Hs.95351 | SS,TM,p450, | lipase, hormone-sensitive | 4.0 |
| 425071 | NM_013989Hs.154424 | SS,T4_deiodinase,T4_deiodinase, | deiodinase, iodothyronine, type II | 4.0 |
| 30 | 424511 BE300512 Hs.193557 | SS,Y_phosphatase,Band_41 | ESTs, Moderately similar to ALU7_HUMAN A | 4.0 |
| 428722 | U76456 Hs.190787 | SS,TIMP, | tissue inhibitor of metalloproteinase 4 | 3.9 |
| 428330 | L22524 Hs.2256 | SS,Peptidase_M10,SS,Peptidase_M10,hemopematrix metalloproteinase 7 (MMP7; uterin | | 3.9 |
| 414831 | M31158 Hs.77439 | SS,cNMP_binding,R1la,HMG_box | protein kinase, cAMP-dependent, regulato | 3.9 |
| 413589 | AW452631 Hs.313803 | SS,abhydrolase | ESTs, Highly similar to AF157833 1 noncl | 3.8 |
| 35 | 418629 BE247550 Hs.86859 | SS,SH2,PH,SS,TM,PH,SH2,Furin-like,pkinas | growth factor receptor-bound protein 7 | 3.8 |
| 413453 | AA129640 Hs.128065 | SS,Peptidase_C1,gpdh | ESTs | 3.8 |
| 403943 | | p450,SS,p450 | C5000355:gil4503225[ref NP_000765.1] cyt | 3.8 |
| 444618 | AV653785 Hs.173334 | | ELL-RELATED RNA POLYMERASE II, ELONGATIO | 3.8 |
| 40 | 408761 AA057264 Hs.238936 | SS,TM,7tm_1, | ESTs, Weakly similar to (define not ava | 3.8 |
| 427809 | M26380 Hs.180878 | SS,lipase,PLAT,Sec7,PH, | lipoprotein lipase | 3.7 |
| 418203 | X54942 Hs.83758 | CKS,SS,CKS, | CDC28 protein kinase 2 | 3.7 |
| 454071 | AI041793 Hs.42502 | TM,7tm_1, | ESTs | 3.7 |
| 424676 | Y08565 Hs.151678 | Glycos_transf_2,Ricin_B_lectin,SS,Glycos | UDP-N-acetyl-alpha-D-galactosamine:polyp | 3.7 |
| 457465 | AW301344 Hs.122908 | SS,Pribosyltran,Sulfatase | DNA replication factor | 3.7 |
| 417601 | NM_014735Hs.82292 | PHD,pkinase,SS | KIAA0215 gene product | 3.7 |
| 446619 | AU076643 Hs.313 | SS,TM,ethand,ion_trans | secreted phosphoprotein 1 (osteopontin, | 3.7 |
| 406625 | Y13647 Hs.119597 | SS,TM,Desaturase,SS | stearoyl-CoA desaturase (delta-9-desatur | 3.6 |
| 428769 | AW207175 Hs.106771 | SS,7tm_1,SPRY, | ESTs | 3.6 |
| 426310 | NM_000909Hs.169266 | SS,TM,7tm_1, | neuropeptide Y receptor Y1 | 3.6 |
| 50 | 417531 NM_003157Hs.1087 | SS,pkinase,vwa,vwa,Glyco_transf_8 | serine/threonine kinase 2 | 3.6 |
| 444781 | NM_014400Hs.11950 | SS,PH,lactamase_B | GPI-anchored metastasis-associated prote | 3.6 |
| 431493 | AI791493 Hs.129873 | SS,p450,p450 | ESTs, Weakly similar to A36036 cytochrom | 3.6 |
| 428966 | AF059214 Hs.194687 | | cholesterol 25-hydroxylase | 3.6 |
| 414175 | AI308876 Hs.103849 | TM,hemopexin,Peptidase_M10,hemopexin,Pep | hypothetical protein DKFZp761D112 | 3.6 |
| 55 | 455325 AW895719 | TM,ion_trans,K_tetra, | gb:QV4-NN0039-290300-154-f06 NN0039 Homo | 3.6 |
| 429597 | NM_003816Hs.2442 | | a disintegrin and metalloproteinase doma | 3.6 |
| 425320 | U29344 Hs.83190 | Acyl_transf,adh_zinc,ketoacyl-synt,pp-bi | fatty acid synthase | 3.5 |
| 431854 | AA383550 Hs.271699 | IMS,SS | polymerase (DNA directed) iota | 3.5 |
| 407104 | S57296 Hs.323910 | SS,TM,SH2,PH,pkinase,Recep_L_domain,Furin-erb-b2 avian erythroblastic leukemia v | | 3.5 |
| 60 | 449051 AW961400 Hs.333526 | SS | HER2 receptor tyrosine kinase (c-erb-b2, | 3.5 |
| 434398 | AA121098 Hs.3838 | pkinase,POLO_box,SS,pkinase,POLO_box, | serum-inducible kinase | 3.5 |
| 454042 | H22570 Hs.172572 | SS,Ig,pkinase,LRRNT,LRRCT, | hypothetical protein FLJ20093 | 3.5 |
| 407756 | AA116021 Hs.38260 | SS,UCH-1,UCH-2,SS,TM,G_glu_transsept | ubiquitin specific protease 18 | 3.5 |
| 401464 | AF039241 Hs.9028 | Peptidase_M24, | histone deacetylase 5 | 3.5 |
| 65 | 412970 AB026436 Hs.177534 | DSPc,Myosin_tail, | dual specificity phosphatase 10 | 3.5 |
| 412049 | N53437 Hs.18268 | SS,adenylatekinase, | adenylate kinase 5 | 3.5 |
| 425776 | U25128 Hs.159499 | SS,TM,7tm_2,SS,TM,7tm_2 | parathyroid hormone receptor 2 | 3.4 |

| | | | | | |
|----|-------------------------------|-----------|-----------|--|-------------|
| 5 | 407846 | AA426202 | Hs.40403 | TM,ABC_membrane,ABC_tran,Ribosomal_S4eCbp/p300-Interacting transactivator, wit | 3.4 |
| | 406925 | L34041 | Hs.9739 | SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE-glycerol-3-phosphate dehydrogenase 1 (so | 3.4 |
| | 445873 | AA250970 | Hs.251946 | SS,rm,PABP,pkinase,14-3-3,rm | 3.4 |
| | 418054 | NM_002318 | Hs.83354 | SS,TM,mito_carr,Lysyl_oxidase | 3.4 |
| | 406815 | AA833930 | Hs.288036 | SS,IPPT, | 3.4 |
| 10 | 410530 | M25809 | Hs.64173 | ATP-synt_ab,SS,7tm_1,ATP-synt_ab | 3.4 |
| | 407021 | U52077 | | | 3.4 |
| | 421168 | AF182277 | Hs.330780 | SS,p450,SS | 3.4 |
| | 431473 | AA825686 | Hs.321176 | SS | 3.4 |
| | 408101 | AW968504 | Hs.123073 | pkinase, | 3.4 |
| 15 | 422083 | NM_001141 | Hs.111256 | lipoygenase,PLAT, | 3.3 |
| | 411393 | AW797437 | Hs.69771 | SS,sushi,trypsin,vwa,rm,fibrinogen_C,fn | 3.3 |
| | 435767 | H73505 | Hs.117874 | SS,Peptidase_S8,P,Peptidase_S8,P | 3.3 |
| | 433068 | NM_006456 | Hs.288215 | SS,Pribosyltran, | 3.3 |
| | 426928 | AF037062 | Hs.172914 | SS,adh_short,TGF-beta,TGFb_propeptide | 3.3 |
| 20 | 414575 | H11257 | Hs.22968 | SS,pkinase,lg, | 3.3 |
| | 445941 | AI267371 | Hs.172636 | SS,SS,lipoygenase,PLAT | 3.3 |
| | 444542 | AI161293 | Hs.280380 | SS,SS,Peptidase_M1,EGF,ig,lectin_c,sushi | 3.3 |
| | 425741 | AF052152 | Hs.159412 | pkinase, | 3.3 |
| | 434228 | Z42047 | Hs.283978 | SS,TM,7tm_1 | 3.3 |
| 25 | 433264 | D85782 | Hs.3229 | | 3.3 |
| | 400419 | AF084545 | | SS,Peptidase_M1, | 3.3 |
| | 439750 | AL359053 | Hs.57664 | TM,integrin_B,Ricin_B_lectin,rm | 3.3 |
| | 417757 | R19897 | Hs.106604 | death,ZU5,pkinase,Activin_rec, | 3.3 |
| | 452194 | AI694413 | Hs.332649 | SS,TM,7tm_3,ANF_receptor,sushi | 3.2 |
| 30 | 421458 | NM_003654 | Hs.104576 | SS | 3.2 |
| | 443767 | BE562136 | Hs.9736 | SS,PCI,RasGEF,hormone_rec,zf-C4, | 3.2 |
| | 422648 | D86983 | Hs.118893 | peroxidase,LRRCT, | 3.2 |
| | 423431 | AA326062 | | SS,p450,p450 | 3.2 |
| | 451264 | AI768235 | | SS,Trehalase | 3.2 |
| 35 | 452110 | T47667 | Hs.28005 | SS,TM,Activin_rec,pkinase | 3.2 |
| | 439963 | AW247529 | Hs.6793 | TM,p450,Ets | 3.2 |
| | 453941 | U39817 | Hs.36820 | SS,DEAD,HRDC,helicase_C, | 3.1 |
| | 406664 | L34041 | Hs.9739 | SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE- | 3.1 |
| | phosphate dehydrogenase 1 (so | | | 3.1 | glycerol-3- |
| 40 | 453487 | R31770 | Hs.23540 | TM,7tm_1, | 3.1 |
| | 420911 | U77413 | Hs.100293 | | 3.1 |
| | 443171 | BE281128 | Hs.9030 | SS,TM,7tm_1,rm,SS | 3.1 |
| | 452256 | AK000933 | Hs.28661 | TM,GDI,7tm_1, | 3.1 |
| | 432201 | AI538613 | Hs.298241 | SS,TM,trypsin,SS,TM,trefoil,trypsin,tref | 3.1 |
| 45 | 419150 | T29618 | Hs.89640 | TM,pkinase,fn3, | 3.1 |
| | 444443 | AI149286 | Hs.55099 | SS | 3.1 |
| | 426283 | NM_003937 | Hs.169139 | | 3.1 |
| | 436291 | BE568452 | Hs.5101 | SS,abhydrolase, | 3.1 |
| | 450223 | AA418204 | Hs.241493 | SS,pro_isomerase, | 3.1 |
| | 424269 | AW137691 | Hs.199754 | SS,TM,7tm_2,GPS | 3.1 |
| | 448105 | AW591433 | Hs.298241 | SS,TM,trefoil,trypsin,trefoil | 3.0 |
| | 452560 | BE077084 | Hs.336432 | SS,rm,zf-RanBP,pkinase,C2,pkinase_C,DAG ESTs | 3.0 |

TABLE 21A

Table 21 A shows the accession numbers for those pkeys lacking unigeneID's for Table 21. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accessions |
|--------|------------|-------------------------------------|
| 420854 | 197072_1 | AW296927 AI684514 AI263168 AA281079 |
| 423431 | 228162_1 | AA326062 AA325758 AW962182 |
| 423945 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| 451264 | 863988_1 | AI768235 R31400 H29082 H23107 |
| 455325 | 1279475_1 | AW895719 N31451 N41451 |
| 456207 | 165078_-1 | AA193450 |

TABLE 21B

5 **Table 21B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 21. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-----------------------------|
| 401045 | 8117619 | Plus | 90044-90184,91111-91345 |
| 402230 | 9966312 | Minus | 29782-29932 |
| 402408 | 9796239 | Minus | 110326-110491 |
| 402578 | 9884928 | Plus | 66350-66496 |
| 403593 | 6862650 | Minus | 62554-62712,69449-69602 |
| 403943 | 7711864 | Plus | 100742-100904,101322-101503 |
| 404091 | 7684554 | Minus | 82121-83229 |

20

**TABLE 22: 739 GENES UP-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT BREAST**

Table 22 shows 739 genes up-regulated in breast cancer compared to normal adult breast. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the denominator was the 85th percentile value for 12 non-malignant breast specimens, and the 96th percentile value amongst the 73 breast cancers was greater than or equal 100 units.

Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 90th percentile tumor to 85th percentile normal breast tissue

| Pkey | ExAccn | UnigeneID | UnigeneTitle | R1 |
|--------|-----------|-----------|--|------|
| 400292 | AA250737 | Hs.72472 | BMP-R1B | 51.5 |
| 424735 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | 38.3 |
| 400297 | AI127076 | Hs.334473 | hypothetical protein DKFZp564O1278 | 29.9 |
| 431448 | AL137517 | Hs.334473 | hypothetical protein DKFZp564O1278 | 26.9 |
| 451110 | AI955040 | Hs.265398 | ESTs, Weakly similar to transformation-r | 25.8 |
| 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 23.2 |
| 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 22.6 |
| 407980 | AA046309 | | gb:zf12f01.s1 Soares_fetal_heart_NbHH19W | 19.8 |
| 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 18.9 |
| 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 18.0 |
| 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 17.6 |
| 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 17.6 |
| 407824 | AA147884 | Hs.9812 | Homo sapiens cDNA FLJ14388 fis, clone HE | 17.1 |
| 453160 | AI263307 | Hs.239884 | H2B histone family, member L | 17.0 |
| 407137 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen | 16.1 |
| 425692 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 16.1 |
| 438533 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypotheti | 16.0 |
| 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (CX | 15.5 |
| 444342 | NM_014398 | Hs.10887 | similar to lysosome-associated membrane | 15.1 |
| 422505 | AL120862 | Hs.124165 | programmed cell death 9 (PDCD9) | 14.9 |
| 430515 | AA746503 | Hs.283313 | ESTs | 14.7 |
| 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 14.4 |
| 452744 | AI267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr14.4 | |
| 412446 | AI768015 | Hs.92127 | ESTs | 14.2 |
| 415539 | AI733881 | Hs.72472 | BMP-R1B | 14.1 |
| 435496 | AW840171 | Hs.265398 | ESTs, Weakly similar to transformation-r | 13.8 |
| 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transl | 13.8 |
| 400205 | NA | | NM_006265*:Homo sapiens RAD21 (S. pombe) | 13.5 |
| 430965 | AA489732 | Hs.154918 | ESTs | 13.4 |
| 415263 | AA948033 | Hs.130853 | ESTs | 13.3 |
| 451952 | AL120173 | Hs.301663 | ESTs | 13.2 |
| 449722 | BE280074 | Hs.23960 | cyclin B1 | 13.2 |
| 406685 | M18728 | | gb:Human nonspecific crossreacting antig | 13.0 |
| 406690 | M29540 | Hs.220529 | carcinoembryonic antigen-related cell ad | 12.8 |
| 429925 | NM_000786 | Hs.226213 | cytochrome P450, 51 (lanosterol 14-alpha | 12.8 |
| 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 12.7 |
| 432378 | AI493046 | Hs.146133 | ESTs | 12.5 |
| 441377 | BE218239 | Hs.202656 | ESTs | 12.5 |
| 456207 | AA193450 | | gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi | 12.4 |
| 422805 | AA436989 | Hs.121017 | H2A histone family, member A | 12.2 |
| 407811 | AW190902 | Hs.40098 | cysteine knot superfamily 1, BMP antagon | 12.2 |
| 407178 | AA195651 | Hs.104106 | ESTs | 12.2 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 12.1 |
| | 421727 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | 12.0 |
| | 434408 | AI031771 | Hs.132586 | ESTs | 12.0 |
| | 446591 | H44186 | Hs.15456 | PDZ domain containing 1 | 11.9 |
| 5 | 431385 | BE178536 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 11.8 |
| | 443348 | AW873596 | Hs.182278 | calmodulin 2 (phosphorylase kinase, delt | 11.7 |
| | 416602 | NM_006159 | Hs.79389 | nel (chicken)-like 2 | 11.7 |
| | 433365 | AF026944 | Hs.293797 | ESTs | 11.6 |
| | 437866 | AA156781 | Hs.74170 | metallothionein 1E (functional) | 11.5 |
| 10 | 412472 | AW975398 | Hs.293836 | ESTs | 11.4 |
| | 416030 | H15261 | Hs.21948 | ESTs | 11.3 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 11.3 |
| | 420757 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 11.3 |
| | 411598 | BE336654 | Hs.70937 | H3 histone family, member A | 11.2 |
| 15 | 423600 | AI633559 | Hs.310359 | ESTs | 11.2 |
| | 430770 | AA765694 | Hs.123296 | ESTs | 11.0 |
| | 421037 | AI684808 | Hs.197653 | programmed cell death 9 (PDCD9) | 10.9 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 10.7 |
| | 409269 | AA576953 | Hs.22972 | hypothetical protein FLJ13352 | 10.6 |
| 20 | 417791 | AW965339 | Hs.111471 | ESTs | 10.6 |
| | 447268 | AI370413 | Hs.36563 | hypothetical protein FLJ22418 | 10.4 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 10.4 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 10.4 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 10.1 |
| 25 | 453619 | H87648 | Hs.33922 | Homo sapiens, clone MGC:9084, mRNA, comp | 10.1 |
| | 442942 | AW167087 | Hs.131562 | ESTs | 10.1 |
| | 434377 | AW137148 | Hs.306593 | Homo sapiens cDNA FLJ11382 fis, clone HE | 10.1 |
| | 427217 | AA399272 | Hs.144341 | ESTs | 10.1 |
| | 445730 | AI624342 | Hs.170042 | ESTs | 10.0 |
| 30 | 432887 | AI926047 | Hs.162859 | ESTs | 10.0 |
| | 452243 | AL355715 | Hs.28555 | programmed cell death 9 | 9.9 |
| | 424590 | AW966399 | Hs.46821 | hypothetical protein FLJ20086 | 9.9 |
| | 432169 | Y00971 | Hs.2910 | phosphoribosyl pyrophosphate synthetase | 9.9 |
| | 438950 | H23789 | Hs.144530 | EST | 9.9 |
| 35 | 418836 | AI655499 | Hs.161712 | ESTs | 9.8 |
| | 430291 | AV660345 | Hs.238126 | CGI-49 protein | 9.8 |
| | 444665 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 9.7 |
| | 407377 | C16391 | | gb:C16391 Clontech human aorta polyA mRN | 9.7 |
| | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 9.7 |
| 40 | 443462 | AI064690 | Hs.171176 | ESTs | 9.7 |
| | 442145 | AI022650 | Hs.8117 | erbB2-interacting protein ERBIN | 9.7 |
| | 435570 | AF212222 | Hs.177812 | uncharacterized bone marrow protein BM04 | 9.7 |
| | 439820 | AL360204 | Hs.283853 | Homo sapiens mRNA full length insert cDN | 9.6 |
| | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 9.6 |
| 45 | 449448 | D60730 | Hs.57471 | ESTs | 9.6 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 9.5 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 9.3 |
| | 411815 | AA156679 | Hs.125790 | leucine-rich repeat-containing 2 | 9.3 |
| | 415385 | R17798 | Hs.7535 | COBW-like protein | 9.3 |
| 50 | 422026 | U80736 | Hs.110826 | trinucleotide repeat containing 9 | 9.2 |
| | 432596 | AJ224741 | Hs.278461 | matrilin 3 | 9.2 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 9.2 |
| | 423945 | AA410943 | | gb:zt32h03.r1 Soares ovary tumor NbHOT H | 9.1 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 9.1 |
| 55 | 446715 | AI337735 | Hs.173919 | ESTs, Moderately similar to ZN91_HUMAN Z | 9.0 |
| | 408771 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 9.0 |
| | 437021 | AI076089 | Hs.292239 | ESTs | 9.0 |
| | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 8.9 |
| | 428839 | AI767756 | Hs.82302 | Homo sapiens cDNA FLJ14814 fis, clone NT | 8.9 |
| 60 | 402408 | NA | | NM_030920*:Homo sapiens hypothetical pro | 8.9 |
| | 418601 | AA279490 | Hs.86368 | calmegin | 8.8 |
| | 426327 | W03242 | Hs.44898 | Homo sapiens clone TCCCTA00151 mRNA sequ | 8.8 |
| | 419519 | AI198719 | Hs.176376 | ESTs | 8.8 |
| | 440621 | AW296024 | Hs.150434 | ESTs | 8.8 |
| 65 | 446142 | AI754693 | Hs.145968 | ESTs | 8.8 |
| | 418196 | AI745649 | Hs.26549 | KIAA1708 protein | 8.7 |
| | 447178 | AW594641 | Hs.192417 | ESTs | 8.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 8.6 |
| | 415857 | AA866115 | Hs.127797 | Homo sapiens cDNA FLJ11381 fis, clone HE | 8.6 |
| | 435061 | AI651474 | Hs.163944 | ESTs | 8.6 |
| 5 | 431374 | BE258532 | Hs.251871 | CTP synthase | 8.4 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 8.4 |
| | 437211 | AA382207 | Hs.5509 | ecotropic viral integration site 2B | 8.3 |
| | 437751 | AA767373 | Hs.35669 | ESTs, Moderately similar to ALU1_HUMAN A | 8.3 |
| | 423887 | AL080207 | Hs.134585 | DKFZP434G232 protein | 8.2 |
| | 440941 | BE268362 | Hs.7535 | COBW-like protein | 8.2 |
| 10 | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | 8.2 |
| | 410193 | AJ132592 | Hs.59757 | zinc finger protein 281 | 8.2 |
| | 431725 | X65724 | Hs.2839 | Norrie disease (pseudoglioma) | 8.1 |
| | 446258 | AI283476 | Hs.263478 | ESTs | 8.1 |
| | 416747 | AW876523 | Hs.15929 | hypothetical protein FLJ12910 | 8.1 |
| 15 | 434424 | AI811202 | Hs.325335 | Homo sapiens cDNA: FLJ23523 fis, clone L | 8.1 |
| | 421650 | AA781795 | Hs.122587 | ESTs | 8.0 |
| | 429534 | AW976987 | Hs.163327 | ESTs, Weakly similar to 2109260A B cell | 8.0 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 8.0 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 8.0 |
| 20 | 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | 8.0 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 8.0 |
| | 418250 | U29926 | Hs.83918 | adenosine monophosphate deaminase (isofo | 7.9 |
| | 400285 | NA | | Eos Control | 7.9 |
| | 401464 | AF039241 | Hs.9028 | histone deacetylase 5 | 7.9 |
| 25 | 407242 | M18728 | | gb:Human nonspecific crossreacting antig | 7.8 |
| | 422232 | D43945 | Hs.113274 | transcription factor EC | 7.8 |
| | 454024 | AA993527 | Hs.293907 | hypothetical protein FLJ23403 | 7.8 |
| | 444542 | AI161293 | Hs.280380 | aminopeptidase | 7.8 |
| | 436396 | AI683487 | Hs.152213 | wingless-type MMTV integration site fami | 7.7 |
| 30 | 437204 | AL110216 | Hs.12285 | ESTs, Weakly similar to I55214 salivary | 7.6 |
| | 408805 | H69912 | Hs.48269 | vaccinia related kinase 1 | 7.6 |
| | 437207 | T27503 | Hs.15929 | hypothetical protein FLJ12910 | 7.6 |
| | 442818 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 7.6 |
| | 426283 | NM_003937 | Hs.169139 | kynureninase (L-kynurenine hydrolase) | 7.5 |
| 35 | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 7.5 |
| | 446315 | NM_016293 | Hs.14770 | bridging integrator 2 | 7.5 |
| | 433426 | H69125 | Hs.133525 | ESTs | 7.5 |
| | 406639 | M97711 | | gb:Human T-cell receptor (V beta 18.1, J | 7.5 |
| | 420077 | AW512260 | Hs.87767 | ESTs | 7.4 |
| 40 | 457332 | AA961694 | Hs.105187 | kinesin protein 9 gene | 7.4 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 7.4 |
| | 447555 | AI391662 | Hs.160963 | Homo sapiens, clone MGC:12318, mRNA, com7.4 | 7.4 |
| | 444618 | AV653785 | Hs.173334 | ELL-RELATED RNA POLYMERASE II, ELONGATIO | 7.3 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 7.3 |
| 45 | 400268 | NA | | NM_003292:Homo sapiens translocated prom | 7.3 |
| | 439509 | AF086332 | Hs.58314 | ESTs | 7.3 |
| | 407771 | AL138272 | Hs.62713 | ESTs | 7.3 |
| | 407202 | N58172 | Hs.109370 | ESTs | 7.3 |
| | 433096 | AU076803 | Hs.282975 | carboxylesterase 2 (intestine, liver) | 7.2 |
| 50 | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 7.1 |
| | 430832 | AI073913 | Hs.100686 | ESTs, Weakly similar to JE0350 Anterior | 7.1 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE7.0 | 7.0 |
| | 423739 | AA398155 | Hs.97600 | ESTs | 7.0 |
| | 448212 | AI475858 | | gb:tc87d07.x1 NCLCGAP_CLL1 Homo sapiens7.0 | 7.0 |
| 55 | 407277 | AW170035 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | 7.0 |
| | 454440 | BE062906 | Hs.28338 | KIAA1546 protein | 7.0 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 7.0 |
| | 421373 | AA808229 | Hs.167771 | ESTs | 6.9 |
| | 431960 | AW241821 | Hs.301927 | c6.1A | 6.9 |
| 60 | 424704 | AI263293 | Hs.152096 | cytochrome P450, subfamily IJ (arachido | 6.8 |
| | 449517 | AW500106 | Hs.23643 | serine/threonine protein kinase MASK | 6.8 |
| | 439840 | AW449211 | Hs.105445 | GDNF family receptor alpha 1 | 6.8 |
| | 414080 | AA135257 | Hs.47783 | B aggressive lymphoma gene | 6.8 |
| | 441243 | AI767056 | Hs.193002 | ESTs | 6.7 |
| 65 | 408380 | AF123050 | Hs.44532 | diubiquitin | 6.7 |
| | 422956 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 6.7 |
| | 446651 | AA393907 | Hs.97179 | ESTs | 6.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 419839 | U24577 | Hs.93304 | phospholipase A2, group VII (platelet-ac | 6.7 |
| | 437740 | AA810265 | Hs.122915 | ESTs | 6.7 |
| | 421582 | AI910275 | Hs.1406 | trefoil factor 1 (pS2) | 6.7 |
| | 427356 | AW023482 | Hs.97849 | ESTs | 6.6 |
| 5 | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 6.6 |
| | 422634 | NM_016010 | Hs.118821 | CGI-62 protein | 6.6 |
| | 421072 | AI215069 | Hs.89113 | ESTs | 6.5 |
| | 427718 | AI798680 | Hs.25933 | ESTs | 6.5 |
| | 411000 | N40449 | Hs.201619 | ESTs, Weakly similar to S38383 SEB4B pro | 6.5 |
| 10 | 449343 | AI151418 | Hs.272458 | protein phosphatase 3 (formerly 2B), cat | 6.4 |
| | 409757 | NM_001898 | Hs.123114 | cystatin SN | 6.4 |
| | 447164 | AF026941 | Hs.17518 | Homo sapiens cig5 mRNA, partial sequence | 6.4 |
| | 456938 | X52509 | Hs.161640 | tyrosine aminotransferase | 6.4 |
| | 418848 | AI820961 | Hs.193465 | ESTs | 6.4 |
| 15 | 424902 | NM_003866 | Hs.153687 | inositol polyphosphate-4-phosphatase, ty | 6.4 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 6.4 |
| | 439452 | AA918317 | Hs.57987 | B-cell CLL/lymphoma 11B (zinc finger pro | 6.4 |
| | 407266 | AJ235664 | | gb:Homo sapiens mRNA for immunoglobulin | 6.3 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 6.3 |
| 20 | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 6.3 |
| | 434340 | AI193043 | Hs.128685 | ESTs, Weakly similar to T17226 hypotheti | 6.2 |
| | 429503 | AA394183 | Hs.26873 | ESTs | 6.2 |
| | 402578 | | | C1001134:gil2117372 pir 65981 fatty ac | 6.2 |
| | 409646 | AW161391 | Hs.709 | deoxycytidine kinase | 6.1 |
| 25 | 430447 | W17064 | Hs.332848 | SWI/SNF related, matrix associated, acti | 6.1 |
| | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 6.1 |
| | 443709 | AI082692 | Hs.134662 | ESTs | 6.1 |
| | 420929 | AI694143 | Hs.296251 | programmed cell death 4 | 6.1 |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 6.1 |
| 30 | 428248 | AI126772 | Hs.40479 | ESTs | 6.0 |
| | 420344 | BE463721 | Hs.97101 | putative G protein-coupled receptor | 6.0 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 6.0 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 6.0 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (MMP1; inters | 6.0 |
| 35 | 428585 | AB007863 | Hs.185140 | KIAA0403 protein | 6.0 |
| | 437608 | AA761605 | Hs.292308 | ESTs, Weakly similar to ALU1_HUMAN ALU S6.0 | 6.0 |
| | 427408 | AA583206 | Hs.2156 | RAR-related orphan receptor A | 6.0 |
| | 406687 | M31126 | Hs.272620 | matrix metalloproteinase 11 (MMP11; stro | 6.0 |
| | 418092 | R45154 | Hs.106604 | ESTs | 6.0 |
| 40 | 447051 | AW139130 | Hs.160951 | ESTs, Weakly similar to Con1 [H.sapiens] | 6.0 |
| | 441233 | AA972965 | Hs.135568 | ESTs | 6.0 |
| | 432239 | X81334 | Hs.2936 | matrix metalloproteinase 13 (collagenase | 6.0 |
| | 435106 | AA100847 | Hs.193380 | ESTs, Highly similar to AF174600 1 F-box | 5.9 |
| | 435525 | AI831297 | Hs.123310 | ESTs | 5.9 |
| 45 | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 5.9 |
| | 410785 | AW803341 | | gb:IL2-UM0079-090300-050-D03 UM0079 Homo5.9 | 5.9 |
| | 422576 | BE548555 | Hs.118554 | CGI-83 protein | 5.9 |
| | 451398 | AI793124 | Hs.144479 | ESTs | 5.9 |
| | 441881 | AW968904 | Hs.179566 | hypothetical protein FLJ22624 | 5.8 |
| 50 | 412022 | AI005043 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 5.8 |
| | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 5.8 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 5.8 |
| | 434094 | AA305599 | Hs.238205 | hypothetical protein PRO2013 | 5.8 |
| | 409151 | AA306105 | Hs.50785 | SEC22, vesicle trafficking protein (S. c | 5.8 |
| 55 | 448807 | AI571940 | Hs.7549 | ESTs | 5.8 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 5.8 |
| | 421281 | AI299139 | Hs.17517 | ESTs | 5.8 |
| | 430361 | AI033965 | Hs.239926 | sterol-C4-methyl oxidase-like | 5.8 |
| | 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (MMP10; str | 5.7 |
| 60 | 440527 | AV657117 | Hs.184164 | ESTs, Moderately similar to S65657 alpha | 5.7 |
| | 434674 | AA831879 | Hs.136985 | ESTs | 5.7 |
| | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 5.7 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 5.7 |
| | 448663 | BE614599 | Hs.106823 | hypothetical protein MGC14797 | 5.7 |
| 65 | 438199 | AW016531 | Hs.122147 | ESTs | 5.7 |
| | 446203 | Z47553 | Hs.14286 | flavin containing monooxygenase 5 | 5.7 |
| | 428336 | AA503115 | Hs.183752 | microseminoprotein, beta- | 5.6 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 430379 | AF134149 | Hs.240395 | potassium channel, subfamily K, member 6 | 5.6 |
| | 422835 | BE218705 | Hs.121378 | metallothionein-like 5, testis-specific | 5.6 |
| | 444758 | AL044878 | Hs.11899 | 3-hydroxy-3-methylglutaryl-Coenzyme A re | 5.6 |
| 5 | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 5.6 |
| | 400301 | X03635 | Hs.1657 | estrogen receptor 1 | 5.6 |
| | 447078 | AW885727 | Hs.301570 | ESTs | 5.6 |
| | 432015 | AL157504 | Hs.159115 | Homo sapiens mRNA; cDNA DKFZp586O0724 (f5.5 | |
| | 438691 | AA906288 | Hs.212184 | ESTs | 5.5 |
| 10 | 439809 | R41396 | Hs.101774 | hypothetical protein FLJ23045 | 5.5 |
| | 415786 | AW419196 | Hs.257924 | hypothetical protein FLJ13782 | 5.5 |
| | 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 5.5 |
| | 401645 | NA | | C16001440*gi12330704 gb AAG52890.1 AF35.5 | |
| | 437967 | BE277414 | Hs.5947 | mel transforming oncogene (derived from | 5.5 |
| 15 | 445885 | AI734009 | Hs.127699 | KIAA1603 protein | 5.4 |
| | 439138 | AI742605 | Hs.193696 | ESTs | 5.4 |
| | 440270 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 5.4 |
| | 437536 | X91221 | Hs.144465 | ESTs | 5.4 |
| | 438167 | R28363 | Hs.24286 | ESTs | 5.4 |
| 20 | 452741 | BE392914 | Hs.30503 | Homo sapiens cDNA FLJ11344 fis, clone PL | 5.4 |
| | 426214 | H59846 | Hs.128355 | ESTs, Moderately similar to ALU7_HUMAN A | 5.4 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 5.4 |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (COM | 5.4 |
| | 434263 | N34895 | Hs.44648 | ESTs | 5.4 |
| 25 | 446382 | AW205168 | Hs.150823 | ESTs | 5.4 |
| | 422406 | AF025441 | Hs.116206 | Opa-interacting protein 5 | 5.3 |
| | 438321 | AA576635 | Hs.6153 | CGI-48 protein | 5.3 |
| | 418310 | AA814100 | Hs.86693 | ESTs | 5.3 |
| | 419625 | U91616 | Hs.91640 | nuclear factor of kappa light polypeptid | 5.3 |
| 30 | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 5.3 |
| | 446900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 5.2 |
| | 449051 | AW961400 | Hs.333526 | HER2 receptor tyrosine kinase (c-erb-b2, | 5.2 |
| | 418758 | AW959311 | Hs.172012 | hypothetical protein DKFZp434J037 | 5.2 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 5.2 |
| 35 | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | 5.2 |
| | 421928 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 5.2 |
| | 428804 | AK000713 | Hs.193736 | hypothetical protein FLJ20706 | 5.2 |
| | 427427 | AF077345 | Hs.177936 | ESTs | 5.2 |
| | 403485 | | | C3001813*gi12737279 ref XP_012163.1 k | 5.2 |
| 40 | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 5.1 |
| | 421937 | AI878857 | Hs.109706 | hematological and neurological expressed | 5.1 |
| | 426752 | X69490 | Hs.172004 | titin | 5.1 |
| | 453310 | X70697 | Hs.553 | solute carrier family 6 (neurotransmitte | 5.1 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 5.1 |
| 45 | 412281 | AI810054 | Hs.14119 | ESTs | 5.1 |
| | 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 5.1 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 5.1 |
| | 404347 | | | Target Exon | 5.1 |
| | 431808 | M30703 | Hs.270833 | amphiregulin (schwannoma-derived growth | 5.1 |
| 50 | 429113 | D28235 | Hs.196384 | prostaglandin-endoperoxide synthase 2 (p | 5.1 |
| | 436291 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 5.1 |
| | 450603 | R43646 | Hs.12422 | ESTs | 5.1 |
| | 434725 | AK000796 | Hs.4104 | hypothetical protein | 5.0 |
| | 435981 | H74319 | Hs.188620 | ESTs | 5.0 |
| 55 | 407376 | AA993138 | Hs.142287 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 5.0 |
| | 431689 | AA305688 | Hs.267695 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 5.0 |
| | 405348 | NA | | C7001664:gi12698061 dbj BAB21849.1 (AB | 5.0 |
| | 436196 | AK001084 | Hs.333498 | Homo sapiens cDNA FLJ10222 fis, clone HE | 5.0 |
| | 437065 | AL036450 | Hs.103238 | ESTs | 5.0 |
| 60 | 410196 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 5.0 |
| | 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 5.0 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 4.9 |
| | 403329 | NA | | Target Exon | 4.9 |
| | 442875 | BE623003 | Hs.23625 | Homo sapiens clone TCCTA00142 mRNA sequ | 4.9 |
| 65 | 442441 | AI820662 | Hs.129598 | ESTs | 4.9 |
| | 430375 | AW371048 | Hs.93758 | H4 histone family, member H | 4.9 |
| | 424128 | AW966163 | | gb:EST378236 MAGE resequences, MAGI Homo | 4.9 |
| | 408873 | AL046017 | Hs.182278 | calmodulin 2 (phosphorylase kinase, delt | 4.9 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 407910 | AA650274 | Hs.41296 | fibronectin leucine rich transmembrane p | 4.9 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | 4.9 |
| | 453204 | R10799 | Hs.191990 | ESTs | 4.8 |
| 5 | 452020 | AA722012 | Hs.255757 | ESTs, Weakly similar to AT2A_HUMAN POTEN4.8 | 4.8 |
| | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | 4.8 |
| | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H7?? transport | 4.8 |
| | 431645 | AF078849 | Hs.266483 | dynein light chain-A | 4.8 |
| | 423575 | C18863 | Hs.163443 | Homo sapiens cDNA FLJ11576 fis, clone HE | 4.8 |
| 10 | 444246 | H93281 | Hs.10710 | hypothetical protein FLJ20417 | 4.8 |
| | 421524 | AA312082 | Hs.105445 | GDNF family receptor alpha 1 | 4.8 |
| | 452827 | AI571835 | Hs.55468 | ESTs | 4.8 |
| | 414222 | AL135173 | Hs.878 | sorbitol dehydrogenase | 4.8 |
| | 456086 | AL161999 | Hs.77324 | eukaryotic translation termination facto | 4.8 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 4.8 |
| 15 | 418973 | AA233056 | Hs.191518 | ESTs | 4.8 |
| | 447033 | AI357412 | Hs.157601 | ESTs | 4.8 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 4.7 |
| | 419968 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 4.7 |
| 20 | 424326 | NM_014479 | Hs.145296 | disintegrin protease | 4.7 |
| | 431585 | BE242803 | Hs.262823 | hypothetical protein FLJ10326 | 4.7 |
| | 429294 | AA095971 | Hs.198793 | Homo sapiens cDNA: FLJ22463 fis, clone H | 4.7 |
| | 416814 | AW192307 | Hs.80042 | dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl | 4.7 |
| | 439897 | NM_015310 | Hs.6763 | KIAA0942 protein | 4.7 |
| | 429687 | AI675749 | Hs.211608 | nucleoporin 153kD | 4.7 |
| 25 | 422880 | AF228704 | Hs.121524 | glutathione reductase | 4.7 |
| | 405801 | | | NM_000390:Homo sapiens choroideremia (Ra4.6 | 4.6 |
| | 432435 | BE218886 | Hs.282070 | ESTs | 4.6 |
| | 439544 | W26354 | Hs.28891 | hypothetical protein FLJ11360; artemis p | 4.6 |
| 30 | 425354 | U62027 | Hs.155935 | complement component 3a receptor 1 | 4.6 |
| | 436027 | AI864053 | Hs.39972 | ESTs, Weakly similar to I38588 reverse t | 4.6 |
| | 424623 | AW963062 | Hs.337404 | ESTs | 4.6 |
| | 403366 | NA | | Target Exon | 4.6 |
| | 402542 | | | Target Exon | 4.6 |
| 35 | 450193 | AI916071 | Hs.15607 | Homo sapiens Fanconi anemia complementat | 4.6 |
| | 411678 | AI907114 | Hs.71465 | squalene epoxidase | 4.6 |
| | 456844 | AI264155 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 4.6 |
| | 448072 | AI459306 | Hs.24908 | ESTs | 4.5 |
| | 408045 | AW138959 | Hs.245123 | ESTs | 4.5 |
| 40 | 423782 | AI472209 | Hs.323117 | ESTs | 4.5 |
| | 447388 | AW630534 | Hs.76277 | Homo sapiens, clone MGC:9381, mRNA, comp4.5 | 4.5 |
| | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 4.5 |
| | 452561 | AI692181 | Hs.49169 | KIAA1634 protein | 4.5 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo4.5 | 4.5 |
| 45 | 428801 | AW277121 | Hs.254881 | ESTs | 4.5 |
| | 428500 | AI815395 | Hs.184641 | fatty acid desaturase 2 | 4.5 |
| | 426075 | AW513691 | Hs.270149 | ESTs, Weakly similar to 2109260A B cell | 4.4 |
| | 437259 | AI377755 | Hs.120695 | ESTs | 4.4 |
| | 400409 | AF153341 | Hs.283954 | Homo sapiens winged helix/forkhead trans | 4.4 |
| 50 | 412863 | AA121673 | Hs.59757 | zinc finger protein 281 | 4.4 |
| | 426989 | AI815206 | Hs.99395 | ESTs | 4.4 |
| | 401866 | | | Target Exon | 4.4 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 4.4 |
| | 406348 | | | Target Exon | 4.4 |
| 55 | 412138 | AW895387 | | gb:QV4-NN0038-300300-157-c10 NN0038 Homo4.4 | 4.4 |
| | 428550 | AW297880 | Hs.98661 | ESTs | 4.4 |
| | 411743 | AW862214 | | gb:QV4-CT0361-301299-074-b05 CT0361 Homo4.4 | 4.4 |
| | 429966 | BE081342 | Hs.283037 | HSPC039 protein | 4.4 |
| | 423291 | NM_004129 | Hs.126590 | guanylate cyclase 1, soluble, beta 2 | 4.4 |
| 60 | 423456 | AL110151 | Hs.128797 | DKFZP586D0824 protein | 4.4 |
| | 452190 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | 4.4 |
| | 424871 | NM_004525 | Hs.153595 | low density lipoprotein-related protein | 4.3 |
| | 429575 | AA706003 | Hs.99387 | ESTs | 4.3 |
| | 429922 | Z97630 | Hs.226117 | H1 histone family, member 0 | 4.3 |
| 65 | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 4.3 |
| | 400300 | X03363 | | HER2 receptor tyrosine kinase (c-erb-b2, | 4.3 |
| | 437258 | AL041243 | Hs.174104 | ESTs | 4.3 |
| | 446595 | T57448 | Hs.15467 | hypothetical protein FLJ20725 | 4.3 |

| | | | | |
|----|--------|-----------|--|-----|
| | 403011 | NA | ENSP00000215330*:Probable serine/threoni | 4.3 |
| | 419055 | AI365384 | Hs.11571 Homo sapiens cDNA FLJ11570 fis, clone HE | 4.3 |
| | 418661 | NM_001949 | Hs.1189 E2F transcription factor 3 | 4.3 |
| 5 | 407786 | AA687538 | Hs.38972 tetraspan 1 | 4.3 |
| | 429183 | AB014604 | Hs.197955 KIAA0704 protein | 4.3 |
| | 442914 | AW188551 | Hs.99519 hypothetical protein FLJ14007 | 4.3 |
| | 441029 | AI091795 | Hs.179246 ESTs | 4.3 |
| | 452194 | AI694413 | Hs.332649 olfactory receptor, family 2, subfamily | 4.3 |
| | 414821 | M63835 | Hs.77424 Fc fragment of IgG, high affinity Ia, re | 4.2 |
| 10 | 410102 | AW248508 | Hs.279727 Homo sapiens cDNA FLJ14035 fis, clone HE | 4.2 |
| | 452110 | T47667 | Hs.28005 Homo sapiens cDNA FLJ11309 fis, clone PL | 4.2 |
| | 442007 | AA301116 | Hs.142838 nucleolar phosphoprotein Nopp34 | 4.2 |
| | 417318 | AW953937 | Hs.12891 ESTs | 4.2 |
| 15 | 431818 | AW510444 | Hs.191705 ESTs, Weakly similar to T47184 hypotheti | 4.2 |
| | 443646 | AI085198 | Hs.164226 ESTs | 4.2 |
| | 419169 | AW851980 | Hs.262346 ESTs, Weakly similar to S72482 hypotheti | 4.2 |
| | 446839 | BE091926 | Hs.16244 mitotic spindle coiled-coil related prot | 4.2 |
| | 423242 | AL039402 | Hs.125783 DEME-6 protein | 4.2 |
| 20 | 432116 | AA902953 | Hs.308538 ESTs | 4.2 |
| | 409038 | T97490 | Hs.50002 small inducible cytokine subfamily A (Cy | 4.2 |
| | 445625 | BE246743 | Hs.288529 hypothetical protein FLJ22635 | 4.2 |
| | 425139 | AW630488 | Hs.325820 protease, serine, 23 | 4.2 |
| | 447397 | BE247676 | Hs.18442 E-1 enzyme | 4.2 |
| 25 | 410166 | AK001376 | Hs.59346 hypothetical protein FLJ10514 | 4.1 |
| | 437295 | AW779318 | Hs.88417 ESTs | 4.1 |
| | 430486 | BE062109 | Hs.241551 chloride channel, calcium activated, fam | 4.1 |
| | 441790 | AW294909 | Hs.132208 ESTs | 4.1 |
| | 410129 | BE244074 | Hs.58831 regulator of Fas-induced apoptosis | 4.1 |
| 30 | 427521 | AW973352 | Hs.290585 ESTs | 4.1 |
| | 425247 | NM_005940 | Hs.155324 matrix metalloproteinase 11 (MMP11; stro | 4.1 |
| | 412886 | AF041163 | Hs.74647 Human T-cell receptor active alpha-chain | 4.1 |
| | 441153 | BE562826 | gb:601336534F1 NIH_MGC_44 Homo sapiens c4.1 | 4.1 |
| | 444301 | AK000136 | Hs.10760 asporin (LRR class 1) | 4.1 |
| 35 | 426711 | AA383471 | Hs.180669 conserved gene amplified in osteosarcoma | 4.1 |
| | 405850 | NA | Target Exon | 4.1 |
| | 440283 | AI732892 | Hs.190489 ESTs | 4.0 |
| | 432441 | AW292425 | Hs.163484 ESTs | 4.0 |
| | 400284 | NA | estrogen receptor 1 | 4.0 |
| 40 | 417341 | N91453 | Hs.102987 ESTs | 4.0 |
| | 429732 | U20158 | Hs.2488 lymphocyte cytosolic protein 2 (SH2 doma | 4.0 |
| | 411393 | AW797437 | Hs.69771 B-factor, properdin | 4.0 |
| | 425704 | U79293 | Hs.159264 Human clone 23948 mRNA sequence | 4.0 |
| | 419594 | AA013051 | Hs.91417 topoisomerase (DNA) II binding protein | 4.0 |
| 45 | 419092 | J05581 | Hs.89603 mucin 1, transmembrane | 4.0 |
| | 443147 | AI034351 | Hs.19030 ESTs | 4.0 |
| | 408633 | AW963372 | Hs.46677 PRO2000 protein | 4.0 |
| | 433404 | T32982 | Hs.102720 ESTs | 4.0 |
| | 421506 | BE302796 | Hs.105097 thymidine kinase 1, soluble | 4.0 |
| 50 | 417900 | BE250127 | Hs.82906 CDC20 (cell division cycle 20, S. cerevi | 3.9 |
| | 414602 | AW630088 | Hs.76550 Homo sapiens mRNA; cDNA DKFZp564B1264 (f3.9 | 3.9 |
| | 413762 | AW411479 | Hs.848 FK506-binding protein 4 (59kD) | 3.9 |
| | 404580 | | NM_014112*:Homo sapiens trichorhinophala | 3.9 |
| | 452046 | AB018345 | Hs.27657 KIAA0802 protein | 3.9 |
| 55 | 459587 | AA031956 | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 3.9 |
| | 416658 | U03272 | Hs.79432 fibrillin 2 (congenital contractural ara | 3.9 |
| | 426647 | AA243464 | Hs.294101 pre-B-cell leukemia transcription factor | 3.9 |
| | 429353 | AL117406 | Hs.200102 ATP-binding cassette transporter MRP8 | 3.9 |
| | 419038 | AW134924 | Hs.190325 ESTs | 3.9 |
| 60 | 418918 | X07871 | Hs.89476 CD2 antigen (p50), sheep red blood cell | 3.9 |
| | 421977 | W94197 | Hs.110165 ribosomal protein L26 homolog | 3.9 |
| | 442567 | AI201183 | Hs.130251 ESTs | 3.9 |
| | 421168 | AF182277 | Hs.330780 cytochrome P450, subfamily IIB (phenobar | 3.9 |
| | 431701 | AW935490 | Hs.14658 Human chromosome 5q13.1 clone 5G8 mRNA | 3.9 |
| 65 | 418526 | BE019020 | Hs.85838 solute carrier family 16 (monocarboxylic | 3.9 |
| | 414998 | NM_002543 | Hs.77729 oxidised low density lipoprotein (lectin | 3.9 |
| | 422790 | AA809875 | Hs.25933 ESTs | 3.9 |
| | 419741 | NM_007019 | Hs.93002 ubiquitin carrier protein E2-C | 3.9 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 430017 | AA263172 | Hs.35 | protein tyrosine phosphatase, non-recept | 3.9 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 3.8 |
| | 428514 | AW236861 | Hs.193139 | ESTs | 3.8 |
| 5 | 434521 | NM_002267 | Hs.3886 | karyopherin alpha 3 (Importin alpha 4) | 3.8 |
| | 409425 | U40462 | Hs.54452 | zinc finger protein, subfamily 1A, 1 (Ik | 3.8 |
| | 439560 | BE565647 | Hs.74899 | hypothetical protein FLJ12820 | 3.8 |
| | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 3.8 |
| | 400021 | | | AFFX control - HUMISGF3A/M97935_MA | 3.8 |
| 10 | 453403 | BE466639 | Hs.61779 | Homo sapiens cDNA FLJ13591 fis, clone PL | 3.8 |
| | 445941 | AI267371 | Hs.172636 | ESTs | 3.8 |
| | 434378 | AA631739 | Hs.335440 | EST | 3.8 |
| | 429220 | AW207206 | Hs.136319 | ESTs | 3.8 |
| | 439176 | AI446444 | Hs.190394 | ESTs, Weakly similar to B28096 line-1 pr | 3.8 |
| | 401045 | | | C11001883*gi 6753278[ref][NP_033938.1] c | 3.8 |
| 15 | 430178 | AW449612 | Hs.152475 | ESTs | 3.8 |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 3.8 |
| | 447630 | AI660149 | Hs.44865 | lymphoid enhancer-binding factor 1 | 3.8 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | 3.8 |
| 20 | 413011 | AW068115 | Hs.821 | biglycan | 3.8 |
| | 422121 | AI767949 | Hs.179833 | ESTs | 3.8 |
| | 452268 | NM_003512 | Hs.28777 | H2A histone family, member L | 3.8 |
| | 427811 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue) | 3.8 |
| | 415579 | AA165232 | Hs.222069 | ESTs | 3.8 |
| 25 | 437330 | AL353944 | Hs.50115 | Homo sapiens mRNA; cDNA DKFZp761J1112 (f | 3.8 |
| | 427122 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 3.7 |
| | 400286 | NA | | C16000922:gi 7499103[pir][T20903 hypothe | 3.7 |
| | 420281 | AI623693 | Hs.191533 | ESTs | 3.7 |
| | 419926 | AW900992 | Hs.93796 | DKFZP586D2223 protein | 3.7 |
| 30 | 417541 | AI992191 | Hs.180040 | hypothetical protein FLJ22439 | 3.7 |
| | 426172 | AA371307 | Hs.125056 | ESTs | 3.7 |
| | 429638 | AI916662 | Hs.211577 | kinectin 1 (kinesin receptor) | 3.7 |
| | 457001 | J03258 | Hs.2062 | vitamin D (1,25- dihydroxyvitamin D3) re | 3.7 |
| | 424109 | AW406878 | | gb:U1-HF-BL0-adg-g-06-0-U1.r1 NIH_MGC_373 | 3.7 |
| 35 | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 3.7 |
| | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fis, clone HE | 3.7 |
| | 430448 | AI633553 | Hs.13303 | Homo sapiens cDNA: FLJ21784 fis, clone H | 3.7 |
| | 432729 | AK000292 | Hs.278732 | hypothetical protein FLJ20285 | 3.7 |
| | 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 3.7 |
| 40 | 421662 | NM_014141 | Hs.106552 | cell recognition molecule Caspr2 | 3.7 |
| | 441633 | AW958544 | Hs.112242 | normal mucosa of esophagus specific 1 | 3.7 |
| | 408761 | AA057264 | Hs.238936 | ESTs, Weakly similar to (define not ava | 3.7 |
| | 406153 | | | Target Exon | 3.7 |
| | 445563 | AW873606 | Hs.149006 | ESTs | 3.7 |
| 45 | 453464 | AI884911 | Hs.32989 | receptor (calcitonin) activity modifying | 3.7 |
| | 448918 | AB011152 | Hs.22572 | KIAA0580 protein | 3.7 |
| | 413936 | AF113676 | Hs.297681 | serine (or cysteine) proteinase inhibito | 3.6 |
| | 448069 | U76248 | Hs.20191 | seven in absentia (Drosophila) homolog 2 | 3.6 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 3.6 |
| 50 | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 419941 | X98654 | Hs.93837 | phosphatidylinositol transfer protein, m | 3.6 |
| | 402397 | AF188625 | Hs.189507 | phospholipase A2, group IID | 3.6 |
| | 430378 | Z29572 | Hs.25556 | tumor necrosis factor receptor superfam | 3.6 |
| | 448106 | AI800470 | Hs.171941 | ESTs | 3.6 |
| | 426431 | NM_000458 | Hs.169853 | transcription factor 2, hepatic; LF-B3; | 3.6 |
| 55 | 431843 | AA516420 | Hs.183526 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 426878 | BE069341 | | gb:QV3-BT0381-270100-073-c08 BT0381 Homo | 3.6 |
| | 434061 | AW024973 | Hs.283675 | NPD009 protein | 3.6 |
| | 445292 | AV653264 | Hs.13982 | Homo sapiens cDNA FLJ14666 fis, clone NT | 3.6 |
| 60 | 452101 | T60298 | Hs.10844 | Homo sapiens cDNA FLJ14476 fis, clone MA | 3.6 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 3.6 |
| | 409047 | AW961434 | Hs.31539 | ESTs | 3.6 |
| | 416820 | NM_000402 | Hs.80206 | glucose-6-phosphate dehydrogenase | 3.6 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 3.6 |
| | 440516 | S42303 | Hs.161 | cadherin 2, type 1, N-cadherin (neuronal | 3.6 |
| 65 | 434360 | AW015415 | Hs.127780 | ESTs | 3.6 |
| | 428970 | BE276891 | Hs.194691 | retinoic acid induced 3 | 3.6 |
| | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 3.6 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 409619 | AK001015 | Hs.55220 | BCL2-associated athanogene 2 | 3.6 |
| | 430044 | AA464510 | Hs.152812 | ESTs | 3.6 |
| | 430829 | AW451999 | Hs.194024 | ESTs | 3.6 |
| | 434224 | AA380731 | Hs.84 | Interleukin 2 receptor, gamma (severe co | 3.6 |
| 5 | 439247 | AF088020 | Hs.46767 | EST | 3.6 |
| | 431542 | H63010 | Hs.5740 | ESTs | 3.5 |
| | 430713 | AA351647 | Hs.2642 | eukaryotic translation elongation factor | 3.5 |
| | 434988 | AI418055 | Hs.161160 | ESTs | 3.5 |
| | 437748 | AF234882 | Hs.5814 | suppression of tumorigenicity 7 | 3.5 |
| 10 | 418322 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 3.5 |
| | 439569 | AW602166 | Hs.222399 | CEGP1 protein | 3.5 |
| | 459583 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 3.5 |
| | 403212 | | | NM_019595:Homo sapiens Intersectin 2 (IT | 3.5 |
| | 409099 | AK000725 | Hs.50579 | hypothetical protein FLJ20718 | 3.5 |
| 15 | 453968 | AA847843 | Hs.62711 | Homo sapiens, clone IMAGE:3351295, mRNA | 3.5 |
| | 436338 | W92147 | Hs.118394 | ESTs | 3.5 |
| | 422890 | Z43784 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 3.5 |
| | 442295 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fis, clone HE | 3.5 |
| | 417975 | AA641836 | Hs.30085 | hypothetical protein FLJ23186 | 3.5 |
| 20 | 433730 | AK002135 | Hs.3542 | hypothetical protein FLJ11273 | 3.5 |
| | 439926 | AW014875 | Hs.137007 | ESTs | 3.5 |
| | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1- | 3.4 |
| | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | 3.4 |
| | 422128 | AW881145 | | gb:QV0-OT0033-010400-182-a07 OT0033 Homo | 3.4 |
| 25 | 414921 | BE390551 | Hs.77628 | steroidogenic acute regulatory protein r | 3.4 |
| | 441134 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 3.4 |
| | 444564 | AI167877 | Hs.143716 | ESTs | 3.4 |
| | 402470 | NA | | Target Exon | 3.4 |
| | 418120 | AA213437 | Hs.192249 | ESTs | 3.4 |
| 30 | 422414 | AW875237 | Hs.13701 | ESTs | 3.4 |
| | 433345 | AI681545 | Hs.152982 | hypothetical protein FLJ13117 | 3.4 |
| | 409213 | U61412 | Hs.51133 | PTK6 protein tyrosine kinase 6 | 3.4 |
| | 422611 | AA158177 | Hs.118722 | fucosyltransferase 8 (alpha (1,6) fucosy | 3.4 |
| | 423554 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 3.4 |
| 35 | 442619 | AA447492 | Hs.20183 | ESTs, Weakly similar to AF164793 1 prote | 3.4 |
| | 402359 | NA | | C19001991*gi12656111 gb AAK00751.1 AF23.4 | 3.4 |
| | 439398 | AA284267 | Hs.221504 | ESTs | 3.4 |
| | 415208 | F01020 | Hs.172004 | titin | 3.4 |
| | 452853 | AA812633 | Hs.10845 | ESTs | 3.4 |
| 40 | 429345 | R11141 | Hs.199695 | hypothetical protein | 3.4 |
| | 449027 | AJ271216 | Hs.22880 | dipeptidylpeptidase III | 3.4 |
| | 412115 | AK001763 | Hs.73239 | hypothetical protein FLJ10901 | 3.4 |
| | 432180 | Y18418 | Hs.272822 | RuvB (E coli homolog)-like 1 | 3.4 |
| | 428977 | AK001404 | Hs.194698 | cyclin B2 | 3.4 |
| 45 | 431611 | U58766 | Hs.264428 | tissue specific transplantation antigen | 3.4 |
| | 418286 | AA622528 | Hs.319825 | Homo sapiens, clone IMAGE:3616574, mRNA | 3.4 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII (tumor antigen H | 3.4 |
| | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 3.4 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 3.3 |
| 50 | 449571 | AW016812 | Hs.200266 | ESTs | 3.3 |
| | 412777 | AI335773 | Hs.270123 | ESTs | 3.3 |
| | 420542 | NM_000505 | Hs.1321 | coagulation factor XII (Hageman factor) | 3.3 |
| | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 3.3 |
| | 418327 | U70370 | Hs.84136 | paired-like homeodomain transcription fa | 3.3 |
| 55 | 449065 | AI627393 | Hs.258998 | ESTs, Weakly similar to high mobility gr | 3.3 |
| | 425999 | AW513051 | Hs.332981 | ESTs, Weakly similar to I38022 hypotheti | 3.3 |
| | 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | 3.3 |
| | 407777 | AA161071 | Hs.71465 | squalene epoxidase | 3.3 |
| | 426516 | BE262660 | Hs.170197 | glutamic-oxaloacetic transaminase 2, mit | 3.3 |
| 60 | 414361 | AI086138 | Hs.204044 | ESTs | 3.3 |
| | 427080 | AW068287 | Hs.173466 | ras-related C3 botulinum toxin substrate | 3.3 |
| | 426429 | X73114 | Hs.169849 | myosin-binding protein C, slow-type | 3.3 |
| | 446163 | AA026880 | Hs.25252 | prolactin receptor | 3.3 |
| | 428566 | U41763 | Hs.184916 | clathrin, heavy polypeptide-like 1 | 3.3 |
| 65 | 418641 | BE243136 | Hs.86947 | a disintegrin and metalloproteinase doma | 3.3 |
| | 436293 | AI601188 | Hs.120910 | ESTs | 3.3 |
| | 411257 | AA628967 | Hs.115274 | ESTs, Highly similar to IHH_HUMAN INDIAN | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 430253 | AK001514 | Hs.236844 | hypothetical protein FLJ10652 | 3.3 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 3.3 |
| | 436469 | AK001455 | Hs.5198 | Down syndrome critical region gene 2 | 3.3 |
| | 437786 | BE142681 | Hs.155573 | polymerase (DNA directed), eta | 3.3 |
| 5 | 444079 | H09048 | Hs.23606 | ESTs | 3.3 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 3.3 |
| | 431215 | AA496078 | Hs.121554 | Human DNA sequence from clone RP11-218C13.3 | 3.3 |
| | 424563 | AA446932 | Hs.151428 | ret finger protein 2 | 3.3 |
| | 450828 | AW270655 | Hs.193804 | ESTs | 3.3 |
| 10 | 408652 | R43409 | Hs.6829 | Homo sapiens mRNA for KIAA1644 protein, | 3.3 |
| | 445142 | AW978484 | Hs.93842 | Homo sapiens cDNA: FLJ22554 fis, clone H | 3.3 |
| | 426761 | AI015709 | Hs.172089 | Homo sapiens mRNA; cDNA DKFZp586I2022 (f3.3 | 3.3 |
| | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 3.3 |
| | 422616 | BE300330 | Hs.118725 | selenophosphate synthetase 2 | 3.3 |
| 15 | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 3.3 |
| | 406663 | U24683 | Hs.302063 | immunoglobulin heavy constant mu | 3.3 |
| | 434137 | AA907734 | Hs.124895 | ESTs | 3.3 |
| | 408877 | AA479033 | Hs.130315 | ESTs, Weakly similar to A47582 B-cell gr | 3.3 |
| | 439101 | C01765 | Hs.38750 | hypothetical protein FLJ11526 | 3.3 |
| 20 | 408221 | AA912183 | Hs.47447 | ESTs | 3.3 |
| | 447519 | U46258 | Hs.339665 | ESTs | 3.3 |
| | 404755 | NA | | Target Exon | 3.3 |
| | 451871 | AI821005 | Hs.118599 | ESTs | 3.2 |
| | 420319 | AW406289 | Hs.96593 | hypothetical protein | 3.2 |
| 25 | 430580 | AA806105 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 3.2 |
| | 400202 | NA | | NM_002795*:Homo sapiens proteasome (pros3.2 | 3.2 |
| | 400222 | NA | | NM_002082*:Homo sapiens G protein-couple | 3.2 |
| | 425988 | BE045897 | Hs.274454 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 458098 | BE550224 | Hs.74170 | metallothionein 1E (functional) | 3.2 |
| 30 | 430589 | AJ002744 | Hs.246315 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 3.2 |
| | 431563 | AI027643 | Hs.120912 | ESTs | 3.2 |
| | 442353 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 3.2 |
| | 422309 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | 3.2 |
| | 419703 | AI793257 | Hs.128151 | ESTs | 3.2 |
| 35 | 420380 | AA640891 | Hs.102406 | ESTs | 3.2 |
| | 410853 | H04588 | Hs.30469 | ESTs | 3.2 |
| | 454417 | AI244459 | Hs.110826 | trinucleotide repeat containing 9 | 3.2 |
| | 432745 | AI821926 | | gb:nt78f05.x5 NCI_CGAP_P3 Homo sapiens | 3.2 |
| | 422032 | AA476966 | Hs.110857 | polymerase (RNA) III (DNA directed) poly | 3.2 |
| 40 | 415339 | NM_015156 | Hs.78398 | KIAA0071 protein | 3.2 |
| | 426384 | AI472078 | Hs.303662 | ESTs | 3.2 |
| | 448030 | N30714 | Hs.325960 | membrane-spanning 4-domains, subfamily A | 3.2 |
| | 418739 | AA310964 | Hs.88012 | SHP2 Interacting transmembrane adaptor | 3.2 |
| | 442053 | R35343 | Hs.24968 | Human DNA sequence from clone RP1-233G163.2 | 3.2 |
| 45 | 434747 | AA837085 | Hs.220585 | ESTs | 3.2 |
| | 427297 | AW292593 | Hs.334907 | Homo sapiens, clone MGC:17333, mRNA, com3.2 | 3.2 |
| | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 3.2 |
| | 452304 | AA025386 | Hs.61311 | ESTs, Weakly similar to S10590 cysteine | 3.2 |
| | 453953 | AW408337 | Hs.36972 | CD7 antigen (p41) | 3.2 |
| 50 | 407758 | D50915 | Hs.38365 | KIAA0125 gene product | 3.2 |
| | 451149 | AL047586 | Hs.10283 | RNA binding motif protein 8B | 3.2 |
| | 430015 | AW768399 | Hs.112157 | ESTs | 3.2 |
| | 433313 | W20128 | Hs.296039 | ESTs | 3.2 |
| | 418334 | AA319233 | Hs.5521 | ESTs | 3.2 |
| 55 | 450223 | AA418204 | Hs.241493 | natural killer-tumor recognition sequenc | 3.2 |
| | 454365 | AW966728 | Hs.54642 | methionine adenosyltransferase II, beta | 3.2 |
| | 451128 | AL118668 | | gb:DKFZp761I0310_r1 761 (synonym: hamy2)3.2 | 3.2 |
| | 417793 | AW405434 | Hs.82575 | small nuclear ribonucleoprotein polypept | 3.2 |
| | 428027 | U22029 | Hs.334345 | cytochrome P450, subfamily IIA (phenobar | 3.2 |
| 60 | 441197 | BE244638 | Hs.166 | sterol regulatory element binding transc | 3.2 |
| | 424634 | NM_003613 | Hs.151407 | cartilage intermediate layer protein, nu | 3.2 |
| | 419986 | AI345455 | Hs.78915 | GA-binding protein transcription factor, | 3.2 |
| | 416714 | AF283770 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 3.2 |
| | 449465 | NM_004380 | Hs.23598 | CREB binding protein (Rubinstein-Taybi s | 3.2 |
| 65 | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 3.2 |
| | 409079 | W87707 | Hs.82065 | interleukin 6 signal transducer (gp130, | 3.2 |
| | 423551 | AA327598 | Hs.233785 | ESTs | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|---|--------|
| | 453553 | AA036849 | Hs.61829 | Homo sapiens cDNA FLJ12763 fis, clone NT | 3.2 |
| | 442580 | AI733682 | Hs.130239 | ESTs | 3.2 |
| | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) | 9923.2 |
| | 425700 | AF076292 | Hs.159251 | forkhead box H1 | 3.2 |
| 5 | 417124 | BE122762 | Hs.25338 | ESTs | 3.2 |
| | 407104 | S57296 | Hs.323910 | v-erb-b2 avian erythroblastic leukemia v | 3.2 |
| | 442215 | AI703172 | Hs.129005 | ESTs, Weakly similar to 2109260A B cell | 3.1 |
| | 430271 | T06199 | Hs.237506 | DnaJ (Hsp40) homolog, subfamily B, membe | 3.1 |
| | 425317 | AW205118 | Hs.210546 | interleukin 21 receptor | 3.1 |
| 10 | 426095 | AI278023 | Hs.89986 | ESTs | 3.1 |
| | 442313 | BE388898 | Hs.8215 | hypothetical protein FLJ11307 | 3.1 |
| | 424709 | AL137589 | Hs.152149 | hypothetical protein DKFZp434K0410 | 3.1 |
| | 429671 | BE379335 | Hs.211594 | proteasome (prosome, macropain) 26S subu | 3.1 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 3.1 |
| 15 | 431574 | AW572659 | Hs.261373 | hypothetical protein dJ434O14.3 | 3.1 |
| | 436876 | AI124756 | Hs.5337 | isocitrate dehydrogenase 2 (NADP), mitoc | 3.1 |
| | 405017 | NA | | Target Exon | 3.1 |
| | 433805 | AA706910 | Hs.112742 | ESTs | 3.1 |
| | 437352 | AL353957 | Hs.284181 | hypothetical protein DKFZp434P0531 | 3.1 |
| 20 | 430105 | X70297 | Hs.2540 | cholinergic receptor, nicotinic, alpha p | 3.1 |
| | 422083 | NM_001141 | Hs.111256 | arachidonate 15-lipoxygenase, second typ | 3.1 |
| | 413507 | BE145360 | Hs.190064 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 415989 | AI267700 | Hs.317584 | ESTs | 3.1 |
| | 422907 | AI879263 | Hs.6986 | Human glucose transporter pseudogene | 3.1 |
| 25 | 425548 | AA890023 | Hs.1906 | prolactin receptor | 3.1 |
| | 422599 | BE387202 | Hs.118638 | non-metastatic cells 1, protein (NM23A) | 3.1 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 3.1 |
| | 453883 | AI638516 | Hs.22630 | cofactor required for Sp1 transcriptiona | 3.1 |
| | 458021 | AI885190 | Hs.156089 | ESTs, Weakly similar to repressor protei | 3.1 |
| 30 | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 3.1 |
| | 400814 | NA | | Target Exon | 3.1 |
| | 402327 | | | Target Exon | 3.1 |
| | 416935 | AA190712 | | gb:zp87f09.r1 Stratagene HeLa cell s3 93 | 3.1 |
| | 439838 | AL355722 | Hs.106875 | Homo sapiens EST from clone 35214, full | 3.1 |
| 35 | 437036 | AI571514 | Hs.133022 | ESTs | 3.1 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 3.1 |
| | 406642 | AJ245210 | | gb:Homo sapiens mRNA for immunoglobulin | 3.1 |
| | 406624 | AF052762 | | gb:Homo sapiens clone csneg8-1 immunoglo | 3.1 |
| 40 | 421924 | BE514514 | Hs.109606 | coronin, actin-binding protein, 1A | 3.1 |
| | 414523 | AU076633 | Hs.76353 | serine (or cysteine) proteinase inhibito | 3.1 |
| | 416379 | N38857 | Hs.203933 | ESTs | 3.1 |
| | 422823 | D89974 | Hs.121102 | vanin 2 | 3.1 |
| | 433904 | AI399956 | Hs.208956 | ESTs | 3.1 |
| | 421904 | BE143533 | Hs.109309 | hypothetical protein FLJ20035 | 3.1 |
| 45 | 428834 | AW899713 | Hs.339315 | ESTs | 3.1 |
| | 436043 | AW963838 | Hs.168830 | Homo sapiens cDNA FLJ12136 fis, clone MA | 3.1 |
| | 452823 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 3.1 |
| | 405381 | NA | | Target Exon | 3.1 |
| | 428746 | AW503820 | Hs.192861 | Spi-B transcription factor (Spi-1/PU.1 r | 3.1 |
| 50 | 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (f3.1 | 3.1 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 3.1 |
| | 423306 | W88562 | Hs.108198 | ESTs | 3.1 |
| | 419123 | AA234276 | Hs.88253 | ESTs | 3.1 |
| | 438581 | AW977766 | Hs.292133 | ESTs, Moderately similar to I78885 serin | 3.1 |
| 55 | 417105 | X60992 | Hs.81226 | CD6 antigen | 3.0 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 3.0 |
| | 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 3.0 |
| | 402606 | | | NM_024626:Homo sapiens hypothetical prot | 3.0 |
| | 401451 | | | NM_004496*:Homo sapiens hepatocyte nucle | 3.0 |
| 60 | 421878 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 3.0 |
| | 409518 | BE384836 | Hs.3454 | KIAA1821 protein | 3.0 |
| | 416933 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 3.0 |
| | 414324 | Y14768 | Hs.890 | lymphotoxin beta (TNF superfamily, membe | 3.0 |
| | 425081 | X74794 | Hs.154443 | minichromosome maintenance deficient (S. | 3.0 |
| 65 | 401519 | | | C15000476*:g 12737279 ref XP_012163.1 | 3.0 |
| | 411704 | AI499220 | Hs.71573 | hypothetical protein FLJ10074 | 3.0 |
| | 428819 | AL135623 | Hs.193914 | KIAA0575 gene product | 3.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 428423 | AU076517 | Hs.184276 | solute carrier family 9 (sodium/hydrogen | 3.0 |
| | 413835 | AI272727 | Hs.249163 | fatty acid hydroxylase | 3.0 |
| | 412600 | L28824 | Hs.74101 | spleen tyrosine kinase | 3.0 |
| 5 | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 3.0 |
| | 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 3.0 |
| | 427666 | AI791495 | Hs.180142 | calmodulin-like skin protein | 3.0 |
| | 452514 | AI904898 | | gb:RC-BT068-130399-085 BT068 Homo sapien | 3.0 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 3.0 |
| | 432485 | N90866 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 3.0 |
| 10 | 437400 | AB011542 | Hs.5599 | EGF-like-domain, multiple 5 | 3.0 |
| | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 3.0 |
| | 413269 | BE167526 | | gb:CM4-HT0509-080300-107-g07 HT0509 Homo | 3.0 |
| | 453216 | AL137566 | Hs.32405 | Homo sapiens mRNA; cDNA DKFZp586G0321 (f | 3.0 |
| | 400929 | | | ENSP00000252232*:Sterol regulatory eleme | 3.0 |
| 15 | 445145 | AI961702 | Hs.147434 | ESTs | 3.0 |
| | 432615 | AA557191 | Hs.55028 | ESTs, Weakly similar to I54374 gene NF2 | 3.0 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 3.0 |
| | 429392 | AL109712 | Hs.296506 | Homo sapiens mRNA full length insert cDN | 3.0 |
| | 408548 | AA055449 | Hs.63187 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3.0 |
| 20 | 451346 | NM_006338 | Hs.26312 | glioma amplified on chromosome 1 protein | 3.0 |
| | 413109 | AW389845 | Hs.110855 | ESTs | 3.0 |
| | 401714 | NA | | ENSP00000241802*:CDNA FLJ11007 FIS, CLON | 3.0 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 3.0 |
| | 421750 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 3.0 |
| 25 | 453293 | AA382267 | Hs.10653 | ESTs | 3.0 |
| | 457085 | AA412446 | Hs.98138 | ESTs | 3.0 |
| | 438930 | AW843633 | Hs.306163 | hypothetical protein AL110115 | 3.0 |

TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Table 22. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accessions |
|--------|------------|---|
| 407980 | 103087_1 | AA046309 AI263500 AA046397 |
| 410785 | 1221055_1 | AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355 |
| 411743 | 1256098_1 | AW862214 AW859811 AW862215 |
| 412138 | 1279172_1 | AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538 |
| 413269 | 1356961_1 | BE167526 BE167651 BE076401 R24654 |
| 416935 | 163179_1 | AA190712 AA190665 AA252564 |
| 422128 | 211994_1 | AW881145 AA490718 M85637 AA304575 T06067 AA331991 |
| 423945 | 233566_1 | AA410943 AW948953 AA334202 AA332882 |
| 424109 | 235506_1 | AW406878 AW966560 AW966151 AW966496 AA336174 AA335376 AA335537 |
| 424128 | 235728_1 | AW966163 AA335983 AA336011 AA335668 AA335973 |
| 425331 | 250199_1 | AW962128 AA355353 AA427363 |
| 426878 | 273265_1 | BE069341 AW748403 AL044891 AI908240 AA393080 |
| 432745 | 353673_1 | AI821926 AA658826 AA564492 AA635129 AI791191 |
| 441153 | 51084_2 | BE562826 BE378727 |
| 448212 | 755099_1 | AI475858 AW969013 |
| 451128 | 859865_1 | AL118668 D78823 AI762176 |
| 452514 | 920172_1 | AI904898 AI904849 AI904899 |
| 456207 | 165078_1 | AA193450 |

TABLE 22B

Table 22B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 22. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| | Pkey | Ref | Strand | Nt_position |
|----|--------|---------|--------|-------------------------------|
| | 400814 | 8569925 | Minus | 72840-72924,74761-74849 |
| | 400929 | 7651921 | Minus | 122033-122241,123483-124028 |
| 20 | 401045 | 8117619 | Plus | 90044-90184,91111-91345 |
| | 401451 | 6634068 | Minus | 119926-121272 |
| | 401519 | 6649315 | Plus | 157315-157950 |
| | 401645 | 7657839 | Minus | 34986-35133 |
| | 401714 | 6715702 | Plus | 96484-96681 |
| 25 | 401866 | 8018106 | Plus | 73126-73623 |
| | 402327 | 7656695 | Minus | 108675-108770,109801-109910 |
| | 402359 | 9211204 | Minus | 40403-41961 |
| | 402408 | 9796239 | Minus | 110326-110491 |
| | 402470 | 9797107 | Plus | 195129-195776 |
| 30 | 402542 | 9801558 | Minus | 67076-67594 |
| | 402578 | 9884928 | Plus | 66350-66496 |
| | 402606 | 9909429 | Minus | 81747-82094 |
| | 403011 | 6693597 | Minus | 3468-3623 |
| | 403212 | 7630897 | Minus | 156037-156210 |
| 35 | 403329 | 8516120 | Plus | 96450-96598 |
| | 403366 | 8783692 | Minus | 49323-49652 |
| | 403485 | 9966528 | Plus | 2888-3001,3198-3532,3655-4117 |
| | 404347 | 9838195 | Plus | 74493-74829 |
| | 404580 | 6539738 | Minus | 240588-241589 |
| 40 | 404755 | 7706327 | Minus | 53729-53846 |
| | 405017 | 6532084 | Plus | 35551-35690 |
| | 405348 | 2914717 | Minus | 43310-43462 |
| | 405381 | 6006920 | Minus | 7636-8054 |
| | 405801 | 2924321 | Plus | 63469-63694 |
| 45 | 405850 | 6164995 | Plus | 13871-14110 |
| | 406153 | 9929734 | Minus | 12902-13069 |
| | 406348 | 9255985 | Minus | 71754-71944 |

**TABLE 23: 320 GENES DOWN-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT BREAST**

5 **Table 23** shows 320 genes down-regulated in breast cancer compared to normal adult breast. These were selected as for Table 22, except that the numerator was set to the median value for 12 non-malignant breast specimens, the denominator was set to the median value amongst the 73 breast cancers, the 90th percentile value amongst the 12 non-malignant breast specimens was greater than or equal 80 units, and the ratio was greater than or equal to 4.0
10 (*i.e.* 4-fold down-regulated in tumor vs. normal breast).

15 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 50th percentile normal body tissue to 75th percentile tumor

| 20 | Pkey | ExAccn | UnigeneID | UnigeneTitle | Ratio |
|----|--------|-----------|-----------|--|-------|
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 22.4 |
| | 428848 | NM_000230 | Hs.194236 | leptin (murine obesity homolog) | 17.4 |
| | 445263 | H57646 | Hs.42586 | KIAA1560 protein | 15.4 |
| 25 | 418935 | T28499 | Hs.89485 | carbonic anhydrase IV | 15.0 |
| | 407228 | M25079 | Hs.155376 | hemoglobin, beta | 14.6 |
| | 417511 | AL049176 | Hs.82223 | chordin-like | 14.6 |
| | 439285 | AL133916 | Hs.172572 | hypothetical protein FLJ20093 | 14.3 |
| | 412442 | AJ983730 | Hs.26530 | serum deprivation response (phosphatidyl | 13.6 |
| 30 | 410544 | AI446543 | Hs.95511 | ESTs | 12.6 |
| | 412047 | AA934589 | Hs.49696 | ESTs | 12.2 |
| | 422667 | H25642 | Hs.133471 | ESTs | 12.0 |
| | 406664 | L34041 | Hs.9739 | glycerol-3-phosphate dehydrogenase 1 (so | 12.0 |
| | 423201 | NM_000163 | Hs.125180 | growth hormone receptor | 11.7 |
| 35 | 422163 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | 10.8 |
| | 428769 | AW207175 | Hs.106771 | ESTs | 10.6 |
| | 407049 | X72632 | | NM_021724*:Homo sapiens nuclear receptor | 10.1 |
| | 412295 | AW088826 | Hs.117176 | poly(A)-binding protein, nuclear 1 | 9.8 |
| | 425126 | N32759 | Hs.172944 | chorionic gonadotropin, beta polypeptide | 9.8 |
| 40 | 406791 | AJ220684 | Hs.272572 | hemoglobin, alpha 2 | 9.5 |
| | 447471 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 9.5 |
| | 451533 | NM_004667 | Hs.26530 | serum deprivation response (phosphatidyl | 9.4 |
| | 419407 | AW410377 | Hs.41502 | hypothetical protein FLJ21276 | 9.0 |
| | 411939 | AJ365585 | Hs.146246 | ESTs | 9.0 |
| 45 | 410532 | T53088 | Hs.155376 | hemoglobin, beta | 8.9 |
| | 425707 | AF115402 | Hs.11713 | E74-like factor 5 (ets domain transcript | 8.8 |
| | 416585 | X54162 | Hs.79386 | leiomodulin 1 (smooth muscle) | 8.7 |
| | 443060 | D78874 | Hs.8944 | procollagen C-endopeptidase enhancer 2 | 8.6 |
| | 435265 | AA779958 | Hs.185932 | ESTs | 8.5 |
| 50 | 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 8.4 |
| | 433138 | AB029496 | Hs.59729 | semaphorin sem2 | 8.3 |
| | 402195 | | | NM_004497*:Homo sapiens hepatocyte nucle | 8.1 |
| | 429350 | AI754634 | Hs.131987 | ESTs | 8.1 |
| | 445107 | AJ208121 | Hs.147313 | ESTs, Weakly similar to I38022 hypotheti | 8.1 |
| 55 | 406643 | N77976 | Hs.272572 | hemoglobin, alpha 2 | 8.0 |
| | 410199 | AW377424 | Hs.205126 | Homo sapiens cDNA: FLJ22667 fis, clone H | 8.0 |
| | 417225 | AA815048 | Hs.24078 | hypothetical protein FLJ12649 | 7.8 |
| | 437569 | AA760849 | Hs.294052 | ESTs | 7.5 |
| | 436062 | AK000027 | Hs.98633 | ESTs | 7.5 |
| 60 | 425078 | NM_002599 | Hs.154437 | phosphodiesterase 2A, cGMP-stimulated | 7.5 |
| | 430327 | AW973636 | Hs.55931 | ESTs | 7.4 |

| | | | | | |
|----|--------|-----------|------------|--|-----|
| | 447577 | AI393693 | Hs.183297 | DKFZP566F2124 protein | 7.4 |
| | 446039 | AI150491 | Hs.90756 | ESTs | 7.2 |
| | 422060 | R20893 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 7.2 |
| 5 | 424455 | AA452006 | Hs.333199 | ESTs | 7.1 |
| | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 7.1 |
| | 442792 | AI352340 | Hs.131194 | ESTs | 7.0 |
| | 406714 | AI219304 | Hs.283108 | hemoglobin, gamma G | 6.9 |
| | 407571 | AI446183 | Hs.9572 | ESTs, Highly similar to CYA5_HUMAN ADENY | 6.8 |
| 10 | 429580 | AA346839 | Hs.209100 | DKFZP434C171 protein | 6.7 |
| | 453500 | AI478427 | Hs.43125 | esophageal cancer related gene 4 protein | 6.7 |
| | 422233 | AB002058 | Hs.113275 | purinergic receptor P2X-like 1, orphan r | 6.7 |
| | 420205 | AA256395 | Hs.88156 | ESTs | 6.6 |
| | 404368 | NA | | ENSP00000241075*:TRRAP PROTEIN. | 6.6 |
| 15 | 447261 | NM_006691 | Hs.17917 | extracellular link domain-containing 1 | 6.5 |
| | 417090 | AA193282 | Hs.85863 | ESTs, Weakly similar to B34612 zinc fing | 6.5 |
| | 410677 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 6.5 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 6.5 |
| | 415011 | AW963085 | | gb:EST375158 MAGE resequences, MAGH Homo | 6.4 |
| 20 | 412068 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 6.4 |
| | 416253 | BE250659 | Hs.15463 | Homo sapiens, clone IMAGE:2959994, mRNA | 6.4 |
| | 435885 | AA701483 | Hs.36341 | ESTs | 6.3 |
| | 402779 | NA | | Target Exon | 6.3 |
| | 418138 | AA213626 | Hs.136204 | EST | 6.3 |
| 25 | 439335 | AA742697 | Hs.62492 | ESTs, Weakly similar to B39066 proline-r | 6.3 |
| | 427019 | AA001732 | Hs.173233 | hypothetical protein FLJ10970 | 6.2 |
| | 411478 | BE143068 | | gb:MR0-HT0158-030200-003-b09 HT0158 Homo | 6.2 |
| | 452654 | BE004783 | | gb:MR2-BN0114-270400-004-e11 BN0114 Homo | 6.1 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 6.1 |
| 30 | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | 6.1 |
| | 441266 | H15968 | Hs.293845 | Homo sapiens, clone IMAGE:3502329, mRNA, | 6.1 |
| | 417011 | F08212 | Hs.234898 | ESTs, Weakly similar to 2109260A B cell | 6.0 |
| | 400089 | NA | | Eos Control | 6.0 |
| | 433614 | W07475 | Hs.277101 | cytochrome c oxidase subunit IV isoform | 5.9 |
| 35 | 440439 | N92818 | Hs.64754 | ESTs, Weakly similar to potential CDS [H | 5.9 |
| | 454404 | BE067414 | | gb:MR4-BT0355-200100-201-e05 BT0355 Homo | 5.9 |
| | 436704 | AA062610 | Hs.148050 | EST | 5.9 |
| | 406563 | NA | | Target Exon | 5.9 |
| | 433490 | AW451023 | Hs.65848 | hypothetical protein DKFZp761O132 | 5.9 |
| 40 | 419313 | AA843387 | Hs.87279 | ESTs | 5.9 |
| | 409196 | NM_001874 | Hs.334873 | carboxypeptidase M | 5.8 |
| | 410882 | AW809163 | | gb:MR4-ST0118-261099-012-a03 ST0118 Homo | 5.8 |
| | 453469 | AB014533 | Hs.33010 | KIAA0633 protein | 5.8 |
| | 441899 | AI372588 | Hs.8022 | TU3A protein | 5.8 |
| 45 | 426210 | AA372052 | Hs.334559 | Homo sapiens cDNA FLJ14458 fis, clone HE | 5.8 |
| | 413065 | BE063555 | | gb:CM1-BT0283-081199-033-d09 BT0283 Homo | 5.8 |
| | 454192 | AW876813 | Hs.3343 | phosphoglycerate dehydrogenase | 5.7 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 5.7 |
| | 429757 | AW452355 | Hs.256037 | ESTs | 5.7 |
| 50 | 420202 | AL036557 | Hs.95910 | putative lymphocyte G0/G1 switch gene | 5.7 |
| | 416284 | AI695473 | Hs.298006 | ESTs | 5.7 |
| | 428553 | AA181641 | Hs.184907 | G protein-coupled receptor 1 | 5.6 |
| | 404689 | NA | | Target Exon | 5.6 |
| | 438887 | R68857 | Hs.265499 | ESTs | 5.6 |
| 55 | 406082 | S47833 | Hs.82927 | adenosine monophosphate deaminase 2 (Iso | 5.6 |
| | 449748 | H23963 | Hs.32043 | ESTs | 5.6 |
| | 431048 | R50253 | Hs.249129 | cell death-inducing DFFA-like effector a | 5.5 |
| | 452205 | C15819 | | gb:C15819 Clontech human aorta polyA mRN | 5.5 |
| | 434040 | AW444613 | Hs.288809 | hypothetical protein FLJ20159 | 5.5 |
| 60 | 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A (ABC1 | 5.5 |
| | 450606 | AI668605 | Hs.60380 | ESTs, Moderately similar to ALU6_HUMAN A | 5.5 |
| | 414629 | AA345824 | Hs.76688 | carboxylesterase 1 (monocyte/macrophage | 5.5 |
| | 401665 | | | C11000703:gil10048448[ref]NP_065258.1 g | 5.5 |
| | 436107 | T99079 | Hs.191194 | ESTs | 5.5 |
| 65 | 444432 | AI161428 | Hs.75916 | splicing factor 3b, subunit 2, 145kD | 5.5 |
| | 434715 | BE005346 | Hs.1164410 | ESTs | 5.5 |
| | 447205 | BE617015 | Hs.11006 | ESTs, Moderately similar to T17372 plasm | 5.5 |
| | 408122 | AI432652 | Hs.42824 | hypothetical protein FLJ10718 | 5.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 454016 | AW016806 | Hs.233108 | ESTs | 5.5 |
| | 414913 | R25621 | | gb:yh45f06.r1 Soares placenta Nb2HP Homo | 5.4 |
| | 459033 | AA017590 | Hs.129907 | ESTs | 5.4 |
| | 441003 | BE172240 | Hs.126379 | ESTs, Weakly similar to I38022 hypotheti | 5.4 |
| | 450637 | N49826 | Hs.18602 | ESTs | 5.4 |
| 10 | 442398 | AA994520 | | gb:ou42g09.s1 Soares_NFL_T_GBC_S1 Homo | 5.4 |
| | 403612 | NA | | Target Exon | 5.3 |
| | 407102 | AA007629 | Hs.9739 | glycerol-3-phosphate dehydrogenase 1 (so | 5.3 |
| | 410057 | R66634 | Hs.268107 | multimerin | 5.3 |
| | 428232 | BE272452 | Hs.183109 | monoamine oxidase A | 5.3 |
| 15 | 432769 | AA620814 | Hs.144959 | ESTs | 5.3 |
| | 431344 | R99530 | Hs.272572 | hemoglobin, alpha 2 | 5.3 |
| | 427032 | AF012023 | Hs.173274 | integrin cytoplasmic domain-associated p | 5.3 |
| | 406305 | BE261320 | Hs.158196 | transcriptional adaptor 3 (ADA3, yeast h | 5.3 |
| | 437411 | AW613948 | Hs.194915 | ESTs | 5.3 |
| 20 | 442800 | AI809481 | Hs.131227 | ESTs | 5.3 |
| | 402054 | NA | | Target Exon | 5.3 |
| | 432085 | AF212829 | Hs.272406 | potassium channel, subfamily K, member 9 | 5.3 |
| | 415313 | R59638 | Hs.6181 | ESTs | 5.2 |
| | 459159 | AI904646 | | gb:QV-BT065-020399-103 BT065 Homo sapien | 5.2 |
| 25 | 427164 | AB037721 | Hs.173871 | KIAA1300 protein | 5.2 |
| | 441391 | BE467930 | Hs.170381 | ESTs | 5.2 |
| | 458959 | AI285901 | Hs.181297 | ESTs | 5.2 |
| | 402698 | NA | | ENSP00000251335*.DJ1003J2.1 (sodium and | 5.2 |
| | 401810 | NA | | Target Exon | 5.2 |
| 30 | 438879 | AA827674 | Hs.189073 | ESTs | 5.2 |
| | 414657 | AA424074 | Hs.76780 | protein phosphatase 1, regulatory (Inhib | 5.2 |
| | 427809 | M26380 | Hs.180878 | lipoprotein lipase | 5.1 |
| | 456063 | NM_006744 | Hs.76461 | retinol-binding protein 4, interstitial | 5.1 |
| | 451186 | AW023469 | Hs.65256 | ESTs, Weakly similar to leucine-rich gli | 5.1 |
| 35 | 451882 | AI821324 | Hs.100445 | ESTs | 5.1 |
| | 402583 | NA | | NM_021620:Homo sapiens PR domain contain | 5.1 |
| | 431130 | NM_006103 | Hs.2719 | HE4; WFDC2; putative ovarian carcinoma m | 5.1 |
| | 458218 | AI435179 | Hs.126820 | ESTs | 5.1 |
| | 416083 | R53467 | Hs.269122 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.1 |
| 40 | 455282 | BE143867 | | gb:MR0-HT0164-070100-013-h02 HT0164 Homo | 5.1 |
| | 426488 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 5.1 |
| | 426156 | BE244537 | Hs.167382 | natriuretic peptide receptor A/guanylate | 5.1 |
| | 407891 | AA486620 | Hs.41135 | endomucin-2 | 5.0 |
| | 408610 | AW026692 | Hs.224829 | ESTs | 5.0 |
| 45 | 445967 | D59597 | Hs.118821 | CGI-62 protein | 5.0 |
| | 434813 | AI524307 | Hs.162870 | ESTs | 5.0 |
| | 437526 | AI076012 | Hs.121388 | ESTs, Weakly similar to MDHC_HUMAN MALAT | 5.0 |
| | 454775 | BE160229 | | gb:QV1-HT0413-090200-062-a12 HT0413 Homo | 5.0 |
| | 409451 | AF012626 | Hs.54472 | fragile X mental retardation 2 | 5.0 |
| 50 | 409853 | AW502327 | | gb:UI-HF-BR0p-aka-a-07-0-UI.r1 NIH_MGC_5 | 5.0 |
| | 405062 | | | Target Exon | 5.0 |
| | 446490 | AK000706 | Hs.15125 | hypothetical protein FLJ20699 | 5.0 |
| | 417622 | AW298163 | Hs.82318 | WAS protein family, member 3 | 5.0 |
| | 421978 | AJ243662 | Hs.110196 | NICE-1 protein | 5.0 |
| 55 | 440338 | R62431 | Hs.12758 | ESTs | 5.0 |
| | 415421 | R35009 | Hs.24903 | ESTs | 5.0 |
| | 417574 | R00348 | | gb:ye69e06.r1 Soares fetal liver spleen | 5.0 |
| | 409882 | AJ243191 | Hs.56874 | heat shock 27kD protein family, member 7 | 5.0 |
| | 447998 | AI768289 | Hs.304389 | ESTs | 4.9 |
| 60 | 445613 | BE550889 | Hs.158491 | ESTs | 4.9 |
| | 443074 | AW341470 | Hs.144907 | ESTs | 4.9 |
| | 451324 | AI783600 | Hs.208052 | ESTs | 4.9 |
| | 432433 | AW014734 | Hs.157969 | ESTs | 4.9 |
| | 449654 | AI989812 | Hs.199850 | ESTs | 4.9 |
| 65 | 414519 | N94587 | Hs.55063 | ESTs | 4.9 |
| | 457531 | AW973716 | Hs.13913 | KIAA1577 protein | 4.9 |
| | 433200 | AA682722 | Hs.192725 | ESTs | 4.9 |
| | 430782 | AF026263 | Hs.247920 | cholinergic receptor, muscarinic 5 | 4.8 |
| | 427555 | AW137094 | Hs.97990 | ESTs | 4.8 |
| | 433545 | AA868510 | Hs.112496 | ESTs | 4.8 |
| | 420334 | AI349351 | Hs.118944 | hypothetical protein FLJ22477 | 4.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 421795 | X63094 | Hs.283822 | Rhesus blood group, D antigen | 4.8 |
| | 427138 | N77624 | Hs.173717 | phosphatidic acid phosphatase type 2B | 4.8 |
| | 413072 | BE063965 | | gb:QV3-BT0296-140200-085-h01 BT0296 Homo | 4.8 |
| 5 | 443721 | AW450451 | Hs.266355 | ESTs | 4.8 |
| | 408053 | AW139474 | Hs.246862 | ESTs | 4.8 |
| | 427067 | AA843716 | Hs.177927 | ESTs | 4.7 |
| | 442969 | AI025499 | Hs.132238 | ESTs | 4.7 |
| | 426220 | AI383475 | Hs.171697 | ESTs, Weakly similar to T13924 sdk prote | 4.7 |
| 10 | 414593 | BE386764 | | gb:601273249F1 NIH_MGC_20 Homo sapiens c | 4.7 |
| | 426893 | AA398716 | Hs.97418 | ESTs | 4.7 |
| | 434046 | AW292618 | Hs.113011 | ESTs | 4.7 |
| | 401590 | NA | | Target Exon | 4.7 |
| | 457971 | AW134679 | Hs.242849 | ESTs | 4.7 |
| 15 | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 4.6 |
| | 443793 | AA045290 | Hs.25930 | ESTs, Weakly similar to 2109260A B cell | 4.6 |
| | 407737 | R49187 | Hs.6659 | ESTs | 4.6 |
| | 441955 | AA972327 | Hs.142903 | ESTs | 4.6 |
| | 441499 | AW298235 | Hs.101689 | ESTs | 4.6 |
| 20 | 447517 | AI382726 | Hs.182434 | ESTs | 4.6 |
| | 403017 | | | Target Exon | 4.6 |
| | 450580 | N40087 | Hs.15248 | ESTs | 4.6 |
| | 404611 | H58589 | Hs.35156 | Homo sapiens cDNA FLJ11027 fls, clone PL | 4.6 |
| | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 4.6 |
| 25 | 459290 | NM_001546 | Hs.34853 | inhibitor of DNA binding 4, dominant neg | 4.6 |
| | 444341 | AI142027 | Hs.146650 | ESTs | 4.6 |
| | 408614 | AL137698 | Hs.46531 | Homo sapiens mRNA; cDNA DKFZp434C1915 (f | 4.6 |
| | 449638 | AW204277 | Hs.250723 | hypothetical protein MGC2747 | 4.6 |
| | 434418 | AF134707 | Hs.278679 | a disintegrin and metalloproteinase doma | 4.6 |
| 30 | 447360 | AI375984 | Hs.167216 | ESTs | 4.6 |
| | 419583 | F00312 | | gb:HSBB0D101 STRATAGENE Human skeletal m | 4.6 |
| | 440698 | AI348455 | Hs.147492 | Homo sapiens cDNA FLJ11777 fls, clone HE | 4.6 |
| | 451199 | AI290653 | Hs.124758 | ESTs | 4.6 |
| | 438338 | NM_014861 | Hs.6168 | KIAA0703 gene product | 4.6 |
| 35 | 433756 | AW015933 | Hs.112654 | Homo sapiens, clone MGC:9764, mRNA, comp | 4.5 |
| | 423301 | S67580 | Hs.1645 | cytochrome P450, subfamily IVA, polypept | 4.5 |
| | 417237 | H86385 | Hs.81737 | palmitoyl-protein thioesterase 2 | 4.5 |
| | 439745 | AL389981 | Hs.149219 | Homo sapiens mRNA full length insert cDN | 4.5 |
| | 424137 | AA335769 | Hs.16262 | ESTs | 4.5 |
| 40 | 449338 | H73444 | Hs.394 | adrenomedullin | 4.5 |
| | 434744 | N94835 | Hs.283828 | Homo sapiens genomic DNA, chromosome 21q | 4.5 |
| | 407402 | AF035303 | | gb:Homo sapiens clone 23943 mRNA sequenc | 4.5 |
| | 443510 | NM_012190 | Hs.9520 | formyltetrahydrofolate dehydrogenase | 4.5 |
| | 415754 | AA169114 | Hs.12247 | hypothetical protein FLJ11413 | 4.5 |
| 45 | 415986 | Z43619 | | gb:HSC1GE121 normalized infant brain cDN | 4.5 |
| | 457416 | BE142052 | Hs.62654 | kringle-containing transmembrane protein | 4.5 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 4.4 |
| | 437120 | AI356125 | Hs.157767 | ESTs, Weakly similar to HXA2_HUMAN HOMEO | 4.4 |
| | 453950 | AA156998 | Hs.211568 | eukaryotic translation initiation factor | 4.4 |
| 50 | 401093 | | | C12000586*:g 6330167 dbj BAA86477.1 (A | 4.4 |
| | 436935 | AW206494 | Hs.253560 | ESTs | 4.4 |
| | 457974 | AW842353 | Hs.321717 | ESTs, Weakly similar to S22765 heterogen | 4.4 |
| | 428222 | AL133112 | Hs.183085 | Homo sapiens mRNA; cDNA DKFZp434K098 (fr | 4.4 |
| | 442705 | AI264634 | Hs.131127 | ESTs | 4.4 |
| 55 | 437409 | AL359599 | Hs.283850 | Homo sapiens mRNA; cDNA DKFZp547C126 (fr | 4.4 |
| | 458494 | AI380906 | Hs.158436 | ESTs | 4.4 |
| | 410490 | H03589 | | gb:yy42d08.r1 Soares placenta Nb2HP Homo | 4.4 |
| | 416069 | R37101 | Hs.20982 | ESTs | 4.4 |
| | 438463 | AA807958 | Hs.314232 | ESTs | 4.4 |
| 60 | 444043 | AI499723 | Hs.135089 | ESTs | 4.4 |
| | 438327 | H87407 | Hs.172944 | chorionic gonadotropin, beta polypeptide | 4.4 |
| | 457711 | AF147401 | Hs.23917 | ESTs | 4.3 |
| | 400870 | | | C11000905:g 11692565 gb AAG39879.1 AF28 | 4.3 |
| | 441425 | AA933590 | Hs.28937 | homeobox protein from AL590526 | 4.3 |
| 65 | 416267 | H45384 | | gb:yn99c10.r1 Soares adult brain N2b5HB5 | 4.3 |
| | 407262 | M12873 | | gb:Human Ig rearranged H-chain mRNA VDJ4 | 4.3 |
| | 444567 | AV654020 | Hs.184261 | ESTs, Weakly similar to T26686 hypothe | 4.3 |
| | 403263 | NA | | Target Exon | 4.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 410034 | BE067414 | | gb:MR4-BT0355-200100-201-e05 BT0355 Homo | 4.3 |
| | 456804 | AI421645 | Hs.139851 | caveolin 2 | 4.3 |
| | 448427 | BE395260 | Hs.309438 | EST | 4.3 |
| 5 | 416931 | D45371 | Hs.80485 | adipose most abundant gene transcript 1 | 4.3 |
| | 421296 | NM_002666 | Hs.103253 | perilipin | 4.3 |
| | 400973 | NA | | ENSP00000236667*:Mucin 5B (Fragment). | 4.3 |
| | 452602 | AW366194 | Hs.55962 | ESTs | 4.3 |
| | 412330 | NM_005100 | Hs.788 | A kinase (PRKA) anchor protein (gravin) | 4.3 |
| 10 | 405016 | | | CY000171*:gij9280405 gb AAF86402.1 AF245 | 4.3 |
| | 435104 | AI475671 | Hs.88607 | ESTs, Highly similar to F-box protein FB | 4.3 |
| | 406118 | | | ENSP00000246632:CDNA FLJ20261 fis, clone | 4.3 |
| | 418556 | T02850 | | gb:FB12A9 Fetal brain, Stratagene Homo s | 4.3 |
| | 429745 | AA480818 | Hs.221736 | ESTs | 4.3 |
| 15 | 433088 | AW451206 | Hs.115899 | ESTs | 4.3 |
| | 444445 | AA342329 | Hs.115920 | Homo sapiens cDNA: FLJ22816 fis, clone K | 4.3 |
| | 453880 | AI803166 | Hs.28462 | ESTs, Weakly similar to I38022 hypotheti | 4.3 |
| | 447384 | AI377221 | Hs.40528 | ESTs | 4.2 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 4.2 |
| | 444975 | AV652165 | Hs.182482 | ESTs, Weakly similar to T00362 hypotheti | 4.2 |
| 20 | 403921 | NA | | C5000212*:gij10047237 dbj BAB13407.1 (A | 4.2 |
| | 451477 | AI798425 | Hs.42710 | ESTs | 4.2 |
| | 406344 | | | C5001660:gij11611537 dbj BAB18935.1 (AB | 4.2 |
| | 416970 | AA191201 | Hs.35861 | DKFZP586E1621 protein | 4.2 |
| 25 | 413662 | BE155866 | Hs.25522 | KIAA1808 protein | 4.2 |
| | 458504 | AW070634 | Hs.144794 | ESTs | 4.2 |
| | 404682 | NA | | C9001188*:gij12738842 ref NP_073725.1 p | 4.2 |
| | 418089 | N69913 | Hs.6858 | ESTs, Weakly similar to I78885 serine/th | 4.2 |
| | 403433 | | | NM_001622:Homo sapiens alpha-2-HS-glycop | 4.2 |
| 30 | 446532 | AW975460 | Hs.143563 | ESTs | 4.2 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 4.2 |
| | 418425 | AI871247 | Hs.6262 | hypothetical protein MGC8407 | 4.2 |
| | 419589 | AW973708 | Hs.201925 | Homo sapiens cDNA FLJ13446 fis, clone PL | 4.2 |
| | 457029 | AA397789 | Hs.161803 | ESTs | 4.2 |
| 35 | 447860 | AF193807 | Hs.131835 | Rhesus blood group, B glycoprotein | 4.2 |
| | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 4.2 |
| | 440610 | AI733098 | Hs.130800 | ESTs | 4.2 |
| | 439590 | AF086410 | | gb:Homo sapiens full length insert cDNA | 4.2 |
| | 427240 | AA399975 | Hs.274151 | ligatin | 4.2 |
| 40 | 408932 | AW594172 | Hs.278513 | TP53TG3 protein | 4.2 |
| | 436112 | T77545 | Hs.187559 | ESTs | 4.2 |
| | 444382 | AI144152 | Hs.58246 | ESTs | 4.2 |
| | 456716 | AA318060 | Hs.135121 | hypothetical protein FLJ22415 | 4.2 |
| | 419846 | NM_015977 | Hs.285681 | Williams-Beuren syndrome chromosome regl | 4.2 |
| 45 | 410036 | R57171 | Hs.57975 | calsequestrin 2 (cardiac muscle) | 4.1 |
| | 400545 | NA | | Target Exon | 4.1 |
| | 403051 | NA | | Target Exon | 4.1 |
| | 420139 | NM_005357 | Hs.95351 | lipase, hormone-sensitive | 4.1 |
| | 450244 | AA007534 | Hs.125062 | ESTs | 4.1 |
| 50 | 453261 | AA034116 | Hs.118494 | ESTs | 4.1 |
| | 440246 | W52010 | Hs.191379 | ESTs | 4.1 |
| | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypotheti | 4.1 |
| | 438232 | AI150595 | Hs.122226 | ESTs | 4.1 |
| | 410233 | AA082947 | | gb:zn10g07.s1 Stratagene hNT neuron (937 | 4.1 |
| 55 | 412179 | BE270758 | Hs.69428 | hypothetical protein MGC3020 | 4.1 |
| | 441871 | AI306150 | Hs.153450 | ESTs, Weakly similar to 1909123A Na gluc | 4.1 |
| | 426411 | AK000708 | Hs.169764 | hypothetical protein FLJ20701 | 4.1 |
| | 453692 | AL110416 | | gb:DKFZp434K0431_r1 434 (synonym: htes3) | 4.1 |
| | 448640 | AW817177 | Hs.102558 | Homo sapiens, clone MGC:5352, mRNA, comp | 4.1 |
| 60 | 417481 | AA203281 | Hs.21798 | ESTs | 4.1 |
| | 412912 | AW118878 | Hs.110835 | ESTs | 4.1 |
| | 454183 | AW807116 | | gb:MR4-ST0062-040100-024-b12 ST0062 Homo | 4.1 |
| | 426328 | AW631296 | | gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens | 4.1 |
| | 435942 | R06285 | Hs.191215 | ESTs | 4.1 |
| 65 | 417629 | T76945 | | gb:yc92c07.r1 Soares Infant brain 1NIB H | 4.1 |
| | 403593 | NA | | Target Exon | 4.0 |
| | 402690 | | | Target Exon | 4.0 |
| | 418190 | R49591 | Hs.270425 | ESTs | 4.0 |

| | | | | | |
|----|--------|----------|-----------|--|-----|
| 5 | 408641 | AW245207 | Hs.5555 | hypothetical protein MGC5347 | 4.0 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 4.0 |
| | 445975 | AI811536 | Hs.145734 | ESTs | 4.0 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 4.0 |
| | 455578 | BE006350 | Hs.14355 | Homo sapiens cDNA FLJ13207 fls, clone NT | 4.0 |
| 10 | 401840 | NA | | Target Exon | 4.0 |
| | 413753 | U17760 | Hs.75517 | laminin, beta 3 (nicein (125kD), kalinin | 4.0 |
| | 445030 | AI205925 | Hs.147238 | ESTs, Highly similar to AAC3_HUMAN ALPHA | 4.0 |
| | 433873 | AW156913 | Hs.150478 | ESTs, Weakly similar to A Chain A, Cryst | 4.0 |
| | 456736 | AW248217 | Hs.1619 | achaete-scute complex (Drosophila) homol | 4.0 |
| | 450112 | BE047734 | Hs.5473 | ESTs, Moderately similar to ALU5_HUMAN A | 4.0 |
| | 448906 | AI589567 | Hs.309719 | ESTs | 4.0 |
| | | | | | |

TABLE 23A

Table 23A shows the accession numbers for those pkeys lacking unigeneID's for Table 23. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accessions |
|--------|------------|---|
| 409853 | 1156226_1 | AW502327 AW502488 AW501829 AW502625 AW502687 |
| 410034 | 1170594_1 | BE067414 BE067958 BE067419 BE067963 AW577127 AW601412 |
| 410233 | 118656_1 | AA082947 AA083036 |
| 410490 | 1205347_1 | H03589 AW750687 AW750688 |
| 410882 | 1225686_1 | AW809163 AW809247 AW809177 AW809190 AW809225 |
| 411478 | 1247073_1 | BE143068 AW849143 AW848705 AW848569 AW848071 AW848475 AW848092 AW848005 |
| 413065 | 1347960_1 | BE063555 BE151321 BE151319 BE151657 BE151655 BE063556 BE151322 |
| 413072 | 1348163_1 | BE063965 BE063968 BE064034 BE064028 BE063874 BE063966 BE063869 BE064043 BE064033 BE063884 |
| 414593 | 1464909_1 | BE386764 BE387560 |
| 414913 | 1506721_1 | R25621 C03959 C04010 |
| 415011 | 151328_1 | AW963085 AA159005 AW963073 |
| 415986 | 1564410_1 | Z43619 R61274 H12206 R12883 |
| 416267 | 1583547_1 | H45384 H49125 H41699 |
| 417574 | 1687770_1 | R00348 R09593 |
| 417629 | 1690392_1 | T76945 R20210 R05755 |
| 418556 | 1767866_1 | T02850 |
| 419583 | 186198_1 | F00312 AA247490 F31427 AA383663 F22045 |
| 426328 | 264901_1 | AW631296 AA375484 |
| 439590 | 47413_1 | AF086410 W94386 W74609 |
| 442398 | 541271_1 | AA994520 AW393574 |
| 452205 | 90415_1 | C15819 AA024741 AA024742 |
| 452654 | 925931_1 | BE004783 BE004947 AI911790 |
| 453692 | 977825_1 | AL110416 AW876759 |
| 454183 | 1049636_1 | AW807116 AW807569 AW807415 AW807338 AW807288 AW807263 AW807316 AW177402 AW807413 AW807068 BE141561 BE141569 AW807401 AW807310 BE141565 AW807318 AW807119 AW807299 AW807241 AW807225 AW807204 AW807345 AW807103 BE141615 AW807431 AW807393 AW807337 AW807406 AW807259 AW807375 AW845890 AW807220 AW807399 AW807064 AW807376 AW807024 BE141595 AW807236 AW807027 AW807112 AW807378 AW807202 BE141593 AW807216 AW807138 AW807244 AW807221 AW807297 AW807050 AW807248 AW807404 AW807075 AW807237 AW807212 AW807308 AW807110 AW807104 BE140912 AW807301 AW807382 AW807294 AW807026 AW807020 AW807108 AW807025 AW807433 AW807124 AW807419 AW807031 AW807264 AW807032 AW807029 AW807052 AW807391 AW807207 AW807215 AW807019 AW807238 AW807201 BE141590 AW807302 AW807323 AW807380 AW807109 BE141588 AW845877 AW807418 AW807407 AW807309 BE141614 AW845861 AW807396 AW807300 AW807348 AW807311 AW807214 AW807132 AW807402 AW807350 AW807028 AW807298 AW807291 AW807305 AW807217 AW807312 AW807261 AW807268 AW807260 AW807266 AW807198 AW807346 AW807315 BE140940 AW807351 AW807122 AW807235 AW807076 AW807314 AW807213 AW807143 AW807131 AW800079 AW807066 AW807077 AW845923 AW807421 BE141619 BE140943 AW807420 AW807381 BE141621 AW845921 BE141629 BE141625 BE141624 BE141636 BE141630 AW807405 AW807290 AW807353 |
| 454404 | 1170594_1 | BE067414 BE067958 BE067419 BE067963 AW577127 AW601412 |
| 454775 | 1234106_1 | BE160229 AW819879 AW820179 AW819882 AW819876 AW820169 BE153201 AW993736 BE152911 |
| 455282 | 1273020_1 | BE143867 AW935060 AW886684 |
| 459159 | 919998_1 | AI904646 BE179494 BE179421 |

TABLE 23B

Table 23B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 23. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-------------------------------------|
| 400545 | 9800107 | Minus | 124618-124881 |
| 400870 | 9838306 | Minus | 34081-35027 |
| 400973 | 7960452 | Minus | 98119-98253 |
| 401093 | 8516137 | Minus | 22335-23166 |
| 401590 | 9966320 | Minus | 33547-33649 |
| 401665 | 7145001 | Plus | 121591-122537 |
| 401810 | 7342191 | Plus | 129063-129476 |
| 401840 | 7684597 | Plus | 56283-56439 |
| 402054 | 8083691 | Minus | 8288-8806 |
| 402195 | 7689778 | Minus | 147901-148884 |
| 402583 | 7684486 | Plus | 94883-95003 |
| 402690 | 8348058 | Plus | 13368-13998 |
| 402698 | 8570304 | Minus | 108641-108903 |
| 402779 | 9588555 | Minus | 38173-39210 |
| 403017 | 6693623 | Plus | 78630-79367 |
| 403051 | 4827080 | Minus | 5269-5411 |
| 403263 | 7770677 | Plus | 52431-52737 |
| 403433 | 9719611 | Minus | 72225-72437 |
| 403593 | 6862650 | Minus | 62554-62712,69449-69602 |
| 403612 | 8469060 | Minus | 94723-94859 |
| 403921 | 7711590 | Minus | 3297-3536 |
| 404368 | 7630956 | Minus | 102053-102199 |
| 404682 | 9797231 | Minus | 40977-41150 |
| 404689 | 7534100 | Plus | 119461-119717 |
| 405016 | 6524300 | Plus | 51997-53308 |
| 405062 | 7657730 | Plus | 101283-101432 |
| 406118 | 9143818 | Plus | 53997-54629 |
| 406344 | 9255974 | Plus | 20254-20374,20526-20659,20835-21097 |
| 406563 | 7711604 | Plus | 34401-34538 |

TABLE 24:

Table 24 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, Pred.Cell.Loc., and ExAccn for all of the sequences in Table 25. The information in Table 24 is linked by Seq ID No. to Table 25.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Pred.Cell.Loc.: Predicted Cellular Localization
 Seq.ID.No.: Sequence Identification Number found in Table 25

| Pkey | ExAccn | UnigeneID | Unigene Title | Pred.Cell.Loc. | Seq. ID. No. |
|--------|--------------------|-----------|--|----------------|----------------|
| 449746 | AI668594 | Hs.176588 | ESTs, Weakly similar to CP4Y_HUMAN CYTOC | | Seq ID 1 & 2 |
| 407276 | AI951118 | Hs.326736 | Homo sapiens breast cancer antigen NY-BR | | Seq ID 3 & 4 |
| 415539 | AI733881 | Hs.72472 | BMP-R1B | | Seq ID 5 & 6 |
| 400297 | AI127076 | Hs.334473 | hypothetical protein DKFZp564O1278 | | Seq ID 7 & 8 |
| 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | | Seq ID 9 & 10 |
| 102457 | NM_001394Hs.2359 | | dual specificity phosphatase 4 | nuclear | Seq ID 11 & 12 |
| 429170 | NM_001394Hs.2359 | | dual specificity phosphatase 4 | nuclear | Seq ID 11 & 12 |
| 424399 | AI905687 | Hs.2533 | aldehyde dehydrogenase 9 family, member | cytoplasm | Seq ID 13 & 14 |
| 422505 | AL120862 | Hs.124165 | ESTs | | Seq ID 15 & 16 |
| 449765 | N92293 | Hs.206832 | ESTs, Moderately similar to ALU8_HUMAN A | | Seq ID 17 & 18 |
| 425692 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | | Seq ID 19 & 20 |
| 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | | Seq ID 21 & 22 |
| 439840 | AW449211 | Hs.105445 | GDNF family receptor alpha 1 | | Seq ID 23 & 24 |
| 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | | Seq ID 25 & 26 |
| 429220 | AW207206 | Hs.136319 | ESTs | | Seq ID 27 & 28 |
| 416276 | U41060 | Hs.79136 | LIV-1 protein, estrogen regulated | | Seq ID 29 & 30 |
| 409079 | W87707 | Hs.82065 | Interleukin 6 signal transducer (gp130, | | Seq ID 31 & 32 |
| 442818 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | | Seq ID 33 & 34 |
| 442082 | R41823 | Hs.7413 | ESTs | | Seq ID 35 & 36 |
| 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothi | | Seq ID 37 & 38 |
| 446163 | AA026880 | Hs.25252 | Homo sapiens cDNA FLJ13603 fis, clone PL | | Seq ID 39 & 40 |
| 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | | Seq ID 41 & 42 |
| 442117 | AW664964 | Hs.128899 | ESTs | | Seq ID 43 & 44 |
| 433043 | W57554 | Hs.125019 | lymphoid nuclear protein (LAF-4) mRNA | | Seq ID 45 & 46 |
| 429353 | AL117406 | Hs.200102 | ATP-binding cassette transporter MRP8 | | Seq ID 47 & 48 |
| 452190 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | | Seq ID 49 & 50 |
| 446733 | AA863360 | Hs.26040 | ESTs, Weakly similar to fatty acid omega | | Seq ID 51 & 52 |
| 452747 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | | Seq ID 53 & 54 |
| 423242 | AL039402 | Hs.125783 | DEME-6 protein | | Seq ID 55 & 56 |
| 417433 | BE270266 | Hs.82128 | 5T4 oncofetal trophoblast glycoprotein | | Seq ID 57 & 58 |
| 432201 | AI538613 | Hs.298241 | Transmembrane protease, serine 3 | | Seq ID 59 & 60 |
| 423961 | D13666 | Hs.136348 | osteoblast specific factor 2 (fasciclin | | Seq ID 61 & 62 |
| 439569 | AW602166 | Hs.222399 | CEGP1 protein | | Seq ID 63 & 64 |
| 114480 | BE066778 | Hs.151678 | UDP-N-acetyl-alpha-D-galactosamine:polyp | | Seq ID 65 & 66 |
| 404561 | NA | | NM_014112*:Homo sapiens trichorhinophala | mitochondria | Seq ID 67 & 68 |
| 325372 | NA | | Phase 2 & 3 Exons | nuclear | Seq ID 69 & 70 |
| 112287 | AB033064 | Hs.334806 | KIAA1238 protein | | Seq ID 71 & 72 |
| 335824 | NA | | ENSP00000249072*:DJ222E13.1 (N-TERMINAL | | Seq ID 73 & 74 |
| 424735 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | | Seq ID 75 & 76 |
| 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin | | Seq ID 77 & 78 |
| 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | | Seq ID 79 & 80 |
| 429925 | NM_000786Hs.226213 | | cytochrome P450, 51 (lanosterol 14-alpha | ER | Seq ID 81 & 82 |
| 429441 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | | Seq ID 83 & 84 |
| 421155 | H87879 | Hs.102267 | lysyl oxidase | extracellular | Seq ID 85 & 86 |
| 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | | Seq ID 87 & 88 |
| 420813 | X51501 | Hs.99949 | prolactin-induced protein | nuclear | Seq ID 89 & 90 |
| 452744 | AI267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | | Seq ID 91 & 92 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----------------|------------------|
| | 420757 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | cytoplasm | Seq ID 93 & 94 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | nuclear | Seq ID 95 & 96 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | | Seq ID 97 & 98 |
| 5 | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | extracellular | Seq ID 99 & 100 |
| | 445537 | AJ245671 | Hs.12844 | EGF-like-domain, multiple 6 | | Seq ID 101 & 102 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | extracellular | Seq ID 103 & 104 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | | Seq ID 105 & 106 |
| | 421727 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | | Seq ID 107 & 108 |
| 10 | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | nuclear | Seq ID 109 & 110 |
| | 419667 | AU077005 | Hs.92208 | a disintegrin and metalloproteinase doma | | Seq ID 111 & 112 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | extracellular | Seq ID 113 & 114 |
| | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | extracellular | Seq ID 115 & 116 |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | extracellular | Seq ID 117 & 118 |
| 15 | 411558 | AA102670 | Hs.70725 | gamma-aminobutyric acid (GABA) A recepto | | Seq ID 119 & 120 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | | Seq ID 121 & 122 |
| | 428398 | AI249368 | Hs.98558 | ESTs | | Seq ID 123 & 124 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | plasma membrane | Seq ID 125 & 126 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | | Seq ID 127 & 128 |
| | 412970 | AB026436 | Hs.177534 | dual specificity phosphatase 10 | | Seq ID 129 & 130 |
| 20 | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | extracellular | Seq ID 131 & 132 |
| | 415752 | BE314524 | Hs.78776 | putative transmembrane protein | | Seq ID 133 & 134 |
| | 444051 | N48373 | Hs.10247 | activated leucocyte cell adhesion molecu | | Seq ID 135 & 136 |
| | 451110 | AI955040 | Hs.265398 | ESTs, Weakly similar to transformation-r | | Seq ID 137 & 138 |

TABLE 24A

Table 24A shows the accession numbers for those pkeys lacking unigeneID's for Table 24. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15 Pkey CAT number Accession
 335824 CH22_3197FG_619_11_LINK_E
 325372 c12_hs

TABLE 24B

5 **Table 24B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 24. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

15

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-------------|
| 404561 | 9795980 | Minus | 69039-70100 |

20

Table 25

The 69 gene sequences identified to be overexpressed in breast cancer may be used to identify coding regions from the public DNA databases (nr and htgs in Genbank). The sequences may be used to either identify genes that encode known proteins, or they may be used to predict the coding regions from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev, 2000, Genome Res. 10:516-522)

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #:

FGENESH predicted ORF

Coding sequence: 1-1518 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCCT CTGGCTTCA GGAATCATG GCTCAACCCT TCTTGCTGCT GATCCTCTC 60
TGCATGTCTC TGCTGCTGTT TCAGGTAATC AGGTTGTACC AGAGGAGGAG ATGGAATGATC 120
AGAGCCCTGC ACCTGTTTCC TGCACCCCT GCCCACTGGT TCTATGGCCA CAAGGAGTTT 180
TACCCAGTAA AGGAGTTTGA GGTGTATCAT AAGCTGATGG AAAAATACCC ATGTGCTGTT 240
CCCTGTGGG TTGGACCTT TACGATGTTT TACAGTGTCC ATGACCCAGA CTATGCCAAG 300
ATTCTCTGA AAAGACAAGA TCCCAAAAGT GCTGTAGGCC ACAAATCTCT TGAATCTCTG 360
GTTGGTCGAG GACTTGTGAC CCTGGATGGT TCTAAATGGA AAAAGCACCG CCAGATTGTG 420
AAACCTGGCT TCAACATCAG CATCTGAAA ATATTTCATCA CCATGATGTC TGAGAGTGTT 480
CGGATGATGC TGAACAAATG GGAGGAACGC ATTGCCAAA ACTCACGTCT GGAGCTCTTT 540
CAACATGTCT CCTGATGAC CCTGGACAGC ATCATGAAAT GTGCCTTCAG CCACGAGGGC 600
AGCATCCAGT TGGACAGTAC CCTGGATCTA TACCTGAAAG CAGTGTTCAA CCTAGCAAAA 660
ATCTCAACC AGCGCATGAA CAATTTTCTA CATCAACACG ACCTGGTTT CAAATTCAGC 720
TCTCAAGGCC AAATCTTTT TAAATTTAAC CAAGAACTTC ATCAGTTCAC AGAGAAAAGTA 780
ATCCAGGACC GGAAGGAGTC TCTTAAGGAT AAGCTAAAAC AAGATACTAC TCAGAAAAGG 840
CGCTGGGATT TTCTGGACAT ACTTTTGAGT GCCAAAAGCG AAAACACCAA AGATTTCTCT 900
GAAGCAGATC TCCAGGCTGA AGTGAAAACG TTATGTTTG CAGGACATGA CACCACATCC 960
AGTGCTATCT CCTGGATCTT TACTGCTTG GCAAAGTACC CTGAGCATCA GCAGAGATGC 1020
CGAGATGAAA TCAGGGAATC CTAAGGGGAT GGGTCTTCTA TTACTGGGGA ACACCTGAGC 1080
CAGATGCCTT ACACCAAGAT GTGCATCAAG GAATGCCTCC GCCTCTACGC ACCGGTAGTA 1140
AACATATCCC GGTACTCGA CAAACCCATC ACCTTTCCAG ATGGACGCTC CTAACCTGCA 1200
GGAATAACTG TGTATTATCA TATTTGGGCT CTTCACCACA ACCCTATTT CTGGGAAGAC 1260
CCTCAGGTCT TTAACCCCTT GAGATTCTCC AGGGAATAAT CTGAAAAAAT ACATCCTAT 1320
GCCTTCAATC CATTCTCAGC TGGATTAAGG AACTGCATTG GGCAGCATTT TGCCATAATT 1380
GAGTGTAAGC AGGCGATGGC ATTAAGTCTG CTCCGCTTCA AGCTGGCTCC AGACCACTCA 1440
AGGCTCCCC AGCCTGTTGG TCAAGTTGTC CTCAAGTCCA AGAATGGAAT CCATGTGTTT 1500
GCAAAAAAAG TTGCTAATT TTAAGTCTCT TCGTATAAGA ATTAATGAGA CAATTTTCCT 1560
ACCAAAGGAA GAACAAAAGG ATAAATATAA TACAAAATAT ATGTATATGG TTGTTTGACA 1620
AATTATATAA CTTAGGATAC TTCTGACTGG TTTTGACATC CATTACAGT AATTTTAATT 1680
TCTTTGCTGT ATCTGGTGAA ACCCACAAAA ACACCTGAAA AAACCAAGC TGACTTCCAC 1740
TGCGAAGGGA AATTATTGGT TTGTGTAAT AGTGGTAGAG TGGCTTTCAA GCATAGTTT 1800
ATCAAACTC CACTCAGTAT CTGCATTACT TTTATCTCTG CAAATATCTG CATGATAGCT 1860
TTATTCTCAG TTATCTTTC CCAATAATAA AAAA

```

Seq ID NO: 2 Protein sequence

Protein Accession #:

FGENESH predicted

```

1      11      21      31      41      51
|      |      |      |      |      |
MEPSWLQELM AHPFLLLILL CMSLLLFQVI RLYQRRRWMI RALHLFPAPP AHWFYGHKEF 60
YPVKEFEVYH KLMEKYPCAV PLWVGPFMTF FSVHDPDYAK ILLKRQDPKS AVSHKILES 120
VGRGLVTLTG SKWKKHQIV KPGFNISILK IFITMMSSEV RMMLNKWEER IAQNSRLELF 180
QHVSLMTLDS IMKCAFHQG SIQLDSTLDS YLKA VFNLSK ISNQRNMNFI HHNDLVFKFS 240
SQGQIFSKFN QELHQFTEK V IQDRKESLKD KLKQDTTQKR RWDFLDILLS AKSENTKDFS 300
EADLQAEVKT FMFAGHDTTS SAISWILYCL AKYPEHQQR CDEIRELLGD GSSITWEHLS 360
QMPYTTMCIK ECLRLYAPVV NISRLLDKPI TFPDGRSLPA GITVFINTWA LHHNPFYFWD 420
PQVFNPLRFS RENSEKHPY AFIPFSAGLR NCIGQHFAL ECKVAVALTL LRFKLAPDHS 480
RPPQVRQVV LKSKNGIHVF AKKVC

```

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #:

NM_052997

Coding sequence: 100-4125 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CTAGTCTATA CCAGCAACGA CTCCTACATC GTCCACTCTG GGGATCTTAG AAAGATCCAT 60
AAAGCTGCTC CCGGGGACA AGTCCGGAAG CTGGAGAAGA TGACAAAGAG GAAGAAGACC 120
ATCAACCTTA ATATACAAGA CGCCAGAGA AGGACTGCTC TACACTGGGC CTGTGCTAAT 180
GGCCATGAGG AAGTAGTAAC ATTTCTGGTA GACAGAAAGT GCCAGCTTGA CGTCTTGTAT 240
GGCGAACACA GGACACCTCT GATGAAGGCT CTACAATGCC ATCAGGAGGC TTGTGCAAT 300
ATTCTGATAG ATTCTGGTGC CGATATAAAT CTCGTAGATG TGTATGGCAA CATGGCTCTC 360
CATATGCTG TTTATAGTGA GATTTGTGCA GTGGTGGCAA AACTGCTGTC CCATGGTGCA 420
GTCATCGAAG TGACAACAA GGCTAGCCTC ACACCACTTT TACTATCCAT AACGAAAAGA 480

```


AGTGAGCAAA TTGTGGAATT TTTGCTGATA AAAAAAGCAA ATGCGAATGC AGTTAATAAG 540
 TATAAATGCA CAGCCCTCAT GCTTGTCTGTA TGTCATGGAT CATCAGAGAT AGTTGGCATG 600
 CTCTTCAGC AAAATGTTGA CGTCTTTGCT GCAGATATAT GTGGAGTAAC TGCAGAACAT 660
 5 TATGCTGTTA CTGTGGATT TCATCACATT CATGAACAAA TTATGGAATA TATACGAAAA 720
 TTATCTAAAA ATCATCAAAA TACCAATCCA GAAGGAACAT CTGCAGGAAC ACCTGATGAG 780
 GCTGCCACCT TGGCGGAAAG AACACCTGAC ACAGCTGAAA GCTTGGTGGG AAAAAACCT 840
 GATGAGGCTG CACCCTTGGT GGAAAGAAAC CCTGACACGG CTGAAAGCTT GGTGGAAAAA 900
 ACACCTGATG AGGCTGCATC CTGGTGGAG GGAACATCTG AAAAAATTCA ATGTTTGGAG 960
 10 AAAGCGACAT CTGGAAGATT CGAACAGTCA GCAGAAGAAA CACCTAGGGA AATTACGAGT 1020
 CCTGCAAAAG AACATCTGA GAAATTTACG TGGCCAGCAA AAGGAAGACC TAGGAAGATC 1080
 GCATGGGAGA AAAAAAGA CACACCTAGG GAAATTATGA GTCCCGCAAA AGAAACATCT 1140
 GAGAAATTTA CGTGGGAGC AAAAGGAAGA CCTAGGAAGA TCGCATGGGA GAAAAAGAA 1200
 ACACCTGTAA AGACTGGATG CGTGGCAAGA GTAACATCTA ATAAAACTAA AGTTTGGAA 1260
 15 AAAGGAAGAT CTAAGATGAT TGCATGTCCT AAAAAAGAAT CATCTACAAA AGCAAGTGCC 1320
 AATGATCAGA GGTTCCTCAT AGAATCCAAA CAAGAGGAAG ATGAAGAATA TTCTTGTGAT 1380
 TCTCGGAGTC TCTTGGAGAG TTCTGCAAG ATTCAAGTGT GTATACCTGA TCTATATAT 1440
 CAAAAATGTA TGGAGATAAA TAGAGAAGTA GAAGAGCCTC CTAAGAAGCC ATCTGCCTTC 1500
 AAGCTTGCCA TTGAAATGCA AAACCTGTGT CCAATAAAG CTTTGAATT GAAGAATGAA 1560
 CAAACATTGA GAGCAGATCC GATGTTCCCA CCAGAATCCA AAAAAAGGA CTATGAAGAA 1620
 20 AATCTTGGG ATCTGAGAG TCTCTGTGAG ACTGTTTCAC AGAAGGATGT GTGTTTACCC 1680
 AAGGCTACAC ATCAAAAAA AATAGATAAA ATAAATGGAA AATTAGAAGA GTCTCCTAAT 1740
 AAAGATGGTC TCTGAAAGGC TACCTGCGGA ATGAAAGTTC CTATTCACAA TAAAGCCTTA 1800
 GAATGAAGG ACATGCAAA TTTCAAAGCG GAGCCTCCGG GGAAGCCATC TGCCTTCGAG 1860
 25 CTGCGCACTG AAATGCAAAA GTCTGTCCCA AATAAAGCCT TGGAAATGAA AAATGAACAA 1920
 ACATGGAGAG CAGATGAGAT ACTCCCATCA GAATCCAAAC AAAAGGACTA TGAAGAAAAA 1980
 TCTTGGGATA CTGAGAGTCT CTGTGAGACT GTTTCACAGA AGGATGTGTG TTTACCCAAG 2040
 GCTGCGCATC AAAAAAGAA AGATAAAATA AATGGAAAT TAGAAGGGTC TCTGTGTTAA 2100
 GATGCTCTC TGAAGGCTAA CTGCGGAATG AAAGTTTCTA TTCCAACTAA AGCCTTAGAA 2160
 30 TTGATGGACA TGCAAACTTT CAAAGCAGAG CCTCCCGAGA AGCCATCTGC CTTGCGCCT 2220
 GCCATTGAAA TGCAAAAGTC TGTTCCAAAT AAAGCCTTGG AATTGAAGAA TGAACAAACA 2280
 TTGAGAGCAG ATGAGATACT CCCATCAGAA TCCAAACAAA AGGACTATGA AGAAAGTTCT 2340
 TGGGATTCTG AGAGTCTCTG TGAGACTGTT TCACAGAAGG ATGTGTGTTT ACCCAAGGCT 2400
 ACACATCAAA AAGAAATAGA TAAATATAAT GGAATTTAG AAGAGTCTCC TGATAATGAT 2460
 35 GGTTTTCTGA AGGCTCCCTG CAGAATGAAA GTTCTATTTC CAACTAAAGC CTAGAATTG 2520
 ATGGACATGC AAACCTTTCA AGCAGAGCCT CCCGAGAAGC CATCTGCCTT CGAGCCTGCC 2580
 ATTGAATGC AAAAGTCTGT TCCAAATAAA GCCTTGAAT TGAAGAATGA ACAAACATTG 2640
 AGAGCAGATC AGATGTTCCC TTCAGAATCA AAACAAAAGA AGGTGAAGA AAATCTTGG 2700
 GATCTGAGA GTCTCCGTGA GACTGTTTCA CAGAAGGATG TGTGTGTACC CAAGGCTACA 2760
 40 CATCAAAAAG AAATGGATAA AATAAGTGA AAATTAGAAG ATTCAACTAG CCTATCAAAA 2820
 ATCTTGGATA CAGTTCAATC TTGTGAAAGA GCAAGGGAAC TTCAAAAAGA TCACTGTGAA 2880
 CAACTGACAG GAAAAATGGA ACAAATGAAA AAGAAGTTTT GTGTACTGAA AAAGAACTG 2940
 TCAGAAGCAA AAGAAATAAA ATCACAGTTA GAGAACCAAA AAGTTAAATG GGAACAAGAG 3000
 CTCTGCACTG TGAGATTGAC TTTAAACCAA GAAGAAGAGA AGAGAAGAAA TGCCGATATA 3060
 45 TTAATGAAA AAATTAGGGA AGAATTAGGA AGAATCGAAG AGCAGCATAG GAAAGAGTTA 3120
 GAAAGTAAAC ACAAACCTGA ACAGGCTCTC AGAATACAAG ATATAGAATT GAAGAGTGTA 3180
 GAAAGTAATT TGAATCAGGT TTCTCACTC CATGAAAATG AAAATTATCT CTTACATGAA 3240
 AATTGCACTG TGAAGAAAGA AATTGCCATG CTAAGACTGG AAATAGCCAC ACTGAAACAC 3300
 CAATACCAGG AAAAGGAAA TAAATCTTT GAGGACATTA AGATTTTAAA AGAAAAAGAT 3360
 50 GCTGAACTTC AGATGACCCT AAAACTGAAA GAGGAATCAT TAATAAAAAG GGCATCTCAA 3420
 TATAGTGGGC AGCTTAAAGT TCTGATAGCT GAGAACACAA TGCTCACTTC TAAATTGAAG 3480
 GAAAAACAAG ACAAAGAAAT ACTAGAGGCA GAAATTGAAT CACACCATCC TAGACTGGCT 3540
 TCTGCTGTAC AAGACCATGA TCAAAATTGT ACATCAAGAA AAAGTCAAGA ACCTGCTTTC 3600
 CACATTGACG GAGATGCTTG TTTGCAAGA AAAATGAATG TTGATGTGAG TAGTAEGATA 3660
 55 TATACAATG AGGTGCTCCA TCAACCATT TCTGAAGCTC AAAGGAAATC CAAAAGCCTA 3720
 AAAATTATC TCAATTATGC AGGAGATGCT CTAAGAGAAA ATACATTGGT TTCAGAACAT 3780
 GCACAAAGAG ACCAACGTGA AACACAGTGT CAAATGAAGG AAGCTGAACA CATGTATCAA 3840
 AACGAACAAG ATAATGTGAA CAAACACACT GAACAGCAGG AGTCTCTAGA TCAGAAATTA 3900
 TTTCAACTAC AAAGCAAAAA TATGTGGCTT CAACAGCAAT TAGTTCATGC ACATAAGAAA 3960
 60 GCTGACAACA AAAGCAAGAT AACAATTGAT ATTCATTTTC TTGAGAGGAA AATGCAACAT 4020
 CATCTCCTAA AAGAGAAAAA TGAGGAGATA TTAAATTACA ATAACCATTT AAAAAACCGT 4080
 ATATATCAAT ATGAAAAAGA GAAAGCAGAA ACAGAAAAC CATGAGAGAC AAGCAGTAAG 4140
 AAACCTCTTT TGGAGAAACA ACAGACCAGA TCTTACTCA CAACATATGC TAGGAGGCCA 4200
 GTCTAGCAT CACCTATGT TGAAATCTT ACCAATAGTC TGTGTCAACA GAATACTTAT 4260
 65 TTTAGAGAAA AAATTCAATG TTCTTCTG AAGCCTACAG ACATAAAATA ACAGTGTGAA 4320
 GAATTACTTG TTCACGAAT GCATAAAGCT GCACAGGATT CCACTCTACC CTGATGATGC 4380
 AGCAGACATC ATCAATCCA ACCAGAACTT CGCTCTGCAC TCCAGCCTAG GTGACAGAGT 4440
 GAGACTCCAC CTCGAAA

70 Seq ID NO: 4 Protein sequence;
 Protein Accession #: NP_443723.1

75 1 11 21 31 41 51
 MTKRKRITNL NIQDAQKRTA LHWACVNGHE EVVTFVLDRK QOLDVLDGEH RTPLMKALQC 60
 HQEACANILI DSGADINLVD VYGNMALHYA VYSEILSVVA KLLSHGAVIE VHNKASLTPL 120
 LLSITRSEQ IVEFLLIKNA NANA VNKYKC TALMLAVCHG SSEIVGMLLQ QNVDFVAADI 180

CGVTAEHYAV TCGFHHIHEQ IMEYIRKLSK NHQNTNPEGT SAGTPDEAAP LAERTPDTA 240
 SLVEKTPDEA APLVERTPDT AESLVEKTPD EAASLVEGTS DKIQCLEKAT SGKFEQSAEE 300
 TPREITPAK ETSEKFTWPA KGRPRKIAWE KKEDTPREIM SPAKETSEKF TWAAGRPRK 360
 IAWKEKTPV KTGCVARVTS NKTKVLEKGR SKMIACPTKE SSTKASANDQ RFPSESKQEE 420
 DEEYSCDSRS LFESSAKIQV CIPESYQKV MEINREVEEP PKKPSAFKPA IEMQNSVPNK 480
 AFELKNEQTL RADPMFPPE KQKDYEENSW DSESLCETVS QKDVCPLKAT HQKEIDKING 540
 KLEESPNKDG LLKATCGMKV SIPTKALELK DMQTFKAEP GKPSAFEPAT EMQKSVPNKA 600
 LELKNEQTWR ADEILPESK QKDYEENSWD TESLCETVSQ KDVCLPKAAH QKEIDKINGK 660
 LEGSPVKDGL LKANCGRMKVS IPTKALELMD MQTFKAEPPE KPSAFEPAT MQKSVPNKAL 720
 ELKNEQTLRA DEILPESKQ KDYESSWDS ESLCETVSQK DVCLPKATHQ KEIDKINGKL 780
 EESPDNDGFL KAPCRMKVS PTKALELMDM QTFKAEPPEK PSAFEPAT MQKSVPNKALE 840
 LKNEQTLRAD QMFPSKQK KVEENSWDSE SLRETVSQKD VCVPKATHQK EMDKISGKLE 900
 DSTLSKILD TVHSCERARE LQKDHCEQRT GKMEQMKKKF CVLKKKLSEA KEIKSQLENQ 960
 KVKWEQELCS VRLTLNQEEE KRRNADILNE KIREELGRIE EQHRKELEVQ QQLEQALRIQ 1020
 DIELKSVESN LNQVSHTHEN ENYLLHENCM LKKEIAMKL EIALTKHQYQ EKENYFEDI 1080
 KULKKEKNAEL QMTLKLKKEE LTKRASQYSQ QLKVLIAENT MLTSKLEKQK DKEILEAIE 1140
 SHHPRLASA V QDHDQIVTSR KQEPAFHIA GDAQLQRKMN VDVSTTYNN EVLHQPLSEA 1200
 QRKSKSLKIN LNYAGDALRE NTLVSEHAQR DQRETQCMK EAEHMYQNEQ DNVNKHTEQQ 1260
 ESLDQKLFLQ QSKNMWVQQ LVHAHKKADN KSKITIDIHF LERKMQHLL KEKNEEIFNY 1320
 NNHLKNRIYQ YEKEKAETEN S

Seq ID NO: 5 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 273-1785 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCGGGGGCG GGAAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGGCGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCGGGAG CGCAGCGCG GGTGGAGTT CAGCCTACTC TTCTTAGAT 120
 GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA TGTACAAGCC 240
 TGCATAAGT GAGAAGGAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCAGAAAGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480
 GGTGCGCTGA GACTAGAAGG CTCAGATTTT CAGTGTGGG ACACCTCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATCTCT CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
 CTGCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 ATATCTGTGA CTGTCTGTAG TTGCTCTTG GTCCTTATCA TATTATTTTG TTAATCCCG 720
 TATAAAGAGC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAGCTTAC 780
 ATTCTCTCT GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
 TCAGGCTCC CTCTGCTGTG CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900
 ATTGAAAAAG TCGCTATGG GGAAGTTTG ATGGGAAAGT GGCGTGGCGA AAGGTAGCT 960
 GTGAAAGTG TCTTACCAC AGAGGAAGCC AGCTGGTCA GAGAGACAGA AATATATCAG 1020
 ACAGTGTGA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
 GGTCCCTGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200
 AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGAAAAAGTA AAACATTTCT GTGAAGAAAA ATGGAAGTTG CTGTATIGCT 1320
 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGATTG GCACCAAGC CTATATGCCT CCAGAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
 CTAGTGGCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTTGCCA AAATGTGAGA GTCCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGCTTC CAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTGTA GCGGAGAAA COGTTGGGTA ACTTGTTCAA GATATGATGC AT

Seq ID NO: 6 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIEED 60
 DSGLPVVTSG CLGLEGDFQ CRDTPPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
 GPIHRLALI SVTVCSLLLV LILFCYFRY KRQETPRYS IGLEQDETYI PPGESLRDLI 180
 EQSSSGSGS GLPLLVRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTTEAS 240
 WFRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLTD YHENGSLYDY LKSTLTDKAS 300
 MLKLAYSVS GLCHLHTEIF STQGPPIAH RDLKSKNIV KKNGTCCIAI LGLAVKFISD 360
 TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGILWEV ARRCVSGGIV 420

EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480
RLTALRVKKT LAKMSESQDI KL

5 Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: none found
Coding sequence: 482-3007(underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
| | | | |
AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGCTGC AGCTTGGATC 60
TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC 120
TGCATTGAGC AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180
ATGCCGTGAA TTTTAAATGA GGGAAAAAGG GACAATTGCT TCAGGATGCT CTAGTATGCA 240
CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTTAA 300
CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTGA GAAGAAAGTA CGCAGTGGTT 360
GGTGTITTTCT TTTTITTAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC 420
ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAAT CGGATTTTCAT CACATGACAA 480
CATGAAGCTG TGGATTCTAT TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540
CCAAACTCCA GTGCTCTCAT CCAGAGGGCTC TTGTGATTCT CTTTGAATT GTGAGGAAAA 600
AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660
TGTGCCACCA TCACGACCTT TCCAACCTAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA 720
CACAAATGAC TTTTCTGGGC TTACCAATGC TATTTCAATA CACCTTGGAT TTAACAATAT 780
TGACAGATTG GAGATAGGTG CATTTAATGG CCTTGGCCTC CTGAAACAAC TTCATATCAA 840
TCACAATTCT TTAGAAATTC TTAAGAGGGA TACTTTCCAT GGACTGGAAA ACCTGGAAAT 900
CCTGCAAGCA GATAACAATT TTATCACAGT GATTGAACCA AGTGCTTTA GCAAGCTCAA 960
CAGACTCAAA GTGTAAATTT TAAATGACAA TGCTATTGAG AGTCTTCTC CAAACATCTT 1020
CCGATTTTGT CCTTTAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA 1080
TGTGTGTTT CTCGAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAAATG 1140
GGCCTGCAAT TGTGACTTAT TGCAGTTAAA AACTTGGTTG GAGAACATGC CTCACAGTCT 1200
TATAATTTGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG 1260
ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCTTC 1320
AGGATCATTAT CATCTGGCAG CAACATCTTC AATAAATGAT AGTCGCATGT CAACTAAGAC 1380
CACGTCCATT TAAAACTAC CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC 1440
ATCCACTCAA CTTCAGGAC CTTACTGCC TATTCTTGT AACTGCAAAG TCCTATCCCC 1500
ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC 1560
TCCTCCGCAA AATCCTAGAA AGTCTATCT AGCGGGAAAT ATTATTCACA GTTTAATGAA 1620
GTCTGATCTA GTGGAATATT TCACITTTGA AATGCTTAC TTGGGAAACA ATCGTATTGA 1680
AGTTCITGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAACTCT ATCTAAATGG 1740
TAACCACTG ACCAAATTA GAAAGGCAT GTTCTTGGT CTCATAATC TTGAATACTT 1800
ATATCTTGAA TACAATGCCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCTTAA 1860
ACTTAAAGTC CTGTATTTTA ATAACAACCT CCTCCAAGTT TTACCACCAC ATATTTTTTC 1920
AGGGGTTCTT CTAACCTAAG TAAATCTTAA AACAAACCAG TTTACCCATC TACCTGTAAG 1980
TAATATTTTG GATGATCTTG ATTTACTAAC CCAGATTGAC CTTGAGGATA ACCCTGGGA 2040
CTGCTCTGT GACTGTTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100
GACAGATGAC ATCCTCTGCA CTTCCCCCGG GCATCTCGAC AAAAAGGAAT TGAAGGCCCT 2160
AAATAGTGAA ATTCTCTGTC CAGGTTTAGT AAATAACCCA TCCATGCCAA CACAGACTAG 2220
TTACCTTATG GTCACCACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280
TCTTACGGAC GCTGTGCCAC TGCTGTCTT AATATTGGGA CTCTGATTA TGTTATCAC 2340
TATGTTTTTC TGTGCTGAG GGATAGTGGT TCTTGTCTT CACCGCAGGA GAAGATACAA 2400
AAAGAAACAA GTAGATGAGC AAATGAGAGA CAACAGTCCT GTGCATCTC AGTACAGCAT 2460
GTATGGCCAT AAAACCACTC ATCACACTAC TGAAGAGCCC TCTGCCTCAC TCTATGAACA 2520
GCACATGGTG AGCCCCATGG TTATGTCTA TAGAAGTCCA TCCITTTGTC CAAAGCATCT 2580
GGAAGAGGAA GAAGAGAGGA ATGAGAAAGA AGGAAGTGAT GCAAAACATC TCCAAAGAA 2640
TCTTTTGGAA CAGGAAAAATC ATTCACCACT CACAGGGTCA AATATGAAAT AAAAAACCAC 2700
GAACCAATCA ACAGAAATTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT 2760
AGAAAAAGAA AGGGAACCTC AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC 2820
TCAGCTCCAG CCTGATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880
GGAAACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940
TTTTGAACIT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA 3000
AACATAGATG GAGAGTTTGA GGGCTTTGCG AGAAATGCTG TGATTCTGTT TTAAGTCCAT 3060
ACCTTGTAAT TAAGTGCTT ACGTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120
AECTATGGGG AAAAAAAGG AAGAAGAAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180
GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCCTTGCA TGTAATAT

Seq ID NO: 8 Protein sequence:
Protein Accession #: none found

70 1 11 21 31 41 51
| | | | |
MKLWIHLFYS SLLACISLHS QTPVLSSRG SCDSLCNCEEK DGTMLNCEA KGIKMYSEIS 60
VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIHGFFNNI ADIEIGAFNG LGLLKQLHIN 120
HNSLEILKED TFHGLENLFF LQADNNFITV IEPFAFSKLN RLKVLILNDN AIESLPPNIF 180
75 RFVPLTHLDL RGNQLQTLFY VGFLEHIGRI LDQLLEDNWK ACNCDLLQK TWLENMPPQS 240
IIGDVVCNSP PFFKGSILSR LKKEICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT 300
TSILKLPTKA PGLPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP 360

PPQNPRKLIL AGNIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG 420
 NHLTKLSKGM FLGLHNLLEYL YLEYNAIKEI LPGTFNPMPK LKVLVYLNNNL LQVLPPIHFS 480
 GVPLTKVNLK TNQFTHLPVS NILDDLDDLT QIDLEDNPWD CSCDLVGLQQ WIKLSKNTV 540
 TDDILCTSPG HLDKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS 600
 5 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660
 YGKHTTHHTT ERPSASLYEQ HMVSPMVHVY RSPSPGPKHL EEEEEERNEKE GSDAKHLQRS 720
 LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA 780
 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ 840
 T
 10
 Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: NM_003474
 Coding sequence: 307-3036 (underlined sequences correspond to start and stop codons)
 15
 1 11 21 31 41 51
 | | | | |
 CACTAACGCT CTTCCTAGTC CCCGGGCCAA CTCGGACAGT TTGCTCATTT ATTGCAACGG 60
 TCAAGGCTGG CTGTGCGCAG AACGGGCGCG GCGGACGCA CGCACACACA CGGGGGGAAA 120
 20 CTTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGGCGGC GCGGGCCGTG CGCGAGGGCT 180
 COGGAGCTGA CTCGCGGAGG CAGGAAATCC CTCGGTGC GACGCCGCGC CCCGCTCGGC 240
 GCCCGGTGG GATGGTGCAG CGCTCGCCGC CGGGCCGAG AGCTGCTGCA CTGAAGGCCG 300
 GCGACGATGG CAGCGCGCCC GCTGCCCGTG TCCGCCGCC GCGCCCTCCT GCTCGCCCTG 360
 GCGGTGCTC TGCTCGCGCC CTGCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA 420
 25 GCTGATGAAG TTGTCACTGC CTCTGTTCCG AGTGGGGACC TCTGGATCCC AGTGAAGAGC 480
 TTCGACTCCA AGAATCATCC AGAAGTCTG AATATTGAC TACAACGGGA AAGCAAAGAA 540
 CTGATCATAA ATCTGGAAG AAATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC 600
 TATCTGCAAG ACGGTACTGA TGTCTCCCTC GCTCGAAAAT ACACGGTAAT TCTGGGTAC 660
 TGTTACTACC ATGGACATG ACGGGGATAT TCTGATTCAG CAGTCAGTCT CAGCACGTGT 720
 30 TCTGGTCTCA GGGGACTTAT TGTGTTTGA AATGAAGCT ATGCTTAGA ACCAATGAAA 780
 AGTGCAACCA ACAGATACAA ACTCTTCCA GCGAAGAAGC TGAAGAAGCT CGGGGGATCA 840
 TGTGGATCAC ATCACAACAC ACCAAACCTC GCTGCAAGA ATGTGTTTCC ACCACCTCT 900
 CAGACATGGG CAAGAAGGCA TAAAGAGAG ACCTCAAGG CAACTAAGTA TGTGGAGCTG 960
 GTGATCGTGG CAGACAACCG AGAGTTTCAG AGGCAAGGAA AAGATCTGGA AAAAGTTAAG 1020
 35 CAGCGATTAA TAGAGATTGC TAATCACGTT GACAAGTTT ACAGACCACT GAACATTCGG 1080
 ATCGTGTGG TAGGCGTGA AGTGTGGAAT GACATGGACA AATGCTCTGT AAGTCAGGAC 1140
 CCATTACCA GCCTCCACG GTACCCATT CCCATGGTGT TCAGCAGTTC CAGCAGGAAG 1200
 TCOCATGACA ATGCGCAGCT TGTCACTGGG GTTTATTTC AAGGGACCAC CATCGGCATG 1260
 40 GCCCAATCA TGAGCATGT CACGGCAGC CAGTCTGGG GAATTGTCAT GGACCATTC 1320
 GACAATCCCC TTGGTGCAGC CGTGACCTG GCACATGAGC TGGGCCACAA TTTGGGATG 1380
 AATCATGACA CACTGGACAG GGGCTGTAGC TGTCAAATGG CGGTTGAGAA AGGAGGCTGC 1440
 ATCATGAACG CTCCACCGG GTACCCATT CCCATGGTGT TCAGCAGTTC CAGCAGGAAG 1500
 GACTTGGAGA CAGCCTGGA GAAAGGAATG GGGGTGTGCC TGTTAACCT GCCGGAAGTC 1560
 45 AGGGAGTCTT TCGGGGCCA GAAGTGTGG AACAGATTG TGAAGAAGG AGAGGAGTGT 1620
 GACTGTGGG AGCCAGAGGA ATGTATGAAT CGTGTGTC AATGCCACAC CTGTACCTG 1680
 AAGCCGGACG CTGTGTGCGC ACATGGGCTG TGCTGTGAAG ACTGCCAGCT GAAGCCTGCA 1740
 GGAACAGCGT GCAGGGACTC CAGCAACTCC TGTGACCTCC CAGAGTTCTG CACAGGGGCC 1800
 AGCCCTCACT GCCAGCCAA CGTGAOCTG CACGATGGC ACTCATGTCA GGATGTGGAC 1860
 50 GGCTACTGCT ACAATGGCAT CTGCCAGCT CACGAGCAGC AGTGTGTAC ACTCTGGGGA 1920
 CCAGGTGCTA AACCTCCCTC TGGGATCTGC TTTGAGAGAG TCAATTCTGC AGGTGATCT 1980
 TATGGCAACT GTGGCAAGAT CTCGAAGAGT TCCTTTGCCA AATGCGAGAT GAGAGATGCT 2040
 AAATGTGGAA AAATCCAGT TCAAGGAGT GCCAGCGGC CAGTCATTGG TACCAATGCC 2100
 GTTTCATAG AAACAAACAT CCCCTGCA CAGGAGGCC GGATTCTGT CCGGGGGACC 2160
 CAOGTGTACT TGGCGATGA CATGCGGAC CCAGGGCTTG TGCTTGCAAG CACAAAGTGT 2220
 55 GCAGATGGA AAATCTGCT GAATCGTCAA TGTCAAATA TTAGTGTCT TGGGGTTTCA 2280
 GAGTGTGCAA TGCAGTGCCA CGGCAGAGGG GTGTGCAACA ACAGGAAGAA CTGCCACTGC 2340
 GAGGCCCACT GGCACCTCC CTTCTGTGAC AAGTTGGCT TTGGAGGAAG CACAGACAGC 2400
 GGGCCCATCC GGCAGGAC TAACCAAGGT TTAACCATAG GAATCTGGT GACCATCTTG 2460
 60 TGTTCTCTTG CTGCGGAT TGTGGTTTAT CTCAAAAGGA AGACCTTGAT ACGACTGCTG 2520
 TTTACAAATA AGAAGACCAC CATTGAAAAA CTAAGGTGTG TGCGCCCTTC CCGGCCACCC 2580
 CGTGGCTTCC AACCTGTGCA GGCTCACCTC GGCCACCTTG GAAAGGCCCT GATGAGGAAG 2640
 COGCCAGATT CCTACCCACC GAAGGACAAT CCCAGGAGAT TGCTGCACTG TCAGAATGTT 2700
 GACATCAGCA GACCCCTCAA CGGCTGAAAT GTCCCTCAGC CCCAGTCAAC TCAGCGAGTG 2760
 65 CTTCCTCCCT TCCACCGGGC CCCACGTGCA CTTAGCGTCC CTGCCAGACC CCGCCAGCC 2820
 AAGCCTGCAC TTAGGCAGGC CCAGGGGACC TGTAAAGCAA ACCCCCTCA GAAGCCTCTG 2880
 CCTGCAGATC CTCTGCCAG AACAACCTCG CTCACCTATG CCTTGGCCAG GACCCAGGA 2940
 CAATGGGAGA CTGGGCTCCG CCTGGCACCC CTCAGACCTG CTCACAATA TCCACACCAA 3000
 GTGCCAGAT CCACACACAC CGCCTATATT AAGTGAAG CCGACACCTT TTTTCAACAG 3060
 TGAAGACAGA AGTTTGCACT ATCTTTCAGC TCCAGTTGGA GTTTTGTGA CCAACTTTTA 3120
 70 GGATTTTITT TAATGTTTAA AACATCATT CTATAAGAAC TTTGAGCTAC TGCCGTGCTG 3180
 GCTGTGCTGT GCTATGGTGC TCTGTCTACT TGCACAGGTA CTGTAAAT ATTAAATTTA 3240
 GCAGAATGTT GATTACAGTG CAGTGGCTG TAGTAGGCAT TTTTACCATC ACTGAGTTT 3300
 CCATGGCAGG AAGGCTGTT GTGCTTTTAG TATTTAGTG AACTTGAAT ATCTGCTTG 3360
 ATGGGATTCT GACAGGATG TGTGCTTT CTGATCAAGG CCTATTGGA AAGCAGTCCC 3420
 75 CCAACTACCC CCAGCTGTGC TTATGGTACC AGATGCAGCT CAAGAGATCC CAAGTAGAAT 3480
 CTCAGTTGAT TTTCTGGATT CCCCATCTCA GGCAGAGCC AAGGGGCTC AGGTCCAGGC 3540
 TGTGTTTGGC TTTCAGGGAG GCCCTGTGCC CTTGACAAC TGGCAGGCAG GCTCCAGGG 3600

ACACCTGGGA GAAATCTGGC TTCTGGCCAG GAAGCTTTGG TGAGAACCTG GGTTCGAGAC 3660
 AGGAATCTTA AGGTGTAGCC ACACCAGGAT AGAGACTGGA AACTAGACA AGCCAGAAGT 3720
 TGACCTGAG CTGAOCAGCC GTGAGCATGT TTGGAAGGGG TCTGTAGTGT CACTCAAGGC 3780
 GGTGCTGAT AGAAATGCCA AGCACTTCTT TTCTCGCTG TCCTTTCTAG AGCACTGCCA 3840
 5 CCAAGTAGGTT ATTTAGCTTG GGAAGGTGG TGTTCCTGTA AGAAACCTAC TGCCAGGCA 3900
 CTGCAAACCG CCACCTCCCT ATACTGCTTG GAGCTGAGCA AATCACCACA AACTGTAATA 3960
 CAATGATCCT GTATTGAGC AGATGAGGAC TTTCATGGG ACCACAATA TTTTCAGATG 4020
 10 TGAACCATTA ACCAGATCTA GTCAATCAAG TCTGTTACT GCAAGGTTC ACTTATTAAC 4080
 AATTAGGCAG ACTCTTATG CTGCAAAAA CTACAACCA TGAATGTGA TGTTCATGGG 4140
 TATAGTTCAT GTCTGCTATC ATTATTCGTA GATATTGGAC AAAGAACCTT CTCTATGGGG 4200
 CATCTCTTTT TTCAACTTG GCTGCAGGAA TCTTTAAAG ATGCTTTTAA CAGAGTCTGA 4260
 15 ACCTATTTCT TAAACACTTG CAACCTACCT GTTGAGCATC ACAGAAATGTG ATAAGGAAAT 4320
 CAACITGCTT ATCAACTTCC TAAATATTAT GAGATGTGGC TTGGGCAGCA TCCCTTGAA 4380
 CTCCTCACTC TTCAAATGCC TGACTAGGGA GCCATGTTT ACAAGGTCTT TAAAGTGACT 4440
 AATGGCATGA GAAATACAAA AATACTCAGA TAAAGTAAAA TGCCATGATG CCTCTGTCTT 4500
 CTGGACTGTT TTTCACATTA GAAGACAATT GACAACAGTT ACATAATTCA CTCTGAGTGT 4560
 TTTATGAGAA AGCCTTCTTT TGGGGTCAAC AGTTTCTTA TGCTTGAAA CAGAAAAATA 4620
 TGTACCAAGA ATCTTGGTTT GCCTCCAGA AAACAAAACT GCATTTCACT TTCCCGTGT 4680
 20 TCCCACTGT ATCTAGGCAA CATAGTATTC ATGACTATGG ATAAACTAAA CACGTGACAC 4740
 AAACACACAC AAAAGGGAAC CCAGCTCTAA TACATTCOA CTCGTATAGC ATGCATCTGT 4800
 TTTATCTATA GTTATTAAGT TCTTTAAAT GTAAAGCAT GCTGAAAAAT AATACTGCTG 4860
 AGATACATAC AGAATTACTG TAACGTATTA CACTTGGTAA TTGTACTAAA GCCAACATA 4920
 TATATACTAT TAAAAAGGTT TACAGAATTT TATGGTGCAT TACGTGGGCA TGTCTTTT 4980
 25 AGATGCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCT CCAATTATA GAGGATATGA 5040
 ACCAAAAAAA AAAAAAAAAA AA

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_003465.2

30 1 11 21 31 41 51
 | | | | |
 MAARPLPVP ARALLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSR DLWIPVKSFD 60
 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTEHYL QDGTDVSLAR NYTVILGHY 120
 35 YHGHVGRGSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLPFAK KLSVRGSGC 180
 SHHNTPLNLA KNPVPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLKVKQR 240
 LIEIANHVDF FYRPLNIRIV LVGVEVWDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300
 DNAQLVSGVY FQGTITGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFNMNH 360
 40 DTLDRGSCSQ MAVEKGCCIM NASTGYPPFM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE 420
 SFGGQKCGNR FVEEGEECDG GEPEECMNRC CNATTCTLKP DAVCAHGLCC EDCQLKPAQT 480
 ACRDSSNSCD LPEFTCTGAS HCPANVYLHD GHSCQDVVDY CYNGICQTHE QQCVTWLGPG 540
 AKPAPGICFE RVNSAGDPYG NOGKVSXSF AKCEMRDAKC GKIQCGGAS RPIVGTNAVS 600
 IETNPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660
 45 AMQCHGRGVC NNRKNCHCEA HWAPPCDKF GFGGSTDSPG IRQADNQGLT IGLVITLCL 720
 LAAGFVVYLL RKTILRLFT NKKTTIEKLR CVRPSRPPRG FQPCQHLGH LGKGLMRKPP 780
 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQVLP PLHRAPRAPS VPARPLPAK 840
 ALRQAGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAFLR PAPQYPHQVP 900
 RSTHTAYIK

Seq ID NO: 11 DNA sequence

Nucleic Acid Accession #: NM_001394

Coding sequence: 400-1584 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 GGCACGAGGG CTGAGCGCCG GAGGAGCGTA GGCAGGGCAG CGCTGGCGCC AGCGGCGACA 60
 GGAGCCGCGC GACCGGCAAA AATACACGGG AGGCGTGC CGAAAAAGT CCGGGTCTCT 120
 CTCTCGTAAA CACACTCTCC TCACGCGCG CCTCCCTC CGCTCTGCGC GCCGCCCGGC 180
 TGGGCGCCCG AGGCGCTCC GACTGCTATG TGACCGCGAG GCTGCGGGAG GAAGGGGACA 240
 60 GGAAGAAGA GGCTCTCCCG CGGAGCCCT TGAGGACCAA GTTTCGGGCC ACTTCTGCAG 300
 GCGTCCCTTC TTAGCTCTCG CTGCCCCCT TCTGACGCT AGGCGGCCCA GGTTCCTTC 360
 TCTTCTCGC GCGCCAGCC GCCTCGGTT CCGGCGACCA TGCTGACGAT GGAGGAGCTG 420
 CGGGAGATGG ACTGCACTGT GCTCAAAAGG CTGATGAACC GGAACGAGAA TGGCGGCGGC 480
 GCGGGCGGCA GCGGACGCA CGGCACCCCT GGGCTGCCGA GCGGCGGCAA GTGCCCTGCTG 540
 65 CTGGAAGTGA GACCGTTCTT GCGCACAGC GCGGGCTACA TCCTAGGTTT GGTCAACGTG 600
 CGCTGTAACA CCATCGTGC GCGGCGGCT AAGGGCTCCG TGAGCTGGA GCAGATCTG 660
 CCGGCGAGG AGGAGGTAG CGCCCGCTTG CGCTCGGGC TCTACTCGG GGTCTATCTG 720
 TACGACGAGC GCAGCCCGCG CGCGAGAGC CTCGCGAGG ACAGCACCGT GTCGTGGTG 780
 GTGACGCGC TCGCGCGCAA CGCGAGCGC ACCGACATCT GCCTGCTCAA AGGCGGCTAT 840
 70 GAGAGGTTT CTTCCGAGTA CCGAGAATT TGTCTAAAA CCAAGGCCCT GGCAGCCATC 900
 CCACCCCGG TTCCCCCAG CGCCACAGAG CCTTGGACC TGGGCTGCG CTCTGTGGG 960
 ACCCACTAC ACGACAGGG GGGTCTGTG GAGATCTTC CTTCTCTTA CTCTGGCAGT 1020
 GCCTACCATG CTGCCCGGAG AGCATGCTG GACGCCCTG GCATCACGGC TCTGTTGAAT 1080
 75 GTCTCTCGG ACTGCCCAA CACTTTGAA GGACACTATC AGTACAAGTG CATCCAGTG 1140
 GAAGATAACC ACAAGGCCGA CATCAGCTCC TGGTTCATGG AAGCATAGA GTACATCGAT 1200
 GCCGTGAAG ACTGCCGTGG GCGGTGCTG GTGCACTGCC AGGCGGGCAT CTCGGGCTCG 1260
 GCCACCATCT GCCTGGCCTA CTGATGATG AAGAAACGGG TGAGGCTGGA GGAGGCCTTC 1320

5 GAGTTCGTTA AGCAGGCGCG CAGCATCATC TCGCCCAACT TCAGCTTCAT GGGGCAGCTG 1380
 CTGCAGTTCC AGTCCCAGGT GCTGGCCACG TCCTGTGCTG CGGAGGCTGC TAGCCCTCG 1440
 GGACCCCTGC GGGAGCGGGG CAAGACCCCC GCCACCCCCA CCTCGCAGTT CGTCTTCAGC 1500
 TTTCCGGTCT CCGTGGGGGT GCACTCGGCC CCCAGCAGCC TGCCCTACCT GCACAGCCCC 1560
 ATCACCACCT CTCCCAGCTG TTAGAGCCGC CCGGGGGGCC CCAGAACCAG AGCTGGCTCC 1620
 CAGCAAGGGT AGGACGGGOC GCATGCGGA GAAAGTTGGG ACTGAGCAGC TGGGAGCAGG 1680
 CGACCGAGCT CCTTCCCCAT CATTTCTCTT TGGCCAACGA CGAGGCCAGC CAGAATGGCA 1740
 ATAAGGACTC CGAATACATA ATAAAAGCAA ACAGAACACT CCAACTAGA GCAATAACCG 1800
 GTGCGCAGC AGCCAGGGAA GACCTTGGTT TGGTTTATGT GTCACTTTCA CTTTTCOGAT 1860
 10 AGAAATTTCT TACCTATTT TTTAAGCAG TAAGGCTTGA AGTGATGAAA CCCACAGATC 1920
 CTAGCAAATG TGCCCAACCA GCTTTACTAA AGGGGGAGGA AGGGAGGCA AAGGGATGAG 1980
 AAGACAAGTT TCCCAAGAT GCCTGGTTCT GGGTACTTGT CCTTTTGTG TCGTGTGTG 2040
 AGTTAAAGGA ATTTCAATTT TAAAAGAAAT CTTCGAAGGT GTGGTTTCA TTTCTCAGTC 2100
 15 ACCAACAGAT GAATAATTAT GCITTAATAA AAAGTATTTA TTAAGACITT CTTCAAGTA 2160
 TGAAGTACA AAAAGTCTAG TTACAGTGGG TTTAGAATAT ATTTATGTTG ATGTCAAACA 2220
 GCTGAGCACC GTAGCATGCA GATGTCAAGG CAGTTAGGAA GTAAATGGTG TCTGTAGAT 2280
 ATGTGCAAGG TAGCATGATG AGCAACTTGA GTTGTGTGCC ACTGAGAAGC AGGCGGGTTG 2340
 GGTGGGAGGA GGAAGAAAGG GAAGAATTAG GTTGAATTG CTTTTTAAAA AAAAAAGAAA 2400
 20 AGAAAAAGAC AGCATCTCAC TATGTTGCCA AGGCTCATCT TGAGAAGCAG GCGGGTTGGG 2460
 TGGGAGGAGG AAGAAAGGGA AGAATTAGGT TTGAATTGCT TTTTAAAAA AAAA

Seq ID NO: 12 Protein sequence:

Protein Accession #: NP_001385

25 1 11 21 31 41 51
 | | | | |
 MVTMEELREM DCSVLKRLMN RDENGCGAGG SGSHGTLGLP SGGKCLLLDC RPFLAHSAGY 60
 ILGSVNVRCN TIVRRRAKGS VSLEQILPAB EEVRARLRSG LYSVIVYDE RSPRAESLRE 120
 30 DSTVSLVVQA LRRNAERTDI CLLKGGYERF SSEYPEFCSK TKALAAIPPP VPFSATEPLD 180
 LGCSSCGTPL HDQGGFVEIL PFLYLGSAHY AARRDMLDAL GITALLNVSS DCPNHFEGHY 240
 QYKCPVEDN HKADISSWFM EAIEYIDAVK DCRGRVLVHC QAGISRSATI CLAYLMMKKR 300
 VRLEEAFEFV KORRSISPN FFSMGQLLQF ESQVLATSCA AEAASPSGPL RERKTPATP 360
 TSQVFVSFPV SVGVHSAFSS LPYLHSPITT SPSC

Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 68-340 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 AGCGCCTTGC CTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60
 CACCACCATG AAGTCTTAG CAGTCCTGGT ACTCTTGGGA GTTTCATCT TCTTGGTCTC 120
 45 TGCCAGAAAT CGACAAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCCTGCTGA 180
 TGATGAAGCC CCGTATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCCTGCA ACCACCGCTG CTCTACCACT TGCTCGTAAA GACATTCCAG TTTTACCCAA 300
 ATGGGTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360
 TCTGCAATTG GGTCAAACT ATTCATGCTT CCTGTGATT CATCCAACCTA CTTACCTTGC 420
 50 CTACGATATC CCTTTATCT CTAATCAGTT TATTTCTTT CAAATAAAAA ATAATATGA 480
 GCGAGCTAAC AT

Seq ID NO: 14 Protein sequence:

Protein Accession #: none found

55 1 11 21 31 41 51
 | | | | |
 MKFLAVLVLL GVSIFLVAQ NPTTAAPADT YPATGPADDE APDAETAAA TTATTAAPT 60
 60 ATTAASTTAR KDIPVLPKWV GDLPNGRVCP

Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: NM_016640.2

Coding sequence: 39-1358 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 | | | | |
 GCITTAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAAGAT GCGGCGGCC AGGTGTTGGA 60
 70 GGCCTTTGCT ACGCGGTCCG AGGCTTTTCA TGACACCCGC GGCTAATGCC GCCGCCACGG 120
 CTACAGAAAC GACCTCCCAA GACGTGCGCG CGACCCCGCT CGCGCGGTAC CCGCCGATTG 180
 TGGCTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG GCGATCGAG CGCTGGCAGG 240
 CGACGTTGCA CGCTGCGGAG TCGGTAGACG AGAAGCTGCG AATCCTACC AAGATGCAGT 300
 75 TTATGAAGTA CATGGTTTAC CCGCAGACCT TCGCACCTGAA TGCCGACCGC TGGTACCAGT 360
 ACTTCACCAA GACGTTGTC CTGTGGGTC TGCCGCGGCC CCCAGCGGAG CCGAGCCCG 420
 AGCCCGAACC CGAACCTGAA CCGTGGCTG ACCTCGCGGC GCTGCGTGG GTGCGCTGCG 480
 ACTGCTGCT GCAGGAGCAC TTCTACCTGC GCGCAGGCG GCGGTGCAC CGTTACGAGG 540

5 AGAGCGAGGT CATATCTTTG CCCTTCCTGG ATCAOCTGGT GTCAACCCCTC GTGGGCCCTCC 600
 TCAGCCCACA CAACCCGGCC CTGGCCGCTG CCGCOCTCGA TTATAGATGC CCAAGTTCATT 660
 TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG 720
 ACTTGGGATA CCAGATAGAT GATAAACCAA ACAACAGAT TCGAATATCC AAGCAACTCG 780
 CAGAGTTTGT GCCATTGGAT TATCTGTTC CTATAGAAAT CCCCCTATA AAATGTAAAC 840
 CAGACAAACT TCCATTATTC AAACGGCAGT ATGAAAACCA CATATTTGTT GGCTCAAAAA 900
 CTGCAGATCC TTGCTGTAC GGTACACACC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960
 GGGAAAGGCT TTTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTTT AGAGCTAATG 1020
 10 CTATTGCAAG CCTTTTGTCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080
 AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT 1140
 CCTTTTCTG CTACCAAGCTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAAATAACC 1200
 CTCGTAACAA TATATGTTGG GGTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA 1260
 ATGATGTGAA AGGTTTTAAT GATGATGTTT TACTTCAGAT AGTTCACITT CTACTGAATA 1320
 15 GACCAAAAGA AGAAAATCA CAGCTGTTGG AAAACTGAAA AAGCATATTT GATTGAGAAC 1380
 TGTGGGAATA TTTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTGTA ACTGTCAACT 1440
 ATTAATAACA TTGATTTTGG AGACAAATAT TTCTTATGTC AACCTGTTAT TAGATCTCTT 1500
 ACTCTGCTCA AATTCATCAC TGAAGATTT AATTTTAGTT ACCTTTGTGTT GATTTAAAAA 1560
 TAATTGCATT TGATATA TGC TAACTGATAA GACAAATTGA GTTATTGAGC TATTAATATG 1620
 20 ACATTTTAAT ATAAATGCAG AAATCCCAA TAAAAAGCTA ACATACTGAA TTCAGTAATT 1680
 AAAAGAACCC ACTGC

Seq ID NO: 16 Protein sequence:
 Protein Accession #: NP_057724.1

25 1 11 21 31 41 51
 | | | | |
 MAAARCWRLR LRGPRLSLHT AANAAATATE TTSQDVAA TP VARYPPIVAS MTADSKAARL 60
 RRJERWQATV HAAESVDKEL RILTKMQFMK YMVYPQTFAL NADRWYQYFT KTVFLSGLPP 120
 30 PPAEPEPEPE PEPEPALDLA ALRA VACDCL LQEHFYLRRL RRVHRYEES VLSPLFDQL 180
 VSTLVGLLSP HNPALAAAAA DYRCPVHFYW VRGEIIPRG HRRGRIDDLR YQIDDKPNNQ 240
 IRISKQLAEF VPLDYSVPIE IPTIKCKPKD LPLFKRQYEN HIFVGSKTAD PCCYGHTQFH 300
 LLPDKLRRLR LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFWSAD VTRPFVSQAV 360
 35 ITDGKYSFF CYQLNTALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDVLLQ 420
 IVHLLNRPK EESQLLEN

Seq ID NO: 17 DNA sequence
 Nucleic Acid Accession #: NM_025059.1
 Coding sequence: 3-2150 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 45 GCATGAGCCT GGACTGCACC AGCCATATCG CGCTGGGTGC CGCTTCGCCA GCGCCCGAGG 60
 AAACCTACGA TCATCTTTG GAAGTCCCGG TCAOOGGGA GCAGTTAAAC CACTATCGGA 120
 ATGTGGCTCA AAATGCTCGA AGTGAACCTG CAGCAACTTT GGTCAAATTT GAATGTGCTC 180
 AGTCTGAGCT TCAAGACCTC CGATCCAAGA TGCTTTCTAA AGAAGTCTCC TGTCAGAAGC 240
 TGAAAGCTGA AATGGAGAGC TACAAGGAAA ACAAATGCCAG AAAATCATCT CTCCTTACCT 300
 50 CTTTGAGAGA CAGAGTTTCA GAACTAGAAG AAGAATCAGC AGCACTTTCC ACTTCTAAAA 360
 TCAGAACAGA AATCACAGCT CACGCTGCAA TCAAGGAGAA CCAGGAATTA AAGAAGAAA 420
 TTGTAGAGTT AAATGAAAAA TTACAAAAGT GTTCAAAAAGA AAATGAGGAG AATAAGAAAC 480
 AAGTTTCAAA GAATTGACG AGAATATGAG AATTCTGAC TCAACTGCGT GACTGCTTGG 540
 ATCCAGATGA GAGGAATGAC AAGGCATCAG ATGAAGATTT AATTTTAAAG CTTAGAGACC 600
 55 TGCGCAAGAA AAATGAATTC GTGAAAGGAC AAATTGTTAT TCTTGAAGAG ACTATAAATG 660
 TCCATGAGAT GGAAGCAAAA GCTAGCAGAG AAACGATCAT GAGGCTGGCT TCAGAAGTCA 720
 ACAGAGAGCA GAAAAAGCT GCCTCCTGTA CTGAAGAGAA AGAGAAGCTG AACCAGGACC 780
 TGCTCAGTGC TGTAGAAGCA AAAGAAGCTC TTGAAGGGA AGTTAAGATC TTCCAAGAAA 840
 GGCTGCTTGC TGCCAGCAGC GTCTGGGATG CCTCAAAGCA GGAAGTGAGC CTCTGGAAGA 900
 60 AAAGCTCTTC TGAGTTGGAG AAGAGTTTGA AGGOCAGTCA GGTGCGATC ACAACCTCAC 960
 AAAGCCAGTA CTCCTCATTT AGGGAGAAAA TCGCAGCCCT CCTTAGGGGC AGATTGAGCA 1020
 TGACTGGGTC CACTGAGGAC ACCATTTTGG AGAAGATTCT AGAATAGGAC AGCCGGGAAG 1080
 AAAGCAGGGA CCGATGGTTC TCCAGCTTG AAGCCCAAAT ATCTGAGCTT GTTGAACAGT 1140
 TGGGAAAGGA GTCTGGGTTT CACCAGAAAG CTCTCCAGAG GGCCAGAGAA GCAGAGAATA 1200
 65 TGTGGAGAGC TCTTCAAGGT CAGCTGACAC ACCTGGAGGC AGAGCTGGTT TCTGGAGGTG 1260
 TTTTGCAGCA CAACCTGAAT TTTGAGAAAC AAAAATATCT TAAATTCTG GATCAGCTTT 1320
 CTCAGAAAAT GAAGTTGGAC CAGATGGCTG CCGAAGTTGG CTITGACACG CGGCTGGACG 1380
 TGGTTTTAGC TCGAACAGAG CAGCTGGTTC GTCTGAGAG CAATGCAGTC ATTGAGAACA 1440
 AGACCAATGC CCACAAATTC CAGAGAAAGC TAAAGACACA GAAAGAGAGA CTGGAGAGCA 1500
 70 AAGAATTACA CATGAGCCTC CTCGGCAGCA AAATAGCCCA GCTGGAGGAG GAGAAGCAGG 1560
 CACGACGGC CTTGGTGTTT GAGAGGGACA ACGCGCATCT TACCATCAGG AACTTGCAGA 1620
 AGAAGGTGGA GAGGCTGCAG AAAGAGCTGA ACAOGTGTCT AGACTTGCAC ACCGAGCTCA 1680
 AAGCCAAACT GGCCGACACC AATGAATGA AGATTAACAA TTTGGAACAG ACTAAAGCCA 1740
 TTGAAGATCT AAACAAATTC AGAGACCAAC TGGAGAAGAT GAAGGAGAAA GCTGAGAAAA 1800
 75 AGCTCATGTC TGTCAGTCA GAACTGGATA CCACAGAACA TGAGGCTAAG GAGAATAAAG 1860
 AAAGGGCCAG AAACATGATA GAAGTGGTAA CCAGTGAAT GAAGACATA AAAAAATCTC 1920
 TGAAGAAGC AGAAAGAGCA GAAAAGCAGC TGGCAGACTT CAGGGAGGTG GTGTCGAGA 1980
 TGCTAGGCTT GAACGTGACC AGCCTTGCTC TTCTGATTA TGAATCATC AAGTGTCTTG 2040

AAAGATTGGT CCATTCACAT CAGCATCACT TTGTTACCTG TGCTGCCTC AAAGATGTGA 2100
 CTACTGGGCA AGAGAGGCAC CCACAAGGCC ATTTACAGCT TCTTCATTGA AACTGTATC 2160
 TCTTGAGAGA GGTGGCCATA AGACATGGCA CACAATCCC AATTTCACAA ATTCTCATG 2220
 TCTTTGAGAT TTGATCAGTT TGTGAATATT TTATGCTTTG ATGATATAGT GAGAATGCAT 2280
 5 CACTTGCAAA AAGATCTCA AAGGTGTCAG CCTTAGATAA ACGTCAGCAT TAAAAAAGC 2340
 CAAAAAAGC AAAAAAAGC ATTTTAGGAT CCAGAAGAAT TCCACCAGAT TGCATGAGTT 2400
 AGATTGGGAA ATGGGAGTGG GAGATAATAT TGGGAGGTAT CTATTTTAAG TCAGGGGCTT 2460
 TACTAGCCGA TTTAGTTCTC ACAATAACCA TGTGGAGAAG CTGTGACATT TTTAATTAC 2520
 AACCTTTCTG GGGCTCAGAC ATAAAGTTAC CTATCCAAGG TTGCAGTTGG GTAGTGGTGG 2580
 10 GACCAGGATG GACAACTCAT TGGCCCTGCC TAAAAAGCCA TACCTCTTCT CCTGCTATGC 2640
 AGAATCTGTT TCTCTGAAT CTCTGTGATG CTGGTGGGAA TTGTTTGCAT AGAGGAAGGA 2700
 CAATAACCTT GCCATCGTGA GTTAATGTCC GGGCTGGTCA CAGTGGTTCA TGCTGTAAAT 2760
 CCCAGCACTT TGGGAGTCCA AGGCAGGCAT ATCATTTGAG GTCAGGAGTT TAAGACCAGC 2820
 CTGGCTAACA TAGTGAGACC CTGTTTCTAC TAAAAATACA AAAATAAGCC AGGTGTGGTG 2880
 15 GTGCATGACT GTAATCCCCA CTACTCAGCA GGAGAAGCAC TTGAACCCAG GAGACGGAGG 2940
 CGGCAGTGAG CCAAGATTGT GCCACTGCAC TCCAGCCTGG GCGACAGAGT GAAACTACAT 3000
 CTCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAGTTAATGT CCAAAAATGA CAGATTACA 3060
 AGTGTAAAGCT ATATGATTTT TCAAAAAGC AAAAGCAATA TACCTAATTC ATTTGGATCA 3120
 AACTTACATA GGTCTCAGGT CCTGTAAGAA ACTTGCCTGT TCTAACTGTT GCTACCAGAT 3180
 20 TATATCTGGT GGTAAATGTT AATGTTTCAG CAGGGCTGGT CTCAGTCTTT TAAAAAGGAA 3240
 AGCTTTATTT GGAGCCCAAC CCTATAAGAT GAAGAAATCC TATATAGTCT TATTACCAA 3300
 TATATCCAAT ACACCCACAG CAATGGTACC TTTTAAAGAT CAGGATTTTA TTATGAATTC 3360
 CTGTCACTTT CTGTTTCCA TTAAATTTT TATTTTACAA ATTTTCAGG GAATCATATT 3420
 25 CTTAACITCA CTGAGAAAAA TGTGTTACTC TTTTGGACAA TTTATCTTAT TCTATCATA 3480
 TAAGATGTAT TTTTATTGTT TCTTAAAG AAGCTCTAGC ATGAAATTA AGGAAAGGGA 3540
 AAGAAATAGA TCTGGTGCAC CCGAACATTA GGAGAAAAATG AAAAAATATAC AACCAACCGT 3600
 TCGTGAGTCA TCAAAAAGTC AAAGTCAGCC TGGCCAACAT GGCAAACTC CGTCTCTGCA 3660
 AAAAAATACA AAATGAGGCC GGTATGTTGG CATATGCCCTG TAATCCCAGC TACTCGAGAG 3720
 30 GCTGAGACAC GAAAAATTGCT TGAACCTGGG AGGCGGAGGT TGCAATGAGC CGAGATGCG 3780
 CTACTGCACT CCAGCCTGGG CAACAGAGAG AGACCTTGTC TCAAAAACA ACAACAACA 3840
 AAAGTCAAAG TCATAATAAG CAAATTATTG GCTTCTTTCT TCTAGACYAA AAGAAATTA 3900
 AGAGATGAAA CAATCAATTG CAAGGGTCAA AACTAGATTG GATCTTGGT TGAATGAAAA 3960
 AAAGCATAAA ATATTCTTGC AATAATTGTA AAAATTTGAA TGTGGACTAA GTCCTAGATT 4020
 ATATATAAT ATTTTAAATT TTTAAGCTT GACAAATGCA CTGATTGTTA TACTTTAAAT 4080
 35 AACTAAAAAT CTGAGAATCC ACAGTGCTAC AGACAATAAA TGATAAAATG GGAAAAA 4140
 AAAAAAAAAA

Seq ID NO: 18 Protein sequence:

Protein Accession #: NP_079335.1

1 11 21 31 41 51
 | | | | |
 45 MSLDCTSHIA LGAASPAP EE TYDHLSEVPV TREQLNHYRN VAQNARSELA ATLVKFECAQ 60
 SELQDLRSKM LSKVSCQEL KAEMESYKEN NARKSSLLTS LRDRVQEELE ESAALSTSKI 120
 RTEITAAHA KEQELKKKV VELNEKLQKC SKENEENKKQ VSKNCRKHEE FLTQLRDCLD 180
 PDERNDKASD EDLILKLRDL RKENEFVKQ IVILEBTINV HEMEAKASRE TIMRLASEVN 240
 REQKKAASCT EEKEKLNQDL LSAVEAKEAL EREVKIFQER LLAGQQVWDA SKQEVSLKK 300
 50 SSSSEKSLK ASQDAVTSQ SQYSSFREKI AALLRGRISM TGSTEDTILE KIREMDSREE 360
 SRDRMVSQL EQLSELVEQL GKESGFHQKA LQRAQKAENM LETLQGQLTH LEAELVSGV 420
 LRDLNLFQEK KYLKFLDQLS QKMKLDQMAA ELGFDTRLDV LARTEQLVR LESNAVLENK 480
 TIAHNLQRKL KTQKERLESC ELHMSLLRQK IAQLEEEKQA RTALVVERDN AHLTIRNLQK 540
 KVERLQKELN TCRDLHTELK AKLADTNELK IKTLEQTKAI EDLNSRDQL EKMKEKAEKK 600
 55 LMSVKSELD TTEHAKENKE RARNMIEVVT SEMKTLKKS EBAEKREKQL ADFREVV SQM 660
 LGLNVTSLAL PDYEIKCLE RLVSHQHFF VTCACLKDVT TGQERHPQGH LQLLH

Seq ID NO: 19 DNA sequence

Nucleic Acid Accession #: AF071552, NM_000662

Coding sequence: 441-1313 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 65 CTTGTATAA GGCTCAGCTA AAAGGGAAAT TGAAGTGGTTC AGGTACCACG GATACTATAC 60
 ACTCTATTGC ATGATTCTCC TGCTACATC AGAAGACGTT TATAAGCCTA TTTAAAGGA 120
 TACCAGTTGG AATCTCTCTT TTATTAATCA CCAAGAGAAC CATGAACAAG CTGTTTATCA 180
 TTTGACTCAT CATTTAATCT TGATTCCAG CTCTCACAC TTGAAAGAAG ACATAATACA 240
 TTTCTCACAG GATTCTGGGA CTATTAACCTG AACTTATGTG TGTAAGGAAG ATTATACAA 300
 70 TGAAGCACT AGAAATAATT ATTATACTTA TAACCATTTG ATTTTACAT GTTTAAATA 360
 TAGCCATAAT TAGCCTACTC AAATCCAAGT GTAAAGTAA AATGATTGTC TTTGTTTGG 420
 TTTTCTTGC TTAGGGGATC ATGGACATTG AAGCATATCT TGAAAGAATT GGCTATAAGA 480
 AGTCTAGGAA CAAATTGGAC TTGGAACAT TAACTGACAT TCTCAACAC CAGATCOGAG 540
 75 CTGTTCCCTT TGAGAACCCT AACATCCATT GTGGGGATGC CATGGACTTA GGCTTAGAGG 600
 CCAATTTTGA TCAAGTTGTG AGAAGAAATC GGGGTGGATG GTGTCTCCAG GTCAATCATC 660
 TTCTGTACTG GGCTCTGACC ACTATTGTTT TTGAGACCAC GATGTTGGGA GGGTATGTTT 720
 ACAGCACTCC AGCCAAAAA ELHAGCACTG GCATAGTATCA CCTTCTCTG CAGGTGACCA 780

5 TTGATGGCAG GAACTACATT GTCGATGCTG GGTTTGGACG CTCATACCAG ATGTGGCAGC 840
 CTCTGGAGTT AATTCTGGG AAGGATCAGC CTCAGGTGCC TTGTGCTTC CGTTTGACGG 900
 AAGAGAATGG ATTCTGGTAT CTAGACCAAA TCAGAAGGGA ACAGTACATT CCAAATGAAG 960
 AATTCTTCA TTCTGATCTC CTAGAAGACA GCAAATACCG AAAAATCTAC TCCTTTACTC 1020
 10 TTAAGCCTCG AACAATTGAA GATTTTGAGT CTATGAATAC ATACCTGCAG ACATCTCCAT 1080
 CATCTGTGTT TACTAGTAAA TCATTTTGT CTTCGCAGAC CCCAGATGGG GTTCACTGTT 1140
 TGGTGGGCTT CACCCTCACC CATAGGAGAT TCAATTATAA GGACAATACA GATCTAATAG 1200
 AGTTCAAGAC TCTGAGTGAG GAAGAAATAG AAAAAGTGCT GAAAAATATA TTTAATATTT 1260
 15 CCTGACAGAG AAAGCTTGTG CCCAAACATG GTGATAGATT TTTACTATT TAGAATAAGG 1320
 AGTAAACAA TCTTGCTAT TTGTCATCCA GCTCACCAGT TATCAACTGA CGACCTATCA 1380
 TGTATCTTCT GTACCCCTAC CTTATTTTGA AGAAAATCCT AGACATCAAA TCATTTTACC 1440
 TATAAAAATG TCATCATATA TAATTAACA GCTTTTAA GAAACATAAC CACAAACCTT 1500
 TTCAATAAT AATAATAATA ATAATAATA ATGATTTTA AAGATGGCT GTGGTTATCT 1560
 TGGAAATGG TGATTTATGC TAGAAAGCTT TTAATGTTG TTTATTGTTG AATTC

Seq ID NO: 20 Protein sequence:

Protein Accession #: NP_000653.1

20 1 11 21 31 41 51
 | | | | |
 MDIEAYLERI GYKKS RNKLD LETLTDILQH QIRAVPFENL NIHCGDAMD LGLEAIFDQVV 60
 RNRNGGAGAG AGGGGAGCAC AAAGGATCCA GGTCTCCGA CGGGAGGTTA ATACCAAGAA 120
 25 VDAGFGRSYQ MWQPLELISG KDQPVQVCFV RLTEENGFWY LDQIRREQYI PNEEF LHS DL 180
 LEDSKYRKIY SFTLKPRTE DFESMNTY LQ TSPSSVFTSK SFCSLQTPDG VHCLVGFTLT 240
 HRRFNKYKDN TDLIEFK TLSE EIEK VLKNI FNISLQRKLV PKHGDRFFTI

Seq ID NO: 21 DNA sequence:

Nucleic Acid Accession #: NM_003714

Coding sequence: 123-1031 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 | | | | |
 35 CGGCACGAGC AAAAAGGAAG AGTGGGAGGA GGAGGGGAAG CGGCGAAGGA GGAAGAGGAG 60
 GAGGAGGAAG AGGGGAGCAC AAAGGATCCA GGTCTCCGA CGGGAGGTTA ATACCAAGAA 120
 CCATGTTGTC CGAGCGGCTG GGCCAGTTCA TGACCTGGC TTTGGTGTG GCCACCTTTG 180
 ACCCGGGCG GGGGACCGAC GCCACCAACC CACCGAGGG TCCTCCAGAC AGGAGCTCCC 240
 40 AGCAGAAAGG CCGCCTGTCC CTGCAGAATA CAGCGGAGAT CCAGCACTGT TTGGTCAACG 300
 CTGGCGATGT GGGGTGTGGC GTGTTTGAAT GTTCGAGAA CAACTCTTGT GAGATTCGGG 360
 GCTTACATGG GATTTCATG ACITTTCTGC ACAACGCTGG AAAATTTGAT GCCCAGGGCA 420
 AGTCATTTCAT CAAAGACGCC TTGAAATGTA AGGCCACGC TCTGCGGCAC AGGTTCCGGCT 480
 GCATAAGCCG GAAGTGCCCG GCCATCAGGG AAATGGTGTG CCAGTTGCAG CGGGAATGCT 540
 45 ACCTCAAGCA CGACCTGTGC GCGGCTGCC AGGAGAACAC CCGGTGATA GTGGAGATGA 600
 TCCATTCAA GGACTTGCTG CTGCACGAAC CCTACGTGA CCTCGTGAAC TTGCTGCTGA 660
 CCTGTGGGGA GGAGGTGAAG GAGGCCATCA CCCACAGCGT GCAGGTTTCAG TGTGAGCAGA 720
 ACTGGGGGAG CTTGTGCTCC ATCTTGAGCT TCTGCACCTC GGCCATCCAG AAGCCTCCCA 780
 CGGCGGCCCG CGAGCGCCAC CCCCAGGTGG ACAGAACCAA GCTCTCCAGG GCCCACCACG 840
 50 GGAAGCAGG ACATCACTC CCAGAGCCCA GCAGTAGGGA GACTGGCGGA GGTGCCAAGG 900
 GTGAGCGAGG TAGCAAGAGC CACCCAAACG CCCATGCCG AGGCAGAGTC GGGGGCCTTG 960
 GGGCTCAGGG ACCTTCCGGA AGCAGCGAGT GGAAGAGCGA ACAGTCTGAG TATTCTGATA 1020
 TCCGAGGTTG AAATGAAAGG CTTGGCCACG AAATCTTTCC TCCACGCGGT CCATTTTCTT 1080
 ATCTATGGAC ATTCCAAAAC ATTTACCATT AGAGAGGGGG GATGTCACAC GCAGGATTCT 1140
 55 GTGGGACTG TGGACTTCAT CGAGGTGTGT GTTCGCGGAA CGGACAGGTG AGATGGAGAC 1200
 CCTGGGGGCC GTGGGGTCTC AGGGGTGCCT GGTGAATTCT GCACTTACAC GTACTCAAGG 1260
 GAGCGCGCCC GCGTTATCTC CGTACCTTTG TCTTCTTCC ATCTGTGGAG TCAGTGGGTG 1320
 TCGGCCGCTC TGTGTGGGG GAGGTGAACC AGGAGGGGGC AGGGCAAGGC AGGGCCCCCA 1380
 GAGCTGGGCC ACACAGTGGG TGCTGGGCCT CGCCCCGAAG CTTCTGGTGC AGCAGCCTCT 1440
 GGTGCTGTCT CCGCGGAAGT CAGGGCGGCT GGATTCCAGG ACAGGAGTGA ATGTAAAAAT 1500
 60 AAATATCGCT TAGAATGCAG GAGAAAGGTT GAGAGGAGGC AGGGGCCGAG GGGGTGCTTG 1560
 GTGCCAAACT GAAATTCAGT TTCTGTGTG GGGCCTTGC GTTCAGAGCT CTTGGCGAGG 1620
 GTGGAGGAG GAGTGTCAAT TCTATGTGTA ATTTCTGAGC CATTGTACTG TCTGGGCTGG 1680
 GGGGACACT GTCCAAGGGA GTGGCCCTA TGAGTTTATA TTTAACCAC TGCTTCAAT 1740
 65 CTCGATTICA CTTTTTTTAT TTATCCAGTT ATATCTACAT ATCTGTATC TAAATAAATG 1800
 GCTTTCAAC AAAAAA AAAAAA AAAAAA

Seq ID NO: 22 Protein sequence:

Protein Accession #: NP_003705

70 1 11 21 31 41 51
 | | | | |
 MCAERLGQFM TLALV LAFD PARGTDATNP PEGPQDRSSQ QKGRSLQNT AEIQHCLVNA 60
 GDVCGGVFEC FENNNSCEIRG LHGICMTFLH NAGKFDAQ GK SFIKDALKCK AHALRHRFGC 120
 75 ISRKPAIRE MVSQLORECY LKHDLC AAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVK EAT HSQVQCEQN WGSLSILSF CTSAIQKPPT APPERQPV DRTKLSRAHHG 240
 EAGHHLPES SRETGRGAKG ERGSKSHPN A HARGRVGGLG AQPQSGSEW EDEQSEYS DI 300

RR

5 Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_005264.1
Coding sequence: 557-1954(underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |
10 GAATTCGGGC CAGAAGAAAT CTGGCCTCGG AACACGCCAT TCTCGCGGCC GCTTCCAATA 60
   ACCACTAACA TCCCTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCCTGGCC 120
   CAACTCGGCC CTTGAGCTC TCGAAGATTA CCGCATCTAT TTTTTTTTTC TTTTTTTTCT 180
   TTTCCTAGCG CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGCGGGGA CACCATTGCC 240
15 CTGAAAGAAT AAATAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACGCGGTCCG 300
   TTGAGTCCAG GTTGGGTCCG ACCTGAAACC CTAAAAGCGG AACCGCTCC CGCCCTCGCC 360
   ATCCCGGAGC TGAGTCGCGG GCGGCGGTGG CTGCTGCCAG ACCCGGAGTT TCCTCTTTCA 420
   CTGGATGGAG CTGAACTTTG GCGGCGCAGA GCAGCACAGC TGTCGGGGGA TCGCTGCACG 480
   CTGAGCTCCC TCGGCAAGAC CCAGCGCGCG CTGGGATTT TTTTGGGGGG GCGGGGACCA 540
20 GCGCGCGGCC GGCACCATGT TCCTGGCGAC CCTGTACTTC GCGCTGCCGC TCTTGGACTT 600
   GCTCCTGTGC GCCAAGTGA GCGGCGGAGA CCGCCTGGAT TCGGTGAAAG CCAAGTGATCA 660
   GTGCGTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCACG CTAAGGCAGT GCGTGGCGGG 720
   CAAGGAGACC AACTTCAGCC TGGCATCCGG CTGGAGGCC AAGGATGAGT GCCGCGCGCG 780
   CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCCGC TGCAAGCGGG GTATGAAGAA 840
25 GGAGAAGAAC TGCTTGGCGA TTTACTGGAG CATGTACCAG AGCCTGCAGG GAAATGATCT 900
   GCTGGAGGAT TCCCATATG AACCAGTTAA CAGCAGATTG TCAGATATAT TCCGGGTGGT 960
   CCCATTCTA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAACTGCCT 1020
   GGATGCAGCG AAGCGCTGCA ACCTGACGA CATTGCAAG AAGTACAGGT CGGCGTACAT 1080
   CACCCCGTGC ACCACGAGCG TGTCCAACGA TGCTGCAAC CGCCGCAAGT GCCACAAGGC 1140
30 CTCCGGCAG TTCTTTGACA AGGTCCCGGC CAAGCACAGC TACGGAATGC TCTTCTGCTC 1200
   CTGCGGGGAC ATCGCTGCA CAGAGCGGAG GCGACAGACC ATCGTGCCTG TGTGCTCCTA 1260
   TGAAGAGAGG GAGAAGCCCA ACTGTTTGA TTTGCAGGAC TCCTGCAAGA CGAATTACAT 1320
   CTGCAGATCT GCGCTTGGCG ATTTTITTTAC CAACTGCCAG CCAGAGTCAA GGTCTGTGAC 1380
   CAGCTGTCTA AAGGAAAACT ACGCTGACTG CCTCCTCGCC TACTGGGGC TTATTGGCAC 1440
35 AGTCATGACC CCCAACTACA TAGACTCCAG TAGCCTCAGT GTGCCCCCAT GGTGTGACTG 1500
   CAGCAACAGT GGGAAAGACC TAGAAGAGTG CTTGAAATTT TTGAATTTCT TCAAGGACAA 1560
   TACATGTCTT AAAAATGCAA TTCAAGCCTT TGGCAATGCG TCCGATGTGA CCGTGTGGCA 1620
   GCCAGCCTTC CCAGTACAGA CCACCCTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA 1680
   CAAGCCCTGC GGGCCAGCAG GGTCTGAGAA TGAATTTCCC ACTCATGTTT TGCCACCGTG 1740
40 TGCAAAATTA CAGGCACAGA AGCTGAAATC CAATGTGTGC GGCAATACAC ACCTCTGTAT 1800
   TTCAAATGAT AATTGAAA AGAAGGTCT OGGTGCTTCC AGCCACATAA CCACAAAATC 1860
   AATGGCTGCT CCTCAAAGCT GTGGTCTGAG CCCACTGCTG GTCTGGTGG TAACCGCTCT 1920
   GTCCACCTTA TTATCTTAA CAGAAATC ATAGCTGCAT TAAAAAATA CAATATGGAC 1980
45 ATGTAAAAAG ACAAAAACCA AGTTATCTGT TTCTGTTCT CTGTATAGC TGAATTTCCA 2040
   GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTTTT TTTTCTTTT 2100
   AAGAAAGCTT CTGTGATCC TTGGGGGCTT CTGTAAAAA CCTGATGCAG TGCTCCATCC 2160
   AAACCTAGAA GGCCTTGGGA TATGCTGTAT TTAAAGGGA CAGTTTGTA CTGGGGCTGT 2220
   AAAGCAAAT GGGGCTGTGT TTTGATGAT GATGATCATC ATGATCATGA TGATTTTAAC 2280
   AGTTTTCATT CTGGCCTTC CTAGCTAGAG AAGGAGTTAA TATTCTAAG GTAACCTCCA 2340
50 TATCTCCTTT AATGACATTG ATTTCTAATG ATATAATTT CAGCCTACAT TGATGCCAAG 2400
   CTTTTTTGCC ACAAGAAGA TTCTTACCAA GAGTGGGCTT TGTGGAAACA GCTGGTACTG 2460
   ATGTTACCTT TTATATATGT ACTAGCATT TCCACGCTGA TGTATTGTA CTGTAACAG 2520
   TTCTGCATCT TGTACAAAA GAAAAACCA CCGGAATTC

```

55 Seq ID NO: 24 Protein sequence:
Protein Accession #: NP_005255

```

1      11      21      31      41      51
|      |      |      |      |
60 MFLATLYFAL PLLDLLSAE VSGGDRLCDV KASDQCLKEQ SCSTKYRTLRL QCVAGKETNF 60
   SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQSL QGNDLLEDSP 120
   YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAAKA CNLDDICKKY RSAYITPCTT 180
   SVSNDVNCRR KCHKALRQFF DKVPAKHSYG MLFCSCRDIA CTERRRQTV PVSYEEREK 240
   PNCLNLQDSC KTNICRSRL ADFFTNCQPE SRSVSSCLKE NYADCLLAYS GLIGTVMTPN 300
65 YIDSSSLSA PWCDSCNSGN DLEECLFLN FFKDNTCLKN AIQAFNGSD VTVWQPAFPV 360
   QTTTATTTTA LRVKNKPLGP AGSENEPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420
   EKEGLGASSH IITKSMAAPP SCGLSPLLVL VVTALSTLLS LTETS

```

70 Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1576(entire sequence represents open reading frame)

```

1      11      21      31      41      51
|      |      |      |      |
75 CTTTGTGTTT GCATGCTTA GTCTAGTGGT ATCTGGAATA ATGGAAGAA ATGGGGGCTT 60
   TGGAGAACTA GGATGTTTCG GGGGAAGCGC TAAGGACCGA GGCTGCTGG AAGACGAGCG 120
   CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCTGGGT TTGGGGGAGC CCCCCGCC 180

```

CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCCGCGCAGC CGACAGCCCC 240
 CCCGACGCCG GCGCCGCCGC CGCCGCCCGC GGGCGCCCCG GCCGCCCCGA CGACGGCCCC 300
 CGCAGCGCAG ACGCCCCAGC CCCCCACGCG CCCCCAAGGG GCGAGCGACG CCAAGCTCTG 360
 CGCTCTCTAC AAAGAGGGCG AGCTGCGCCT GAAGGGCAGC AGCAACAACA CGGAGTGTGT 420
 TCCCGTGCCC ACCTCCGAGC AGCTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480
 GGCCTTGAGG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGGGCG AGGAACCACT 540
 GTTCATGGTG ACAGGGCGAC GGGAGGACGT GGCCACAGCC CGGCGGGAAA TCATCTCAGC 600
 AGCGGAGCAC TTCTCCATGA TCCGTGCCTC CGCAACAAG TCAGGCGCCG CCTTGTGTGT 660
 GGCTCCTGCT CTGCCCCGCC AGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG 720
 GCTGGTGGTG GGGCCCCAAG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780
 CATTATCACA CCAAGCCGTG ACGCGACCC CGTGTTCGAG ATCACGGGTG CCCCAGGCAA 840
 CGTGGAGCGT GCGCGCGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900
 CGAGTACAAC AATGAAAAAG ACTTCTTGGC GGGGAGCCCC GACGCGAGCA TCGATAGCCG 960
 CTACTCCGAC GCCTGGCGGG TGCACCAGCC CGGCTGCAAG CCCCTCTCCA CCTTCCGGCA 1020
 GAACAGCCTG GGCTGCATCG GCGAGTGGCG AGTGGACTCT GGCTTTGAGG CCCCACGCTT 1080
 GGGTGAGCAG GCGCGGGGACT TTGGCTACGG CGGGTACCTC TTTCGGGGCT ATGGCGTGGG 1140
 CAAGCAGGAT GTGTACTACG GCGTGGCCGA GACTAGCCCC CCGCTGTGGG CGGGCCAGGA 1200
 GAACGCCACG CCCACTCCCG TGCTCTCTCT CTCTGCTCTC TCCTCTCTCT CCTTTCGCG 1260
 CAAGGCCCGC GCTGGGCCCG CGGGCGCACA CCGCTCCCCT GCCACTTCCG CGGGACCCGA 1320
 GCTGGCCGGA CTCCGAGGCG GCGCCCGGGG AGAGCCGCTC CAGGGCTTCT CTAACCTTGG 1380
 TGGGGCGGCG CTGCGGAGCC CCGCGGGGG GCGGGATTGC ATGGTCTGCT TTGAGAGGGA 1440
 AGTGACTGCC GCCCTGTGTC CCGCGGACA CAACCTGTTC TGCATGGAGT GTGCAGTACG 1500
 CATCTGCGAG AGGACGGACC CAGAGTGTCC CGTCTGCCAC ATCACAGCCA CGCAAGCCAT 1560
 CCGAATATTC TCCTAA

Seq ID NO: 26 Protein sequence:
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 FCFAMPSLVV SGIMERNNGGF GELGCFGSSA KDRGLEDER ALQLALDQLC LLGLGEPPAP 60
 RAGEDGGGGG GGAPAQPTAP PQPAPPPPPA APPAAPPTAP AAQTPQPPTA PKGASDAKLC 120
 ALYKEAELRL KGSNTTECV PVPTSEHVAE IVGRQCKIK ALRAKTNTYI KTPVRGEEPV 180
 FMVTRREDV ATARREIISA AEHFSMIRAS RNKSGAAGFV APALPGQVTI RVRVPYRVVG 240
 LVVGPKGATI KRIQQQNTYI ITPSRDRDP VFEITGAPGN VERAREEIEI HIAVRTGKIL 300
 EYNNENDFLA GSPDAAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360
 GEQGGDFGYG GYLFPYGVVG KQDVYYGVAE TSPLWAGQE NATPTSVLFS SASSSSSSSA 420
 KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGLRSPGGG RDCMVCFESE 480
 VTAALVPCGH NLCMECAVR ICERTDPECP VCHITATQAI RIFS

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: FGENSEH predicted
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120
 CTCAGGCAGA GCGACCCGCA GAAACGGAACT CTGGACCTGG AGAAAAAGCCT GCAGTTCTCT 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAACACAAG GTGAGCCGGC GCGGGGCCCT AGGCGGGCCC TGCCTCCCA GGCACACTCA 300
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCCCTCCAG ACTGTCTTGG CCCACTTGGC TGCACTGGCC 420
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACTCT 480
 AGCCGTGGCT GGACGATGTT ATGCAGCAA GCACAGCAGC TGCTGCTCTC GGAAGGCCA 540
 GGGCCTGAGG TCATTGCAGG GCGCAGGTG GCCACAGGTG GCTCCCCAGA CCTCCCTCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGACAGGCC CCGCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGOCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCCTTGCCA CTGTGTCAG 840
 GCACTTCCCCT ATCTGACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCC TTCCAGGGA 1020
 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080
 CTGTTCTGGG CAAAGTGTGG CCAAGTCCG CAGCCCCAGC CCTGAGTGC TGGGACGCT 1140
 GACAGGACAC GGGGAAGAGG CATGCTTCC CTGGGACCT GCTGTCCAT GTGTCCAAAG 1200
 CCTCTGCT GTCCAGATGG CCCCACAGGA AACCACTTT CCAGGGGCTC TGCTCCCTTG 1260
 GGGCTCGCT GGGTCTGAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
 AGGTGAAGG AGGGCTCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380
 GGGGTAGCG CGGACACTGT GCGCTCTCT GCAGACAGCC TCTCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCACTCTCAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
 TCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGGA GGCCAGAAAG 1620
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGCC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCCA ATGATCTGCG CCTTCCCT GCGAAAGGCC 1740
 ACCACACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCGAG 1800

ACCCAAGAGC TCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 COGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCGCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGGG AGCGTGCCAT CTGCGCCGCA 1980
 CTGAAGCAGA CCCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
 AAACGGCGCC TGCATCGCTC AGTGCTTGA

Seq ID NO: 28 Protein sequence:

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MSGAGVAAGT RPPSPTPGS RRRRQRPVSG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHSEMLAK LHEIEHLKR ENKGEARGP RPALPPQAHSL TPLPQHRNT AINSSTRLGSL 120
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAAITS SRGWTMLCSQ AQHVLLSGSP 180
 GFEVIAGRQV ATGCSFDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240
 MLGAQGIWTH SIQGSPLAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
 AHFPLSLGLG LTSQGHLLTGG WSQPGNIAAG AVPRALPSQG DMEKGVVEGGP FPSRCGNSE 360
 LFWAKCGPSR QPQPCSGADA DRTREEAMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420
 GARWVCINGV WVEPGGSPSA RLKEGSSRTH RFGGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
 SVKSISNSAN SQGKARPOFG SFNKQDSKAD VSQKADLEE PLLHNSKLDK VPGVQGGARK 540
 EKAEASNAGA ACMGNSHQHG RQMGAGAHPP MILPLLRKP TTLRQCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEBSQRPAQA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTPKNFA ERQKRLQAMQ KRRLHRSVL

Seq ID NO: 29 DNA sequence

Nucleic Acid Accession #: NM_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CTGTTGCCGA ATTTCGGCACG AGACCCGCTG TTCGCGCCTG GTAGAGATT CTGGAAGACA 60
 CCAAGTGGCCG OGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCGGTGGGA CAACGAGGCC 120
 GCGGAGAAGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTGATCTCTG ACCTTTGCC 180
 TCTCTGTAC AAATCCCTT CATGAACATA AAGCAGCTGC TTCCGCCAG ACCACTGAGA 240
 AAATTAGTCC GAATTGGGAA TCTGGCATT ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT 360
 TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
 AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
 CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCGA CCATGACTCA GATAGTTTCA 600
 GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
 TCTCTGAAG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTTCC 780
 CCAAGAGATG AAGCAGCTCC ACTCCACCCA GTGTACATC AAAGAGCCGG GTGAGCCGGC 840
 TGGCTTGTAG TAAAAATAAG GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
 GAAACACAAA TGAATATCCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960
 GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
 TCAACCAAT TAGTGTCTGA TCTTGTCTGA TTCATACAAG TGAAGAAGAG GCTGAAATCC 1080
 CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTATAGGCC ATTTCCATCA 1140
 TCAGTTTCTT GTCTCTGCTG GGGGTTATCT TAGTGCTCT CATGAATCGG GTGTTTTTCA 1200
 AATTTCCTT GAGTTTCTT GTGGCACTGG CCGTTGGGAC TTGAGTGGT GATGCTTTT 1260
 TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
 CAATGGAAAT GAAAAGAGGA CCACCTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
 GTGCTATTTT TGATTCCACG TGAAGGGTTC TAACAGCTCT AGGAGGCCCTG TATTTCATGT 1440
 TTCTTGTGA ACATGTCTC ACATTGATCA AACAAATTTA AGATAAGAAG AAAAAGAATC 1500
 AGAAGAAACC TGAATATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT 1560
 CTCACCTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTC 1620
 GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG 1680
 AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
 GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
 TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCAACATC 1860
 CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT 1920
 TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAAATT CAGCGATGGC CTAGCAATTG 1980
 GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGCT GTGTCTCTG 2040
 ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTCTACT AAAGGCTGGC ATGACCGTTA 2100
 AGCAGGCTGT CTTTATAAT GCATTGTGAG CCATGCTGGC GTATCTTGA ATGGCAACAG 2160
 GAATTTTCAT TGGTCATTAT GCTGAAATG TTTCTATGT GATATTGCA CTACTGCTG 2220
 GCTTATTCAT GTATGTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
 GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
 GTTTTGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATGTTGTT CGTATAAATT 2400
 TCTAGTTTAA GCTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460
 AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT 2520
 TTGTATTGAA TATTGTGCTC TGTACAAAAG TCAGTTAAAG GTACGTTTTA ATATTTAAGT 2580
 TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
 TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCA GGAATAATGT CTTTAATGCT 2700

TTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTITA GGTCTCTGAA GAACTGCTGG 2760
 TGTITAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
 AGCAAAAGAAA TAAAGGAGAA AAGAGAAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
 AAAAAACACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAAG 2940
 CAGAAATTAGT ATAGAGTACA TTTATTAAAC ATTTTGTCA GGATTATTTT CCGTAAAAAC 3000
 GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
 AAAATATATT AATGAATCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
 TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
 TATGCCAAG TTATATATCA CCAAAGCTG TATGACTGGA TGTCTGGTT ACCTGGTTTA 3240
 CAAAATATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACCTAAGTA 3300
 TCATTGTATT CGATTACAGAA AGTACTTTGA TATCTCTCAG TCGTTCAAGT CTATCATTGT 3360
 GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
 GATGTTTCTT TTTTACCAA TAAATTCCTT ATATCAGCTT G

15 Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_036451.2

1 11 21 31 41 51
 | | | | |
 20 MARKLSVILI LTFALSVTNP LHELKAAAFQ QTTEKISPNW ESGINVDLAI STRQYHLQQL 60
 FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDHHS DHEHSDHER HSDHEHSDH 120
 EHSDHDHHS HIHHAASGKN KRKALCPDHD SDSSGKDPRN SQKGGAHRPE HASGRRNVKD 180
 SVSASEVTST VYNTVSEGTH FLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT 240
 NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGMGIQV PLNATEFNLY CPAINQIDA 300
 25 RSCLHTSEK KAEIPPKTYS LQIAWVGFI AISISFLSL LGVILVPLMN RVFFKFLLSF 360
 LVALA VGTLS GDAFLHLLPH SHASHHSHS HEPPAMEMKR GPLFSLSSQ NIEESAYFDS 420
 TWKGLTALGG LYFMFLVEHV LTLKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN 480
 EEKVDTDDRT EGYLRADSQE PSFDFSQQA VLEEEVEMIA HAHPEQVYNE YVPRGCKNKC 540
 HSHFHDLTGQ SDDLHHHHHD YHHILHHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600
 30 MGDGLHNFSD GLAIGAAFTG GLSSGLSTSV AVFCHPELPH LGDFAVLLKA GMTVKQAVLY 660
 NALSAMLAYL GMATGFIHGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
 RWGYFFLQNA GMLLGFIML LISIFEKIV FRNF

35 Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: NM_002184.1
 Coding sequence: 256-3012 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 40 GAGCAGCCAA AAGGCCCGCG GAGTCGCGCT GGGCCGCCCC GGCGCAGCTG AACCGGGGGC 60
 CGCGCTGCC AGGCCGACGG GTCTGGCCCA GCCTGGCGCC AAGGGGTTCG TGCCTGTGG 120
 AGACGCGGAG GGTTCGAGGCG GCGCGGCCCT AGTGAAACCC AATGGAAAAA GCATGACATT 180
 TAGAAGTAGA AGACTTAGCT TCAATCCCT ACTCCTTCAC TTAATAATT TGTGATTGG 240
 45 AAATATCCGC GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300
 CTCACCACTG AATCTACAGG TGAACCTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
 CCAGTTGTAC AACTTCATTC TAATTTCCT GCAGTTGTG TGCTAAAGGA AAAATGTATG 420
 GATTATTTTC ATGATAATGC TAATTACATT GTCTGGAAAA CAAACCATTT TACTATTCCT 480
 AAGGAGCAAT ATACTATCAT AAACAGAAAC GCATCCAGTG TCACCTTTAC AGATATAGCT 540
 50 TCATTAAATA TTCAGCTAC TTGCAACATT CTTACATTCG GACAGCTTGA ACAGAATGTT 600
 TATGGAATCA CAATAATTC AGGCTTGCCT CCAGAAAAAC CTAATAATTT GAGTTGCATT 660
 GTGAACGAGG GGAAGAAAAA GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACCTTGGAG 720
 ACAAACTTCA CTTTAAAAATC TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780
 CGTGACACCC CCACCTCATG CACTGTTGAT TATTCTACTG TGTATTTTGT CAACATTGAA 840
 55 GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGAT 900
 CCTGTATATA AAGTGAAGCC CAATCCGCCA CATAATTTAT CAGTGATCAA CTCAGAGGAA 960
 CTGTCTAGTA TCTTAAATTT GACATGGACC AACCCAAGTA TTAAGAGTGT TATAATACTA 1020
 AAATAAACA TTCAATATAG GAACAAAGAT GCCTCAACTT GGAGCCAGAT TCCTCTGAA 1080
 GACACAGCAT CCACCCGATC TTCATTCCT GTCCAAGACC TTAACCTTT TACAGAATAT 1140
 60 GTGTTTAGGA TTCGCTGTAT GAAGGAAGAT GGTAAAGGAT ACTGGAGTGA CTGGAGTGAA 1200
 GAAGCAAGTG GGATCACCTA TGAAGATAGA CCATCTAAAG CACCAAGTTT CTGGTATAAA 1260
 ATAGATCCAT CCCATACCTA AGGCTACAGA ACTGTACAAC TCGTGTGGAA GACATTGCCT 1320
 CCTTTTGAAG CCAATGGAAA AATCTTGGAT TATGAAGTGA CTCTCAAG AGTGAAATCA 1380
 CATTACAAA ATTACACAGT TAATGCCACA AAACGACAG TAAATCTCAC AAATGATCGC 1440
 TATCTAGCAA CCCTAACAGT AAGAAATCTT GTTGGCAAT CAGATGCAGC TGTTTTAACT 1500
 65 ATCCCTGCCT GTGACTTTCA AGCTACTCAC CCTGTAATGG ATCTTAAAGC ATTCCCAAAA 1560
 GATAACATGC TTTGGGTGGA ATGGACTACT CCAAGGGAAT CTGTAAGGAA ATATATACTT 1620
 GAGTGGTGTG TGTATCAGA TAAAGCACC TGTATCACAG ACTGCAACA AGAAGATGGT 1680
 ACCGTGCATC GCACCTATTT AAGAGGGAAC TTAGCAGAGA GCAATGTCTA TTTGATAACA 1740
 GTTACTCCAG TATATGCTGA TGGACAGGA AGCCCTGAAT CCATAAAGGC ATACCTTAAA 1800
 70 CAAGTCCAC CTTCCAAAGG ACCTACTGTT CGGACAAAAA AAGTAGGGAA AAACGAAGCT 1860
 GTCTTAGAGT GGGACCAACT TCCTGTTGAT GTTCAGAAATG GATTATCAG AAATATACT 1920
 ATATTTTATA GAACCATCAT TGGAAATGAA ACTGCTGTGA ATGTGGATT TCCTCACACA 1980
 GAATATACAT TGTCTCTTT GACTAGTGAC ACATTGTACA TGGTACGAAT GGCAGCATAC 2040
 ACAGATGAAG GTGGGAAGGA TGGTCCAGAA TTCACITTTA CTACCCCAAA GTTTGCTCAA 2100
 75 GGAGAAATT AAGCAATAGT CGTGCCTGTT TGTCTAGCAT TCCTATTGAC AACTCTCTG 2160
 GGAGTGCTGT TCTGCTTTAA TAAGCGAGAC CTAATTAATA AACACATCTG GCCTAATGTT 2220
 CCAGATCCTT CAAAGAGTCA TATTGCCAG TGGTCACCTC ACATCTCC AAGGCACAA 2280

5 TTAATTCAA AAGATCAAAT GTATTACAGAT GGCAATTTCCTA CTGATGTAAG TGTTGTGGAA 2340
 ATAGAAGCAA ATGACAAAAA GCCTTTTCCA GAAGATCTGA AATCATTGGA CCTGTTCAA 2400
 AAGGAAAAA TTAATACTGA AGGACACAGC AGTGGTATTG GGGGGTCTTC ATGCATGTCA 2460
 TCTTCTAAGC CAAGCATTTT TAGCAGTGTG GAAAATGAAT CTTCACAAAA CACTTCGAGC 2520
 ACTGTCCAGT ATTCTACOGT GGTACACAGT GGCTACAGAC ACCAAGTTCC GTCAGTCCAA 2580
 GTCTTCTCAA GATCCGAGTC TACCCAGCCC TTGTTAGATT CAGAGGAGCG GCCAGAAGAT 2640
 CTACAATTAG TAGATCATGT AGATGGCGGT GATGGTATTT TGCCAGGCA ACAGTACTTC 2700
 10 AACAGAACT GCAGTCAGCA TGAATCCAGT CCAGATATTT CACATTTTGA AAGGTCAAAG 2760
 CAAGTTTCAT CAGTCAATGA GGAAGATTTT GTTAGACTTA AACAGCAGAT TTCAGATCAT 2820
 ATTTCACAAT CCTGTGGATC TGGGCAAAATG AAAATGTTTC AGGAAGTTTC TGCAGCAGAT 2880
 GCTTTTGGTC CAGGTCAAGTA GGGACAAGTA GAAAGATTTG AAACAGTTGG CATGGAGGCT 2940
 GCGACTGATG AAGGCATGCC TAAAGTTAC TTACCACAGA CTGTACGGCA AGGCGGCTAC 3000
 ATGCTCAGT GAAGGACTAG TAGTTCTGC TACAACCTCA GCAGTACCTA TAAAGTAAAG 3060
 15 CTAATATGAT TTTATCTGTG AATTC

Seq ID NO: 32 Protein sequence:

Protein Accession #: NP_002175.1

20 1 11 21 31 41 51
 | | | | |
 MLTLQTWVVQ ALFILTETES TGEILDPCGY ISPESPVVQL HSNFTAVCVL KEKCMDYFHV 60
 NANYIVWKTN HFTFKEQYT IINRTASSVT FTDIASLNIQ LTCNLTFGQ LEQNVYGITI 120
 ISGLPEKPK NLSQVNEKG KMRCEWDGGR ETHLETNFTL KSEWATHKFA DCKAKRDTPT 180
 25 SCTVDYSTVY FVNEVWVEA ENALGKVTSD HINFDPVYKV KPNPPHNLV INSEELSSIL 240
 KLTWNPNSIK SVILKYNQI YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300
 CMKEDGKGYW SDWSEESAGI TYEDRPSKAP SFWYKIDPSH TQGYRTVQLV WKTLPPEAN 360
 GKILDYEVTL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420
 FQATHPVM DL KAFKDNMLW VEWTTPRESV KKYILEWCVL SDKAPCITDW QQEDGTVHRT 480
 YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPS KGPTVTRTKV GKNEAVLEWD 540
 30 QLPVDVQNGF IRNYYTIFRT IHNETA VNV DSSHTYETLS SLTSDTLYMV RMAAYTDEGG 600
 KDGPEFTFT PKFAQGEIEA IVVPVCLAF LTTLLGVLC FNKRDLLKH IWPNVDPDSK 660
 SHIAQWSPT PPRHNFNSKD QMYS DGNFTD VSVVEIEAND KKPFPEDLKS LDLFKKEKIN 720
 TEGHSSGIGG SSCMSSSRPS ISSSDENESS QNTSSTVQYS TVVHSGYRHQ VPSVQVFSRS 780
 ESTQPLDSE ERPELQLVD HVDGGDGLP RQYFKQNC QHESPDISH FERSKQVSSV 840
 35 NEEDFVRLKQ QSDHISQSC GSGQMKMFQE VSAADAFGPG TEGQVERFET VGMEAATDEG 900
 MPKSYLPQTV RQGGYMPQ

Seq ID NO: 33 DNA sequence:

Nucleic Acid Accession #: NM_018255.1

Coding sequence: 11-2491 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 AGTTGGCGAC ATGGTGGCAC CCGTGCTGGA GACTTCTCAC GTGTTTTGCT GCCCAAACCG 60
 GGTGCGGGGA GTCTGAACT GGAGCTCTGG GCCCAGAGGA CTCTGGCCT TTGGCACGTC 120
 CTGCTCCGTG GTGCTCTATG ACCCCTGAA AAGGGTTGTT GTTACCAACT TGAATGGTCA 180
 CACCGCCCGA GTCAATTGCA TACAGTGGAT TTGTAACAG GATGGCTCCC CTCTACTGA 240
 ATTAGTTTCT GGAGGATCTG ATAATCAAGT GATTCACTGG GAAATAGAGG ATAATCAGCT 300
 50 TTTAAAGCA GTGCATCTC AAGGCCATGA AGGACCTGTT TATGCGGTGC ATGCTGTTA 360
 CCAGAGGAGG ACATCAGATC CTGCATTATG TACACTGATC GTTCTGCGAG CTGCAGATTC 420
 TGCTGTTGCA CTCTGGTCTA AAAAGGGTCC AGAAGTAATG TGCTTCAGA CTTTAAACTT 480
 TGGAAATGGA TTGCTTTGG CTCTCTGCTT ATCTTTTTTG CCAAATACTG ATGTACCAAT 540
 ATTAGCATGT GGCAATGATG ATTGCAGAAT TCACATATTT GCTCAACAAA ATGATCAGTT 600
 TCAGAAAGTG CTCTCTCTCT GTGGACATGA GGATTGGATT AGAGGAGTGG AATGGGCAGC 660
 55 CTTTGGTAGA GATCTTTTCC TAGCAAGCTG TTCACAAGAT TGCTGATAA GAATATGGAA 720
 GCTGTATATA AAGTCAACAT CTTTAAAGAA TCAGGATGAC GATAACATAA GACTGAAAGA 780
 AAATACTTTT ACCATAGAAA ATGAAAGTGT TAAATAGCA TTGCTGTGA CTCTGGAGAC 840
 AGTGTAGCC GGTATGAAA ACTGGGTAAT TGCAGTTTAC TGGCAACCTG TGTTTTACAA 900
 AGATGGTGTG CTACAGCAGC CAGTGAGATT ATTATCTGCT TCCATGGATA AAACCATGAT 960
 60 TCTCTGGGCT CCAGATGAAG AGTCAGGAGT TTGGCTAGAA CAGGTTGAG TAGGTGAAAT 1020
 AGGTGGGAAT ACITTTGGGAT TTTATGATTG CCAGTTCAAT GAAGATGGCT CCATGATCAT 1080
 TGCTATGCT TTCCAGGAG CGTTGCACCT TTGAAACAG AATACAGTTA ACCCAAGAGA 1140
 GTGGACTCCA GAGATTGTCA TTTCAAGACA CTTTGATGGT GTCCAAGACC TAGTCTGGGA 1200
 TCCAGAAGGA GAATTTATTA TCACTGTTGG TACTGATCAG ACAACTAGAC TTTTGTCTCC 1260
 65 ATGGAAGACT CTGCTTGCCT CAGCTTGTA GGCAGCTAAG AAAGAGCATG CAGCTATCAT 1320
 TGGGTATGAC CTGAAATGTT TGGCAATGAT TAATCGGTTT CAGTTTGTAT CTGAGCAGA 1380
 TGAAAAAGTT CTCTGGGTTT TTCTGCACC TCGGAATTTT GTGGAAAAAT TTTGTGCCAT 1440
 TACAGGACAA TCACTGAATC ATGTGCTCTG TAATCAAGAT AGTGATCTTC CAGAAGGAGC 1500
 CACTGTCCCT GCATTGGGAT TATCAAAATA AGCTGTCTTT CAGGAGAGATA TAGCTTCTCA 1560
 70 GCCTTCTGAT GAAGAGGAGC TGTTAACTAG TACTGGTTTT GAGTATCAGC AGGTGGCCTT 1620
 TCAGCCCTCC ATACTACTG AGCTCCAC TGAGGATCAT CTCTGCAGA ATACTTTGTG 1680
 GCCTGAAGTT CAAAACTAT ATGGGCACGG TTATGAAATA TTTGTGTTA CTGTAAACAG 1740
 TTTCAAGACT CTGCTTGCCT CAGCTTGTA GGCAGCTAAG AAAGAGCATG CAGCTATCAT 1800
 TCTTTGGAAC ACTACATCTT GGAACAGGT GCAGAAITTA GTTTCCACA GTTTGACAGT 1860
 75 CACGAGATG GCCTTCTCAC CTAATGAGAA GTTCTTACTA GCTGTTTCCA GAGATCGAAC 1920
 CTGGTCATTG TGGAAAAAGC AGGATACAAT CTCACCTGAG TTCAGGCCAG TTTTGTGCT 1980
 TTTTGCTCT ACCAACAAAA TTACTTCTGT GCACAGTAGA ATTATTGCT CTGTGATTG 2040

5 GAGTCTGAC AGCAAGTATT TCTTCACTGG GAGTCGAGAC AAAAAGGTGG TTGCTCTGGGG 2100
 TGAGTGGCAG TCCACTGATG ACTGTATTGA GCACAACATT GGCCCTCTGT CCTCAGTCTCT 2160
 GGACGTGGGT GGGGCTGTGA CAGCTGTCAG CGTCTGCCCA GTGCTCCACC CTCTCAACG 2220
 ATACGTGGTT GCAGTAGGAT TGGAGTGTGG AAAGATTGTC TTATATACCT GGAAAAAGAC 2280
 TGATCAAGTT OCAGAAATAA ATGACTGGAC CCACTGTGTA GAAACAAGTC AAAGCCAAAG 2340
 TCATACACTG GCTATCAGAA AATTATGCTG GAAGAATTGC AGTGGAAAAA CTGAACAGAA 2400
 GGAAGCAGAA GGTGCTGAGT GGTACACTT TGCAAGCTGT GGTGAAGATC ACACGTGAA 2460
 GATACACAGA GTCAATAAAT GTGCACTGTA ATTGG

10 Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_060725.1

15 1 11 21 31 41 51
 MVAPVLETS VFCCPNRVRG VLNWSSGPRG LLAGFTSCSV VLYDPLKRVV VTNLNGHTAR 60
 VNCIQWICKQ DGSPSTELVS GSDNQVIHW EIEDNQLLKA VHLQGHGPV YAVHAVYQRR 120
 TSDPALCTLI VSAADSAVR LWSKKGPVEM CLQTLNFGNG FALALCLSL PNTDVPILAC 180
 GNDDCRHIF AQNDQFQKV LSLCGHEDWI RGVWAAFR DLFLASCSD CLIRWKLYI 240
 KSTSLQDD DNIRLKENTF TIENESVKIA FAVTLETVA GHENWVNAVH WQPVFYKDG 300
 20 LQQPVRLLSA SMDKTMILWA PDEESGVWLE QVRVGEVGGN TLGFYDCQFN EDGSMIAHA 360
 FHGALHLWKQ NTVNPREWTP EIVISGHFDG VQDLVWDPEG EHIITVGTQD TTRLFAPWKR 420
 KDQSQVTWHE IARPIQHGYD LKCLAMINRF QVSGADEKV LRVFSAPRNF VENFCATTGQ 480
 SLNHVLCNQD SLDPEGATVP ALGLSNKAVF QGDIASQSPD EEELLTSTGF EYQQVAFQPS 540
 25 ILTEPTEDH LLQNTLWPEV QKLYGHGYEI FCVTCNSSKT LLASACKAAK KEHAAHLWN 600
 TTSWKQVQNL VFHSLTVTQM AFSPEKFL AVSRDRTWL WKKQDTSPE FEPVFSLF 660
 TNKITSVHSR IWSCDWSPD SKYFFTGSRD KKVVVWGED STDDCEHNI GPCSSVLDVG 720
 GAVTAVSVP VLHPSQRYV AVGLECGKIC LYTWKKTQV PEINDWTHCV ETSQSQSHTL 780
 AIRKLCWKNC SGTETQKEAE GAEWLHFASC GEDHTVKIHR VNKCAL

30 Seq ID NO: 35 DNA sequence
 Nucleic Acid Accession #: NM_022131
 Coding sequence: 11-2878 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 TGCTGOGAGG ATGCTGCCTG GCGGCTGTG CTGGGTGCCG CTCCTGCTGG CGCTGGGCGT 60
 GGGGAGCGGC AGCGGCGGTG GCGGGGACAG CCGGCAGCGC CGCCTCTCG CGGCTAAAGT 120
 CAATAAGCAC AAGCCATGGA TCGAGACTTC ATATCATGGA GTCATAACTG AGAACAAATGA 180
 CACAGTCATT TTGGACCCAC CACTGGTAGC CTTGGATAAA GATGCACCGG TTCCTTTTGC 240
 40 AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCCTTTGAGG CTGTGGTGTCT 300
 CAACAAGACA TCAGGAGAGG GCCGGCTCCG TGCCAAGAGC OCCATTGACT GTGAGTTGCA 360
 GAAGGAGTAC ACATTTCATCA TCCAGGCCA TGACTGTGGT GCTGGGCCCC ACGAGACAGC 420
 CTGGAAAAAG TCACACAAGG CCGTGGTCCA TATACAGGTG AAGGATGTCA ACGAGTTTGC 480
 TCCACCTTC AAGAGCCAG CCAACAAGGC TGTGTGACG GAGGGCAAGA TCTATGACAG 540
 45 CATTCTGCAG GTGGAGGCCA TTGACGAGGA CTGCTCCCA CAGTACAGCC AGATCTGCAA 600
 CTATGAAATC GTCACCACAG ATGTGCTTT TGCCATCGAC AGAAATGGCA ACATCAGGAA 660
 CACTGAGGAG CTGAGCTATG ACAAACAACA CCAAGTATGAG ATCCTGGTGA CCGCCTACGA 720
 CTGTGGACAG AAGCCCGCTG CTCAGGACAC CTTGGTGACG GTGGATGTGA AGCCAGTTTG 780
 CAAGCTGGC TGGCAAGAT GGAACAAGAG GATTGAGTAC CAGCCTGGCT CCGGGAGCAT 840
 50 GCCCTGTTC CCCAGCATCC ACCTGGAGAC GTGCGATGGA GCGGTGCTT CCCTCCAGAT 900
 CGTCACAGAG CTGCAGACTA ATTACATTGG GAAGGGTTGT GACCGGGAGA CCTACTCTGA 960
 GAAATCCCTT CAGAAGTTAT GTGGAGCCTC CTCTGGCATC ATTGACCTCT TGCCATCCCC 1020
 TAGCGCTGCC ACCAACTGGA CTGCAGGACT GCTGGTGAC AGCAGTGAGA TGATCTTCAA 1080
 GTTGACGGC AGGCAAGGTG CCAAAATCCC CGATGGGATT GTGCCAAGA ACCTGACCGA 1140
 55 TCAGTTCAAC ATCACCATTG GGATGAAACA CGGCCAGC CTTGGTGTGA GAGCCGAGAA 1200
 GGAAACCATC CTCTGCAACT CAGACAAAAC CGAAATGAAC CGGCATCACT ATGCCCTGTA 1260
 TGTGCAACA TGCCGCTCG TCTTCTCTT GCGGAAGGAC TTCGACAGG CTGACACCTT 1320
 TCGCCCCCGG GAGTTCACCT GGAAGCTGGA TCAGATTGT GACAAAGAGT GGCCTACTA 1380
 TGTATCAAT GTGGAGTTTC CTGTGGTAAC CTTATACATG GATGGAGCAA CATATGAACC 1440
 60 ATACCTGGTG ACCAACGACT GGCCCAATTCA TCCATCTCAC ATAGCCATGC AACTCACAGT 1500
 CGGCGCTTGT TGGCAAGGAG GAGAAGTCAC CAAACCACAG TTTGCTCAGT TCTTTATG 1560
 AAGCTGGCC AGTCTCACCA TCCGCCCTGG CAAATGGA AGCCAGAAGG TGATCTCTG 1620
 CCTGCAGGCC TGCAAGGAAG GGCTGGACAT TAATTCCTTG GAAAGCCTTG GCCAAGGAAT 1680
 AAAGTATCAC TTCAACCCCT CGCAGTCCAT CTTGGTGATG GAAGGTGACG ACATTGGGAA 1740
 65 CATTAAACCGT GCTCTCCAGA AAGTCTCCTA CATCAACTCC AGGCAGTTCC CAACGCGGG 1800
 TGTGCGGCGC CTCAAAGTAT CCTCCAAAGT CAGTGTCTT GGGGAAGACG TATGCATCAG 1860
 TATCCCTGAG GTAGATGCCT ATGTGATGGT CTTCCAGGCC ATCGAGCCCC GGATCACCC 1920
 CCGGGGACCA GACCACTTCT GGAGACCTGC TGCCAGTTT GAAAGTGCCA GGGGAGTGAC 1980
 CCTCTTCCCT GATATCAAGA TTGTGAGCAC CTTGCCAAA ACCGAAGGCC CCGGGGACGT 2040
 70 GAAACCCACA GACCCCAAAT CAGAAGTCTT AGAGGAAATG CTTCACTAAT TAGATTTCTG 2100
 TGACATTTTG GTGATCGGAG GGGACTTGGA CCCAAGGCAG GAGTGTGG AGCTCAACCA 2160
 CAGTGAGCTC CACCAACGAC ACCTGGATGC CACTAATTCT ACTGCAGGCT ACTCCATCTA 2220
 CGGTGTGGGC TCCATGAGCC GCTATGAGCA GGTGTACAT CATATCCGCT ACCGCAACTG 2280
 GCGTCCGGCT TCCCTTGAAG CCCGGCGTTT CCGGATTAAG TGCTCAGAAC TCAATGGGCG 2340
 75 CTACACTAGG AATGAGTTCA ACTGGAGGT CAGCATCCT CATGAAGACC AAGTCTCAGA 2400
 TAAGGAGCAT GTCAATCATC TGATTGTGCA GCCTCCCTTC CTCAGTCTG TCCATCATCC 2460
 TGAGTCCCGG AGTAGACTTC AGCACAGTTC AGTGGTCCA AGCATTGCCA CAGTGGTCAT 2520

CATCATCTCC GTGTGCATGC TTGTGTTGT CGTGGCCATG GGTGTGTACC GGGTCCGGAT 2580
 CGCCCACCAG CACTTCATCC AGGAGACTGA GGCTGCCAAG GAATCTGAGA TGGACTGGGA 2640
 CGATTTCTGCG CTGACTATCA CAGTCAACCC CATGGAGAAA CATGAAGGAC CAGGGCATGG 2700
 GGAAGATGAG ACTGAGGGAG AAGAGGAGGA AGAAGCCGAG GAAGAAATGA GCTCCAGCAG 2760
 TGGCTCTGAC GACAGCGAAG AGGAGGAGGA GGAGGAAGGG ATGGGCAGAG GCAGACATGG 2820
 GCAGAATGGA GCCAGGCAAG CCCAGCTGGA GTGGGATGAC TCCACCTCC CTTACTAGTG 2880
 CCCAGGGGTC TGCTGCCTGG CCCACATGTC CTTTGTGTA ACCCTGACCC AGTGATGACC 2940
 CATGTCTATC ATACCTCACC TCTGATGTCT GTGACATGTC TGGGAAGGCC TTCTCCAGCT 3000
 TCCTGGAGCC CACCCITTA GCTTGGGCA CTCCTGTGT TTCATCCATG GGGAAATTCC 3060
 AAGAAGCCCA GCATGGCCAT CAGTGAGGAC TTCAGGGTAG ACTTGTCTCT GTAGCCTCCA 3120
 CTTCTGCCCT AAGTTCGCCA GCATCTGAC TACCTGTCTG CAGAGTTTGC CTTTGTITTT 3180
 TCCTGCAGGG AAGAAGGCC ACCTTTGTGT CACTCACCTC CCCAGGCTCA GAGTCCCAA 3240
 GGCCCTGGGG TTCCAACCTA CTGTGCGTCT CCTCCACACA GACCAGTAGG TTCTCCTATG 3300
 CTGACTCCAG GTTGCTTCAT ACAAGGAGGG TGGTTGAACT TCACACACGT AAGTCTTAG 3360
 TGCTTAACAG TTTAAAGGAA AGTCCCTGTT GAGGCAGAAC TAAGTTTACA GGGAAAGGTA 3420
 CACACATTTCT CTCTCTCTCT CTCTCTGT CTATCTAGTT CCCAGCTTG GAGAGCCTTT 3480
 CCCCTGTGCT CTTTCTGAGG CCATATAAGC TTATAAGAAA AGTCCCAAAC CAAGAATAGG 3540
 TCCTTGGCCA CAAGCAGGGT CTGATCCCC ATCAGAGCTA TCTGAGCCTG CCGTCTGGG 3600
 CACCTGTGTC AACCATGCGT CTACCTGCCC AGGGGCACTC AGCAAACAGA ACCACAGGGC 3660
 CCAGGAGGCA TTCCACACAG GCACTGCCCC AGGACAACAC AACAGGACA GTCACAACAA 3720
 GGACAACAAG GACACAACAC AACACAACAC AAGGACAGTC ACAACAAGCC TAGAGCCAGA 3780
 AAGCAGATGG AATGCTAAT GAGGTCAAAC GTAGGCTTCA TGGTGGGTGG AGTGGGGGTG 3840
 GCTGGGCTCC CCCAGGACAG AGGGGACCTT GAGGTTGGA AGGCTCTCAC CACTCAGCCT 3900
 TATGGTCCCT TATCTCTCTAT CTTCCTCTT GAGAAAATAC ACGCTTCTG CATGTATTAG 3960
 AAACGCACGA GCTCCACCAA GTCTACAATG AAAGTTTGAA ATTAACTGC AAGGAATTAG 4020
 AAGCATATTT GCAATCATG CAGCTTCTT TTTCTTCTG TCATAAAGG AGGAACACTT 4080
 TAGATAGAGG GCAATATAT CTGAAAACCT AATTCTTTC TTTTITGAT AAGGAAATCT 4140
 TTTCCATCTC CATCTAACA TGCACAACCT GTGAAGAGAA TTGTTTCTAT AGTAACTGGT 4200
 CTGTGATCTT TTGTGGCCAA GAGAATAGCA GGCAAGAATT AGGGCCTTGA CAGAATTTC 4260
 ACGAAGCTCT GAGAACATGT TTGTTTCGAA TGCTGATTC CTCTTTGTC TCAATGTGTA 4320
 TGCTCTGCC CCATCTTCA CTCTCTCA AGCTCACACC AATTGGTTTG GCACAGGCAC 4380
 AGAGCTGGTC CCTAGTTAAG TGGCATTAT GTTAAAAAAA AATAGTTCAG AATCTCAGCC 4440
 TTTTCTTTGT GTCATCAAAA CAGCTTAAGA AGGGGACTAC TGCCAATGTC CTCTAGTCTG 4500
 ACCTCCACCC AGGGAGGACC CATGGCAGGT CTTTCAACT TTCTGATTCA TGAGAACAAC 4560
 CTTGTGAAGC TTTTCCACC TCCTAAAGTG TTTCTGCACT CTGTCCTTC CTTTGGACCT 4620
 CACAACAAAT CCTGTGAAGT AACTGAGACA TCTGTTGTTA GATACATTTT TGTGATGAGT 4680
 AAACAGGAGC TTGC

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP_071414.1

1 11 21 31 41 51
 | | | | |
 MLPGRLCWVP LLLALGVSG SGGGDSRQR RLLAAKVNKH KPWIETSYHG VITENNDTVI 60
 LDPPLVALDK DAPVPFAGEI CAFKIHGQEL PFEAVVLNKT SGEGRRLAKS PIDCELQKEY 120
 TFIIQAYDCG AGPHETA WKK SHKAVVHIQV KDVNEFAPTF KEPAYKAVVT EGKIYDSILQ 180
 VEAIDEDCSP QYSQICNYEI VTTDVPFAID RGNIRNTEK LSYDKQHQYE ILVTAYDCGQ 240
 KPAAQDTLVQ VDVKPVCKPG WQDWTKRIEY QPGSGSMPLF PSIHLETCDG AVSSLQIVTE 300
 LQTNVIGKGC DRETYSEKSL QKLCGASSGI IDLLPSPSAA TNWTAGLLVD SSEMIFKFDG 360
 RQGAKIPDGI VPKNLTDQFT ITMWMKHGFS PGVRAEKETI LCNSDKTEMN RHHYALYVHN 420
 CRLVFLLRKD FDQADTFRPA EFHWKLDQIC DKEWHYYVIN VEFPPVTLYM DGATYEPYLV 480
 TNDWPIHPSH IAMQLTVGAC WQGGVETKPK FAQFFHGLSLA SLTIRPGKME SQKVISCLQA 540
 CKEGLDINSL ESLGGGIKYH FNPSQSILVM EGDDIGNINR ALQKVSYSINS RQFETAGVRR 600
 LKVSSKVOQCF GEDVCISIFE VDAYVMVLQA IEPRTLRTG DHFWPAAQF ESARGVTLPF 660
 DIKIVSTFAK TEAPGDVKTT DPKSEVLEEM LHNLDPCDIL VIGGDLDPHQ ECLELNHSEL 720
 HQRHLDATNS TAGYSIYGVG SMSRYEVLH HIRYRNWRPA SLEARRFRK CSELNGRYTS 780
 NEFNLEVSIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIIIS 840
 VCMLVFVVM GYVRVRIHQ HFIQETAAK ESEMDWDDSA LTITVNPMEK HEGPQHGEDE 900
 TEGEEEEEE EEMSSSSGSD DSEEEEEEE MGRGRHQNG ARQAQLEWDD STLPY

Seq ID NO: 37 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 143-874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCGCC TCCAGCTCCG 120
 CGCTGCCCGG CAGCGGGGAG CCATGCGACC CCAGGCCCCC GCGGCTCCG CGCAGCGGCT 180
 CCGCGGCTC CTGCTGCTCC TGCTGCTGCA GCTGCGCGCG CCGTGGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 CATTCCGGGT ACACCTGGGA TCCAGGTCG GGATGGATT CAAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGA AGCTTTGAGG AGTCTGGGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATTAT GGCATGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCACTGG CTCACTTCGG CTAATATGCA GAAATGCATG 600
 CTGTACGCGT TGGATTTCAT CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTA 660

AGCTATAATT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTTCATCG 720
 CACTTCTTCT GTGGAAGGAC TTGTGAAGG AATTGGTGTCT GGATTAGTGG ATGTTGCTAT 780
 CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATTGAAG AACTACCCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 5 TTTTATTATT ATGCCTTGGG ATGGTTCCTT TAAATGACAT TTTAATAAG TTTATGTATA 960
 CATCTGAATG AAAAGCAAAG CTAATATATG TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTC A TTTTGTCTCA ATCAAAAGTG GTTCAATAT TTTTITTAGT 1080
 TGGTTAGAA ATCTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
 10 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200
 TGTACAATT GTAAATGTTA AGAATTTTT TTATATCTGT TAAATAAAAA TTATTTCCTA 1260
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 38 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 | | | | |
 15 MRPQGPAA SP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60
 20 GVPGRDGS PG ANIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLYNGIDL 120
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAEC SGPL PIEAHYLDQ 180
 GSPFMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRHIEE 240
 LPK

Seq ID NO: 39 DNA sequence

Nucleic Acid Accession #: NM_000949

Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 30 GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACTCCTT 60
 CTCCCTCTTT CTGGAATTTT CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120
 ATGTCTCTGT CGAAGGAAGTA CTCATCGACT GATGTGGCAG ACTTGTCTCC CTGACAAAAC 180
 TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCCTGAA 240
 35 GTGAACCTTT GATACTTTC CTGACGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
 CATCTGCAAC CGTTTTCCT CTGCTACTTT TTCTCAACAC CTGCTTCTG AATGGACAGT 360
 TACCTCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCCTCC CAATAAGGAA ACATTACCT 420
 GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCATG ACTTACCACA 480
 GGGGAAGGAG GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAATCCT 540
 40 GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 CTAACAGAT GGGGAAGCAGT TTCTCGGATG AACTTTATGT GGAGGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGGAG CTGGGCTGTT AAGTAAACAA GCCAGAAGAC AGAAAACCT 720
 ACTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTACGC 780
 TCCTGTATGA AATTTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGTCT 840
 45 GGAGCAAAAC AGAGTTTAAG ATTCTAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
 TTGCTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960
 TACCTAGTGA CTTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTCTG 1020
 CTGTCTCTG TTGATTTATT GTCTGGGCA TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
 GCATCTTCC GCCAGTTCCT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTGGGAGA 1140
 50 AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCCA AGACTTTCCT CCCACTTCTG 1200
 ACTATGAGGA CTGTCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
 TGTCAGTCCA TTCAAAAGAA CACCAAGTC AAGGTATGAA AOCACATAC CTGGATCCTG 1320
 ACACGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
 AACCAGGC CAATCCCTCC ACATTCTATG ATCTGAGGT CATTGAGAAG CCAGAGAATC 1440
 55 CTGAAACAAC CCACACCTGG GACCCCACT GCATAAGCAT GGAAGGCAAA ATCCCTATT 1500
 TTCATGCTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCAGC CAGCAACAAC 1560
 CCAGATCCTT TACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGG CCTGCAGGTG 1620
 CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATT 1680
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740
 60 CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAAGATGG TGCATTATCA TTGCTACCAA 1860
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980
 CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAAGAGGC CCCACCATCA CTGGAACAGA 2040
 65 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
 TGGGTGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCTTTTCA TATAGCTTGT 2160
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAAG TAACACTACA GAGTACGTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280
 TTTTAAACA CTGCTCTCTT TCCTCAGCAG CTGATTCCAG AACAATCAT TATGTTTCT 2340
 70 AACTGTGATT TGTAGATTTA CTTTTGTCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
 AAAAGCACAC TGCCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAGAG 2460
 GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAATTTGT TTACCATAGA 2520
 AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC 2580
 75 AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCTTT 2640
 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAGA AAT

Seq ID NO: 40 Protein sequence:

Protein Accession #: NP_000940.1

1 11 21 31 41 51
 5 MKENVASATV FTLLFLNTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPITNY 60
 SLTYHREGT LMHECPDIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSFSELYVD 120
 VTYIVQDPP LELAVEVKQF EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180
 EHFAGGQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIQPSDF TMNDITVWIS 240
 10 VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKKGSE ELLSALGQCD 300
 FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGSCDSPSL 360
 SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420
 PSQHNPRSSY HNTDVCELA VGPAGAPATL LNEAGKDALK SSQTKSREE GKATQQREVE 480
 SFHSETDQDT PWLLPQEKTP FGSAPLDYV EHKVNKDGA LSLLPKQREN SGKPKKPGTP 540
 15 ENNKEYAKVS GYMDNNILVL VPDPAKNVA CFEEAKEAP PSLEQNQAEK ALANFTATSS 600
 KCRLQLGGLD YLDPACFTHS FH

Seq ID NO: 41 DNA sequence

Nucleic Acid Accession #: none found, Eos cloned sequence

Coding sequence: 1-1572 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ATGACCCAAA ATAAATTAAG GCTTGTTC AAAGCCAATG TGTACTGA AGTGCCTGAT 60
 GGAGGATGGG GCTGGGCGGT AGCTGTTTCA TTTTCTTCG TTGAAGTCTT CACCTACGGC 120
 25 ATCATCAAGA CATTGGGTGT CTCTTTAAT GACTTAATGG ACAGTTTAA TGAATCCAAT 180
 AGCAGGATCT CATGGATAAT CTCAATCTGT GTGTTTGTCT TAACATTTT AGCTCCCTC 240
 GCCACAGTCC TGAGCAATCG TTTCCGACAC CGTCTGGTAG TGATGTTGGG GGGGCTACTT 300
 GTCAGCACCG GGATGGTGGC CGCTCTCTC TCACAAGAGG TTCTCATAT GTAOGTCGCC 360
 30 ATCGGCATCA TCTCTGTCT GGGATACTGC TTTAGTTTT TCCCACTGT AACCATCCTA 420
 TCACAAATAT TTGGCAAAAG ACGTTCATA GTCAGTGCAG TTGCTTCCAC AGGAGAATGT 480
 TCGCTGTGT TTGCTTTCG ACCAGCAATC ATGGCTCTGA AGGAGCGCAT TGGCTGGAGA 540
 TACAGCTCC TCTCTGGGG CTTACTACAG TTAACATTG TCATCTTCGG AGCACTGCTC 600
 AGACCATCT TTATCAGAG ACCAGCGTCA CGAAATAG TCATCCAGGA AAATCGGAAA 660
 35 GAAGCGCAGT ATATGCTTGA AAATGAGAAA ACACGAACCT CAATAGACTC CATTGACTCA 720
 GGAGTGAAGC TAACACTCTC ACCTAAAAAT GTGCCTACT ACCTAACCT GGAAGTGGAG 780
 CGGAAGGCCG ACATGCAGCA GGTCTGGTG AAGACCAGCC CCAGGCCAAG CGAAAAGAAA 840
 GCCCGCTAT TAGACTTCTC CATTITGAAA GAGAAAAGTT TTATTGTGA TGCATTATT 900
 GGTCTCTTG CAACACTGGG ATCTTTTGA CCTTCCTGT ACATCATTC TCTGGGCATT 960
 40 AGTCTGGGCA TTGACAGGA CCGCGTCTT TTTTATTAT CTACGATGGC CATTGCAGAA 1020
 GTTTTCGGA GGATCGGAGC TGGTTTGTG CTCACAGGG AGCCCATTCG TAAGATTTAC 1080
 ATTGAGTCA TCTGCTCAT CITATTGACT GTGCTCTGT TTGCTTTAC TTTTGTACT 1140
 GAATCTGGG GTCTAATGTC ATGCAGCATA TTTTGGGT TTATGGTTGG AACAAATAGGA 1200
 GGGACTCACA TTCACTGCT TGCTGAGGAT GATGTCGTGG GCATTGAGAA GATGCTTCT 1260
 45 GCAGTGGGG TCTACATCTT CATTAGAGC ATAGCAGGAC TGGCTGGACC GCCCTTGCA 1320
 GGTTTGTTGG TGGACCAAG TAAGATCTAC AGCAGGGCCT TCTACTCTG CGCAGCTGGC 1380
 ATGGCCCTGG CTGCTGTGT CCTCGCCCTG GTGAGACCGT GTAAGATGGG ACTGTGCCAG 1440
 CATCATCACT CAGGTGAAAC AAAGGTAGT AGCCATCGTG GGAAGACTT ACAGGCATA 1500
 CCTGAAGACT TTCTGGAAT GGATCTTGA AAAAATGAGC ACAGAGTTCA CGTGCAAATG 1560
 50 GAGCCGGTAT GA

Seq ID NO: 42 Protein sequence:

Protein Accession #: none found, Eos cloned sequence

1 11 21 31 41 51
 55 MTQNKLLCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IKTFGVFFN DLMDSFNESN 60
 SRISWIIIS VFVLTSAPL ATVLSNRFGH RLVMGLGGL VSTGMVAASF SQEVSHMYVA 120
 IGIISGLGYC FSFLPTVTL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180
 60 YSLFVGLLQ LNIVIFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
 GVELTSPKN VPHTNLELE PKADMQQVLV KTSRPFSEKK APLLDFSILK EKSIFYALF 300
 GLFATLGFFA PSYIHPGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLAED DVVGIEKMSS 420
 65 AAGVYIFQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
 HHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 43 DNA sequence

Nucleic Acid Accession #: FGENESH predicted ORF

Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 ATGCTGTCTG GCTTCTGTAG GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120
 75 GACCGGGAGA GGGAGAGCCG GCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGCGCG AGAAGGGGAA CCGGGGCGAG CCGCCCGCTT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCCCG CGCCAGCTGG GCAGGCTCC GGGACTGCGG CTGGGGGCGC GCAGGACCT 300
 CGCTGCGCT CTGGACGTTT CCGGGGGAGG GTCCGGTTGC CAGTGAACC TCCAGAGGCT 360

TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAAG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGA TGGCTTAGGA 480
 GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCCGCGG GACAGTCACT GACGAGGCCC GGGGGTCCGC GGGGGCACGA 600
 5 CTCTCTCGGAG ACCGTCTCTG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTCG TCGTCTCTCT CATCTGGAA CGCCGCTTCG CTCCTGCAGC 720
 TGTGCTGGC TGCCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
 10 GGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCGTGGC 960
 CCGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGTACCCAA 1020
 GGAGACGGCG AGGGTGGCC CCCACCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 TCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGG TGCTGCCCG TGCCAGACGC 1140
 CGCGGATTCC CATCTCTCC ACAGCGGGCG CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200
 15 ATCTACGTGG CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CCTTTATCAT CTGGGGGTCC 1260
 CTGGTGGCAG CCGTGTCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320
 GCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCCAGTGC CAGCACCTCC 1380
 CCGGGGTCGT CCTCAGGCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAATCC 1440
 20 GGGGGCCGGG CGCCCCCAAC AAGGTACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500
 AACAACGTGT ATGTCAACAT GCCACGAAT TTCTCTGTGC TGAACGTGTA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
 CAGCACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 25 ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCAOGATT CCTTTGGATG 1860
 GCTTCATTGG CCCCCAGCT GTATGAAAAC ATCTCCGAAT TAGCATTCTT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 30 AAGAATTTTA TAACTGATA AATTAAGGAT TTTTATTATG TGTATTAT TATTTCTTTT 2100
 TGTGTTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCATT GGCTAATTTT TTGTATTTT 2340
 35 TGTAGAGATG GGGTTTACC ATGTTGGCTG GGCTGGTCTC ACTCTCTGA CCTCAAGCAA 2400
 TCTGCTGTC TCAGCTCCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCTTTT TTGTCTTAG ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGACACCTT AATTTCATTG TAAAAGATA TATATATTT GTCTATTTT GTGCTTTGG 2640
 40 GGGCTATTT TGTGCTTTT TACCTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTAAGAGAG ACTGAAATAA ATGTATAGT TACTTAATA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCATT CATCCCTTC 2820
 TTGATTGAT CTAAATTTT TGGCTTAAAG GTGACATCTG AGAGGTAATG CATTCCTTT 2880
 TATATTGAAA TCATAACTA TCACCGCTG CTCTCTGAG TACTTTTAA TTTTGCCTT 2940
 45 TGGTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCT 3000
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCCA GATCTGATA 3060
 AAAAAATTT TTGTCTTAG TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTACTTT 3180
 GCAGATCATA AGCTTTTTA TACTCTGTT ATCAAAATGG CTTATTTTC AGGCACTAAG 3240
 50 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTT CTCTCCAC ACTGTTCTT 3300
 ATTTCTCTC TCCTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTA 3360
 CAAATTCAG TGAATTTAT TGTGTGTTT TACTTATAT AAAAAAAGT AACTTAAAG 3420
 ATGTGCAAGT ACATTTCOA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
 GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTCTTATTC 3540
 55 TGTTCATGA CTGAATAATG TAAAACAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTATAATA ACCAAAGGCA GGGGAAAATC ATTTACTTA TTAATAATA TTTTATGATG 3660
 TGAIAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 44 Protein sequence:

Protein Accession #: FGENSEH predicted

60 1 11 21 31 41 51
 | | | | |
 65 MLGFLMSPS TQHRAQYTPG GKLPWEASI GAHSTRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEGNRGE PPAWIRAQQ PRPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
 SGRQPRGSD CIPRPSASA THKAVPKGTG PPAEDGDLG APGPRARRRR LLGVAEAGSG 180
 PRGKRRTVS DEARGSPGR LLGDRPALSG DALAPRVVP CGALAAFPSP HPGTPLRSCS 240
 CCWLRCWRRG RGPSGEYCHG WLDAGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQGGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPV RAWQRCSPG 360
 70 SPKGRQLLRA FGLLPARR RGFSPRGG PSPLQFPALP IYVFLIVGS VFVAFILGS 420
 LVAACCCRL RPKQDPQQR APGGNRLMET IPMPSASTS RGSSRSQST AASSSSANS 480
 GARAPTRSQ TNCCLPEGTM NNVVYNNMPTN FSVLNCQAT QIVPHQGYL HPPVVGTVQ 540
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMPYAV TV

Seq ID NO: 45 DNA sequence:

Nucleic Acid Accession #: NM_002285

Coding sequence: 55-3738 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 5 GGGCGAGCCT CGGCGGCGGC GGTAGCGGCG GCGGCGACGC TGACACCTCC CACCATGGAC 60
 AGCTTCGACT TAGCCCTGCT CCAGGAATGG GACCTCGAGT CACTGTGTGT CTATGAACCA 120
 GATAGAAATG CATTACGGAG GAAAGAACGA GAAAGAAGAA ATCAAGAAAC TCAACAGGAT 180
 GATGGCACTT TTAATTCTAG TTAATCTCTC TTCAGTGAGC CCTACAAGAC TAACAAGGGG 240
 GATGAACTCT CCAACCGGAT CCAGAACACT TTAGGCAATT ATGATGAAAT GAAAGACTTT 300
 TTAACGTATA GAACCAATCA GAGTCATCTC GTTGGAGTTC CCAAACCTGG GGTTCCTCAG 360
 10 ACTCCTGTGA ACAAGATCGA TGAACATTTT GTTGCAAGTT CAAGAGCCCA GAACCAAGCC 420
 TCGTCTATCT GTAGCACTAC AACTTCCACA CCAGCAGCTG TCCCGTGTGA GCAGAGTAAA 480
 AGAGGCACTA TGGGCTGGCA GAAAGGCTGG CACCCACCTT CTGACGGCCA ACAGAGAGCA 540
 ACACAACAGG GCTCTCTCAG GACCTTGCTT GGAGATGGTG TTGGCAGACA GCAGCCTCGG 600
 GCCAAACAGT TGTGCAATGT GGAGGTGGGC CTCAGAGACC AGGAGAGGCC ACCTGCCATG 660
 GCGGCCAAGC ACAGCAGCAG CGGACACTGT GTTCAGAACT TTCTCCATC CCTAGCTTCA 720
 15 AAACCCAGCC TGGTCCAGCA GAAACCGACC GCGTATGTGA GGCCAATGGA CGGCCAAGAT 780
 CAGGCCCCCTG ATGAGTCTCC TAAGCTGAAG TCGTCTTCGG AAACCAAGCT GCAGTGCACA 840
 TCATACAGGG GAGTCCTGCG CAGCAAGCCG GAGCCTGCCA GAGCCAAGGC CAAGCTCTCC 900
 AAGTTCAGCA TCCCAAGCA GGGGGAGGAG AGTAGATCTG GAGAAACCAA CAGCTGTGTT 960
 GAAGAAATAA TCCGGGAGAT GACCTGGCTT CCACCACTTT CTGCTATTCA AGCACCTGGC 1020
 20 AAAGTGGAA CCAACCAATT TCCATTTC AATAAGGACT CTCAGCTTGT ATCTCTGGA 1080
 CACAATAATC CAAAGAAAGG TGATGCAGAG CCAGAGAGTC CAGACAATGG CACATCGAAT 1140
 ACATCAATGC TGGAAAGATGA CCTTAAGCTA AGCAGTGATG AAGAGGAGAA TGAACAGCAG 1200
 GCAGCTCAGA GAACGGCTCT CCGCGCTCTC TCTGACAGCG CCGTGGTCCA GCAGCCCAAC 1260
 25 TGCAAGAACT CCGTGGCTTC CAGCAAGGGC AGCAGCAGCA GCAGCAGCAG CGGCACGAGC 1320
 AGCTCTCCA GCGACTCAGA GAGCAGCTCC GGATCTGACT CGGAGACCGA GAGCAGCTCC 1380
 AGCGAGAGTG AGGGCAGCAA GCCCCCCAC TTCTCCAGCC CCGAGGCTGA ACCGGCATCC 1440
 TCTAACAGT GGCAGCTGGA TAAATGGCTA AACAAAGTTA ATCCCAACA GCCTCCTATT 1500
 CTGATCCAAA ATGAAAGCCA CGGGTCAGAG AGCAATCAGT ACTACAACCC GGTGAAAGAG 1560
 30 GAGTCCAGG ACTGTGGGAA AGTCCCGAC GTTGGCCAGC CCAGCCTGAG AGAGAAGGAG 1620
 ATCAAGAGCA CTGCAAGGA GGAGCAAAAG CCAAGGACAG CCAACAAGGC CCCTGGGAGT 1680
 AAAGGCGTGA AGCAGAAAGT CCGCGCCGCG GCGCTGGCCG TGCGGTGAG CGCAGCCGCC 1740
 CCGCCACCCG CAGTGGCCTG TGCGCCCGCG GAGAACGCGC CCGCGCTGC CCGGAGGTCC 1800
 GCGGGCAAGA AGCCCAACG GCGCACCGAG AGGACCTCAG CCGGGGACCG CGCCAACCTG 1860
 35 CACCGGCCCG AGGAGCCCGC GGCCGCGGAC GCGCTGGGGA CGAGCGTGGT GGTCCCCCG 1920
 GAGCCCAACA AAACCAAGGC CTGTGGCAAC AACAGAGCGA GCCACCGCAA GGAGCTGCGC 1980
 TCCTCGGTGA CCGCAGAGAA GCGCCGACAG CGGGGGCTAA GCAGGATCGT CCCCAAATCC 2040
 AAGGAGTCA TTGAGACAGA GTGCTCATCT TCATCTCTCT CCTCGGACTC GCAGCTGGAG 2100
 TCGAGCAGG AGGAGTACCC TTGTGCTCAA GCACAGACCG TGGCTGCCTC TGCCTCTCTC 2160
 40 GGGAAATGAT AGAGGCTGAA GGAGGCGGCT GCCAAGCGGG GCAGTGGTCC TAGGGCCCTT 2220
 GTAGGCTCCA TCAACGCCAG GACCACCACT GACATCGCCA AGGAGCTGGA GGAGCAGTTC 2280
 TACACATCG TCCCTTTGG CCGGAACGAA CTCTCTCTCC CTCTAAAGGA CAGTGATGAG 2340
 ATCAGGTCTC TCTGGGTCAA AATCGACCTG ACCCTCTGT CCAGGATCCC AGAACACCTG 2400
 CCCCAGGAGC CAGGGGTATT GAGCGCCCTT GCCACCAAGG ACTCTGAGAG CGCACCGCCC 2460
 45 AGCCACACCT CGGACACACC TGCAGAAAAG GCTTTGCCAA AATCCAAGAG GAAACGCAAG 2520
 TTGTGACAAG AAGACGACTA CAGGGAGATC AAGAAGTCCC AGGGAGAGAA AGACAGCTCT 2580
 TCAAGACTGG CCACCTCCAC CAGTAATACT TTGTCTGCAA ACCACTGCAA CATGAACATC 2640
 AACAGTGTGG CAATACCAAT AAATAAAAAAT GAAAAAATGC TTGGTGCGCC CATCTCACCC 2700
 CTCTCTGATG CATCTAAACA CAAATACACC AGCGAGGACT TAACTTCTTC CAGCCGACCT 2760
 50 AATGGCAACA GTTTGTTTAC TTCAAGCTCT TCCAGCAAAA AGCCTAAGGC CGACAGCCAG 2820
 CTGCGAGCTC ACGGGGAGGA CCTCAGGAAA GCAGCTCACA ACAATTCTGA AAACATTCCC 2880
 CTCCACAAGT CAGGCGCGCA GACGAAGCCG TGGTCTCCAG GCTCCAACGG CCACAGGGAC 2940
 TGCAAGAGGC AGAAACTTGT CTTGATGAT ATGCCTGCGA GTGCCGATTA TTTTATGCAA 3000
 GAAGCTAAAC GAATGAAGCA TAAAGCAGAT GCAATGGTGG AAAAGTTTGG AAAGGCTTTG 3060
 55 AACTATGCTG AAGCAGCATT GTCGTTTATC GAGTGTGGAA ATGCAATGGA ACAAGGCCCC 3120
 ATGGAATCCA AATCTCCTTA TTACCTGATG TATTCAGAAA CAGTAGAGCT CATCAGGTAT 3180
 GCTATGAGAC TAAAAACCCA CTCAGGCCCC AATGCCACAC CAGAAGACAA ACACTGGCT 3240
 GCATTATGTT ACCGATGCTT GGCCCTCTCT TACTGGCGGA TGTTCGACT CAAAAGGGAC 3300
 CAAGCTGTAA AGTATTCAA AGCACTAATC GACTATTTC AAGACTCATC TAAAGCCGCC 3360
 60 CAAAGCCCCC CTCGCTGGGG GGCCAGTGGG AAGAGCACTG GAACCCCATC CCCCATTCT 3420
 CCAACCCCTT TTCCCGGCGA CTCGCTGGGG TCTCAGGGCA GCCTCTCAA CGCCAGCGCC 3480
 CTGTCCCCCT CGACCATCGT CAGCATCCCA CAGCGCATCC ACCAGATGGC GGCCAACCC 3540
 GTCAGCATCA CCAACAGCAT CCTGCACAGC TACGACTACT GGGAGATGGC CGACAACCTG 3600
 GCCAAGGAAA ACCGAGAATT CTTCACAGC CTGGATCTGC TCATGGGGCC GGTCAACCTG 3660
 65 CACAGCAGCA TGGAGCACCT GGTCCAGTAC TCCCAACAGG GCCTGCACTG GCTGCGGAAC 3720
 AGCGCCACC TGTCATAGGG ACCTCACCTT GGGGCCAGAG TGGGCTCTGG TCTCCACAGA 3780
 TGGCTCAAGG TTTTGGACA CTGTGCTACT GAAACTCCCA GCCACAGCAT TTATAGACTG 3840
 CGGTGAACAT TTCCTCA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_002276

1 11 21 31 41 51
 | | | | |
 75 MDSFDLALLQ EWDLESVCVY EPDRNALRRK ERERRNQETQ QDDGTFNSSY SLFSEPYKTN 60
 KGDELSNRIQ NTLGNYDEM K DFLTDRTNQS HLVGVKPGV PQTPVNKIDE HFVADSRAQN 120
 QPSSICSTTT STPAAPVPVQ SKRGTMGWQK AGHPPSDGQQ RATQQGLSLR LLGDGVGRQQ 180
 PRAKQVCNVE VGLQTQERPP AMAAKHSSG HCVQNFPPL ASKPSLVQK PTAYVRPMDG 240

QDQAPDESPK LKSSSETSVH CTSYRGVPAS KPEPARAKAK LSKFSIPKQG EESRSGETNS 300
 CVEEIREMT WLPLSAIQA PGKVEPTKFP FPNKDSQLVS SGHNNPKKG DAEPESPDNGT 360
 SNTSMLEDDL KLSSEEEENE QQAQRTALR ALSDSAVVQQ PNCRTSVPS KSSSSSSSG 420
 TSSSSDSES SSGSDSETES SSSSESGSKP PHFSSPEAEP ASSNKWQLDK WLNKVNPHKP 480
 5 PILIQNEHSG SESNQYYPV KEDVQDCGKV PDVCQPSLRE KEIKSTCKEE QRPRTANKAP 540
 GSKGVKQKSP PAAVAVAVSA AAPPAVPCA PAENAPAPAR RSAGKKPTRR TERTSAGDGA 600
 NCHRPPEEAA ADALGTSVVV PPEPTKTRPC GNNRASHRKE LRSSTCEKR RTRGLSRIVP 660
 KSKFEIETES SSSSSSDSD LESEQEYPL SKAQTVAAAS SSGNDQRLKE AAANGGSGPR 720
 10 APVGSINART TSDIAKELEE QFYTLVPFGR NELLSPKDS DEIRSLVWKI DLTLLSRIPE 780
 HLPQEPGVLS APATKDSESA PPSHTSDTPA EKALPKSKRK RKCDNEDDYR EIKKSQGEKD 840
 SSSRLATSTS NTLNANHCNM NINSVAIPIN KNEKMLRSP SPLSDASKHK YTSEDLTSS 900
 RPNGNLSFTS ASSSKPKAD SOLQPHGGDL TKAHNNSNEN IPLHKSRPQT KPWSFGSNGH 960
 RDCKRQKLVF DDMPRADYF MQEAKRMKHK ADAMVEKFGK ALNYAEAALS FIECGNAMEQ 1020
 15 GPMEKSPYY LMYSETVELI RYAMRLKTHS GPNATPEDKQ LAALCYRCLA LLYWRMFRLK 1080
 RDHAVKYSKA LIDYFKNSSK AAQAPSPWGA SGKSTGTPSP ISPNPFGSS VGSQGSLSNA 1140
 SALSPSTIVS IPQRHQMAA NHVSTNSIL HSYDYWEMAD NLAKENREFF NDLDLLMGPV 1200
 TLHSMMEHLV QYSQGLHWL RNSAHL

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_033151
 Coding sequence: 351-4499 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 25 ACTGGGATAA AGCAAGAAGA CTGATTTTAT GAGCAGGGGT TTGATACATC AAAGGAGATT 60
 GCCCAGGATC AAGGGTGC GG GTTGGGGT GGGTGGGGA GGGTGGTTAG AGAAGGTTTC 120
 ACTAAGTGAT TTGGGCTGAG GGCTGAGAA GATGTTTAAA AAGAGGGATC AACACAGGC 180
 30 TAAGGAGAGG AAAGAGCAGG CACCCAAACC TCTGCATGGC CCAATATGC TCCCTGCAGG 240
 GTAGTGCCCC CTCTTCTGGC TGCTCAAGGC GAGATCTAAG CTCTCTCTAA CTCTGCTGT 300
 CTTTTCATAT TCTCTGATTC TGGGAAACGA AGAATTGGCA GAACTGAAA ATGACTAGGA 360
 AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCTCGT GAATCGTGGC ATCGACATAG 420
 GCGATGACAT GGTTCACGGA CTTATTATA AAACCTATAC TCTCCAAGAT GGCCCTCGGA 480
 35 GTACGACAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCACCACG TGGGGGAAGT 540
 ATGATGCTGC CTTGAGAACC ATGATTCCTT TCCGTCCCAA GCCGAGGTTT CCTGCCCTCC 600
 AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGGTC ACCCCGCTCA 660
 TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG TCAGTCCATG 720
 ATGCCTCAGA CAAAATATGC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA GTCTCAAGGC 780
 40 GAGGATTTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA ACAAGTTTGA 840
 TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG CCAATATTGA 900
 TTATACAAA GATCCTGGAA TATTCAGAAG AGCAGTTGGG GAATGTTGTC CATGGAGTGG 960
 GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTT TCCTCCAGTT 1020
 GGATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTCTCTCC TTGCTCTTG 1080
 45 AGAAGCTCAT CCAATTTAAG TCTGAATAC ACATCACCTC AGGAGAGGCC ATCAGTCTCT 1140
 TCACCGGTGA TGTAAGACTC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA GTACTGATCA 1200
 CCTGCGCATC GCTGGTCATC TGCAGCAATT CTCTCACTT CATTATTGGA TACACTGCAT 1260
 TTAITGGCAT CTTATGCTAT CTCTGGTTT TCCCACTGGC GGTATTCTAT ACAAGAATGG 1320
 CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT GTGACCAAGT 1380
 AAGTTCTCAC TTGCATTAAG CTGATTAAAA TGTACACATG GGAGAAACCA TTGCAAAAA 1440
 50 TCATTGAAGA CCTAAGAGAG AAGGAAAGGA AACTATTGGA GAAGTGCGGG CTTGTCCAGA 1500
 GCCTGACAA GATAACCTTG TTCATCATCC CCACAGTGGC CACAGCGGTC TGGGTTCTCA 1560
 TCCACACATC CTTAAAGCTG AAACCTACAG CGTCAATGGC CTTACAGATG CTGGCTCTCT 1620
 TGAATCTCT TCGGCTGTCA GTGTTCTTTG TGCTATTGC AGTCAAAGGT CTCACGAATT 1680
 CCAAGTCTGC AGTGATGAGG TTCAAGAAGT TTTCTCTCCA GGAGAGCCCT GTTCTCTATG 1740
 55 TCCAGACATT ACAAGACCC AGCAAAGCTC TGGTCTTTGA GGAGGCCACC TTGTCATGGC 1800
 AACAGACCTG TCCCGGGATC GTCAATGGGG CACTGGAGCT GGAGAGGAAC GGGCATGCTT 1860
 CTGAGGGGAT GACCAAGCCT AGAGATGCC TCGGGCCAGA GGAAGAAGGG AACAGCCTGG 1920
 GCCCAGAGTT GCACAAGATC AACCTGGTGG TGTCCAAGGG GATGATGTTA GGGGTCTGCG 1980
 60 GCAACACGGG GAGTGGTAAG AGCAGCCTGT TGTACGCCAT CCTGGAGGAG ATGCACTTGC 2040
 TCGAGGGGCT GGTGGGGGTG CAGGGAAGCC TGGCTATGT CCCCAGCAG GCCTGGATCG 2100
 TCAGCGGGAA CATCAGGGAG AACATCTCA TGGGAGGCGC ATATGACAAG GCCCGATACC 2160
 TCCAGGTGCT CCACTGCTGC TCCCTGAATC GGGACCTGGA ACTTCTGCC TTGAGAGACA 2220
 TGACAGAGAT TGGAGAGCGG GGCTCAACC TCTTGGGGG GCAGAAACAG AGGATCAGCC 2280
 TGGCCCGCGC CGTCTATTCC GACCGTCAGA TCTACCTGCT GGACGACCCC CTGTCTGCTG 2340
 65 TGGACGCCCA CGTGGGGAAG CACATTTTG AGGAGTGCAT TAAGAAGACA CTCAGGGGGA 2400
 AGACGGTCTG CTTGGTGACC CACCAGCTGC AGTACTTAGA ATTTGTGGC CAGATCAATT 2460
 TGTTGAAAAA TGGGAAAATC TGTGAAAATG GAACACAG TGAGTTAATG CAGAAAAAGG 2520
 GGAAATATGC CCAACTTATC CAGAAGATGC ACAAGGAAGC CACTTCGGAC ATGTTCAGG 2580
 ACACAGCAAA GATACAGAG AAGCCAAAGG TAGAAAGTCA GGCTCTGGCC ACCTCCCTGG 2640
 70 AAGAGTCTCT CAACGGAAAT GCTGTGCCG AGCATCAGCT CACACAGGAG GAGGAGATGG 2700
 AAGAAGGCTC CTTGAGTTGG AGGGTCTACC ACCACTACAT CCAGGCAGCT GGAGGTACA 2760
 TGGTCTCTIG CATAATTTT TTCTCTGTGG TGCTGATCGT CTCTTAACG ATCTTCAGCT 2820
 TCTGGTGGCT GGTGAGTGG TTGGAGCAGG GCTCGGGGAC CAATAGCAGC CGAGAGAGCA 2880
 75 ATGGAACCAT GGCAGACCTG GGCAACATTG CAGACAATCC TCAACTGTCC TTCTACCAGC 2940
 TGGTGTACGG GCTCAACGCC CTGCTCTCA TCTGTGTGG GGTCTGCTCC TCAGGGATT 3000
 TCACCAAAGT CACGAGGAAG GCATCCACGG CCTGCACAA CAAGCTCTTC AACAGGTTT 3060
 TCCGCTGCC CATGAGTTT TTTGACACCA TCCAATAGG CCGGCTTTT AACTGCTTC 3120

5 CAGGGGACTT GGAACAGCTG GACCAGCTCT TGCCCATCTT TTCAGAGCAG TTCTGGTCC 3180
 TGCTCTTAAT GGTGATCGCC GTCCTGTTGA TGTGAGTGT GCTGTCTCCA TATATCCTGT 3240
 TAATGGGAGC CATAATCATG GTTATTTGCT TCATTTATTA TATGATGTC AAGAAGGCCA 3300
 TCGGTGTGTT CAAGAGACTG GAGAACTATA GCCGGTCTCC TTTATTCTCC CACATCCTCA 3360
 10 ATTCTCTGCA AGGCTGAGC TCCATCCATG TCTATGGAAA AACTGAAGAC TTCATCAGCC 3420
 AGTTTAAGAG GCTGACTGAT GCGCAGAATA ACTACCTGCT GTTGTCTTA TCTTCCACAC 3480
 GATGGATGGC ATTGAGGCTG GAGATCATGA CCAACCTTGT GACCTTGGCT GTTGCCCTGT 3540
 TCGTGGCTTT TGGCATTTC TCCACCCCT ACTCCTTTAA AGTCATGGCT GTCAACATCG 3600
 TGCTGAGCT GGGCTCCAGC TTCCAGGCCA CTGCCCGGAT TGGCTTGGAG ACAGAGGCAC 3660
 AGTTCAGGC GTAGAGAGG ATACTGCACT ACATGAAGAT GTGTGTCTCG GAAGCTCCTT 3720
 TACACATGGA AGGCACAAGT TGTCCCAAG GGTGGCCACA GCATGGGAA ATCATATTTC 3780
 AGGATTATCA CATGAAATAC AGAGACAACA CACCCACCGT GCTTCACGGC ATCAACCTGA 3840
 CCATCCGCGG CCACGAAGTG GTGGGCATCG TGGGAAGGAC GGGCTCTGGG AAGTCTCCT 3900
 TGGGCATGGC TCTCTCCG CTGGTGGAGC CCATGGCAGG CCGGATTCTC ATTGACGGCG 3960
 15 TGGACATTTG CAGCATCGGC CTGGAGGACT TGGGTCCAA GCTCTCAGTG ATCCCTCAAG 4020
 ATCCAGTGCT GCTCTCAGGA ACCATCAGAT TCAACCTAGA TCCCTTTGAC CGTCACACTG 4080
 ACCAGCAGAT CTGGGATGCC TTGGAGAGGA CATTCCTGAC CAAGGCCATC TCAAAAGTTC 4140
 CCAAAAAGCT GCATACAGAT GTGGTGGAAA ACGGTGGAAA CTCTCTGTG GGGGAGAGGC 4200
 AGCTGCTCTG CATTGCCAGG GCTGTGCTTC GCAACTCCAA GATCATCCTT ATCGATGAAG 4260
 20 CCACAGCCTC CATTGACATG GAGACAGACA CCTGATCCA GCGCACAATC CGTGAAGCCT 4320
 TCCAGGGCTG CACCGTGCTC GTCAATTGCC ACCGTGTAC CACTGTGCTG AACTGTGACC 4380
 ACATCTGTGT TATGGGCAAT GGAAGGTGG TAGAATTGA TCGGCGGAG GTACTGCGGA 4440
 AGAAGCTGG GTCAATTGTC GCAGCCCTCA TGGCCACAGC CACTCTTCA CTGAGATAAG 4500
 25 GAGATGTGGA GACTTCATGG AGGTGGCAG CTGAGCTCAG AGGTTACAC AGGTGCAGCT 4560
 TCGAGGCCCA CAGTCTGCGA CCTCTTGT TGGAGATGAG AACTTCTCT GGAAGCAGG 4620
 GTAAATGTAG GGGGGGTGGG GATTGCTGGA TGGAAACCT GGAATAGGCT ACTTGATGGC 4680
 TCTCAAGACC TTAGAACCCC AGAACCATCT AAGACATGGG ATTCAGTGAT CATGTGGTTC 4740
 30 TCCTTTTAAC TTACATGCTG AATAATTTTA TAATAAGGTA AAAGCTTATA GTTTCTGAT 4800
 CTGTGTAGA AGTGTGCAA ATGTGTACT GACTTTGTAA AATATAAAAC TAAGGAAAAC 4860
 TC

Seq ID NO: 48 Protein sequence:
 Protein Accession #: NP_149163.2

35 MTRKRTYVWPNSSGGLVNRIGIDGDMVSGLIYKTYTLQDGPWSQERNPEAPGRAAVPPWGKYDAALRT
 MIFRFPKPRFPAQPLDNAGLFSYLTVSWLTPMLIQSLRSRLDENTPPLSVHDASDKNVQRLHRLWEEE
 VSRRIEASVLLVMLRFQRTLLIFDALLGICFIASVLGPILIPKILEYSEELGNVHVGLCFALF
 40 LSECVKLSFSSSWINQRTAIRFRAAVSSFAFEKLIQFQSVIHITSGEAISFTGDVNYLFEVVCYGPL
 VLITCASLVICISSYFIIGYAFIALCYLLVFPLAVFMTMAVKAQHHTSEVSDQIRVTVSEVLTCK
 LIKMYTWKPFKILIEDLRKLEKLEKCGLVQSLTSLFIHPTVATAVWVLIHTSLKLLTASMAFSM
 LASLLRLSVFFVPIAVKGLTNSKSAVMRFKFFLQESPVFYVQTLQDPSKALVFEEATLSWQQTCPGI
 45 VNGALELERNGHASEGMRPRDALGPEEEGNSLGPHELHKNLVSKGMMLGVCNGTSGSKSLLSAILEE
 MHLEGSVGVQGSLAYVPQQAIVVSGNIRENIMGGAYDKARYLQVLHCCSLNRDLELPPGDMTEIGER
 GLNLGGQKQRISLARAVYSDRQYLLDDPLSAVDAHVGKHIFEECKKTLRGKTVVLVTHQLQYLEFCG
 50 QILLENKICENGTHSELMQKKGKYAQLIQKMHKEATSDMLQDTAKIAEKPKVESQALATSEELNNGN
 AVPEHQLTQEEEMEEGSLWRVYHHYIAAGGYMVSCIFFVVLIVFLTIFSFWWLSYWLQEGSGTNS
 RESNGTMADLGNIDNPQLSFYQLVYGLNALLICVGVCSGIFTKVTAKALHNKLFNKVFRCPMSF
 FDTPIGRLLNCFAGDLEQLDQLPIFSEQLVLSLMVIAVLLIVSVLSPYILMGAIMVICITYMMF
 55 KKAIGVFKRLNENYRSPLFSHILNSLQGLSSIHVYKTEDFISQFKRLTDAQNNYLLFLSSTRWMA LRL
 EIMTNLVTALVALFVAFGISSTPYFVKVMAVNIVQLASSFQATARIGLETEAQTAVRILQYMKMCVS
 EAPLHMEGTSQPGWPQHGEIIFQDYHMKYRDNTPTVLHGINLTIRGHEVVIGVGRGSGKSSLGMA LFR
 LVEPMAGRILIDGVDCISLEDLRSKLSVIPQDPVLLSGTIRFNLDPDRHTDQIQWALERTFLTKAI
 SKFPKKLHTDVVENGGNFVSGERQLLCIARAVLRNSKILLIDEATASIDMETDTLIQRTIREAFQGGCTVL
 VIAHRVTVTLNCDHILVMGNKGKVEFDRPEVLRKPGSLFAALMATATSSLR

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: NM_033419
 Coding sequence: 18-980 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 CGAGCCAGGG AGAAAGGATG GCCGGCCTGG CGGCGCGGTT GGTCTGCTA GCTGGGGCAG 60
 CGGCGCTGGC GAGCGGCTCC CAGGGCGACC GTGAGCCGGT GTACCGGCAC TGCCTACTGC 120
 65 AGTGCGAAGA GCAGAACTGC TCTGGGGGCG CTCTGAATCA CTCCGCTCC CGCCAGCCAA 180
 TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240
 TCACCGTTGG GCTCTACCTC CAGGAAGGTC ACAAAGTGCC TCAGTTCCAT GGCAAGTGCC 300
 CCTCTCCCG GTTCTCTGTC TTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG 360
 GCCTGGCCAG CTGTGTGATG CTCTGCCGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA 420
 70 TGTACCACAC CTGTGTGGCC TTCGCTGGG TGTCCTCAA TGCATGGTTC TGGTCCACAG 480
 TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTTCTGT GCCTCCACTG 540
 TCATCTACA CTAATCTAC CTGTGCTGCG TCAGGACCGT GGGGCTGCG CACCCAGCTG 600
 TGGTCAGTGC CTCCGGCTC CTCTGCTGC TCATGCTGAC CGTGCACTG TCCTACCTGA 660
 GCCTCATCCG CTTCGACTAT GGCTACAACC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA 720
 75 ACGTGTGTGT GTGGCTGGCC TGGTGCCTGT GGAACACGCG GCGGCTGCT CACGTGCGCA 780
 AGTGGCTGGT GGTGCTCTTG CTGCTGCAGG GGCTGTCCCT GCTCGAGCTG CTTGACTTCC 840
 CACCGCTCTT CTGGGTCTG GATGCCCATG CCATCTGGCA CATCAGCACC ATCCCTGTCC 900
 ACGTCTCTT TTTCAGCTTT CTGGAAGATG ACAGCCTGTA CCGCTGAAG GAATCAGAGG 960

5 ACAAGTTCAA GCTGGACTGA AGACCTTGA GCGAGTCTGC CCCAGTGGGG ATCCTGCCCC 1020
 CGCCCTGCTG GCCTCCTTC TCCCCTCAAC CCTTGAGATG ATTTTCTCTT TTCAACTTCT 1080
 TGAAGTTGGA CATGAAGGAT GTGGGCCCCAG AATCATGTGG CCAGCCCACC CCCTGTTGGC 1140
 CCTCACCAGC CTTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG 1200
 GGCAGGCCCT CTACCTCTCG GAGCTGAACT GGGGTGGAAC TGAGTGTGCT CTTAGCTCTA 1260
 CCGGGAGGAC AGCTGCCTGT TTCTCCCCA TCAGCCTCCT CCCACATCC CCAGCTGCCT 1320
 GGCTGGGTCC TGAAGCCCTC TGTCTACCTG GGAGACCAGG GACCACAGGC CTTAGGGATA 1380
 CAGGGGGTCC CCTTCTGTTA CCACCCCCA CCTCCTCCA GGACACCACT AGGTGGTGCT 1440
 10 GGATGCTTGT TCTTTGGCCA GCCAAGGTTT ACGGCGATTC TCCCATAGG ATCTTGAGGG 1500
 ACCAAGCTGC TGGGATTGGG AAGGAGTTT ACCTGACCA TTGCCCTAGC CAGGTTCCCA 1560
 GGAGGCCCTCA CCATACTCCC TTTCAGGGCC AGGGCTCCAG CAAGCCCAGG GCAAGGATCC 1620
 TGTGCTGCTG TCTGGTTGAG AGCCTGCCAC CGTGTGTCGG GAGTGTGGGC CAGGCTGAGT 1680
 GCATAGGTGA CAGGGCCGTG AGCATGGGCC TGGGTGTGTG TGAGCTCAGG CTTAGGTGCG 1740
 CAGTGTGGAG ACGGGTGTGT TCGGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGGG 1800
 15 GGTGGGTGTG TTAGCGTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGGTGG GCATGTGAGA 1860
 TGAGTGACTG CCGGTGAATG TGTCCACAGT TGAGAGGTTG GAGCAGGATG AGGGAATCCT 1920
 GTCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCCC AAGGCGCCAC CTGGGCGGAC 1980
 AGCCAGGAGC TCTCCATGGC CAGGCTGCCT GTGTGCATGT TCCTGTCTG GTGCCCTTT 2040
 GCGCCCTCC TGCAAACTCT ACAGGTGCC CACACAACAG TGCCCTCCAG AAGCAGCCCC 2100
 20 TCGGAGGCAG AGGAAGGAAA ATGGGGATGG CTGGGGCTCT CTCCATCCTC CTTTCTCCT 2160
 TGCTTCCCA TGGCTGGCCT TCCCCTCAA AAOCTCCATT CCCCTGCTGC CAGCCCCCTT 2220
 GCCATAGCCT GATTTTGGG AGGAGGAAGG GGCGATTGA GGGAGAAGGG GAGAAAGCTT 2280
 ATGGCTGGGT CTGGTTTCTT CCCTCCAG AGGGTCTTAC TGTTCAGGG TGCCCCAGG 2340
 GCAGGCAGGG GCCACACTAT GCCTGCCGCC TGGTAAAGGT GACCCCTGCC ATTTACCAGC 2400
 25 AGCCCTGGCA TGTTCCTGCC CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTTCCAT 2460
 CCAAAGGCA GTCTCCGTGG TTGAAGCAGA CTGGATTTT GCTCTGCCCC TGACCCCTTG 2520
 TCCCTCTTTG AGGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGGAATC GGGTGGCCTG 2580
 CGTAGCTTC TTTTGATACT GAAAACTTT AAGGTGGGAG GGTGGCAAGG GATGTGCTTA 2640
 ATAAATCAAT TCCAAGCTC AAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 50 Protein sequence:
 Protein Accession #: NP_219487.1

35 1 11 21 31 41 51
 MKDVGPESCQ QPTPCWPSA LESVLGKASQ HLGLESQPL YLLELNWGGT ECALSSTGR 60
 AACFLPSILL PTSPAALWLP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTTRWCWMLV 120
 40 LWPAKVHGDG PHGLRDQAA GIGKEFHPDH CPSQVPRRP HTPFQGGQSS KPRARILCC 180
 LVESLPPCVG SVGQAECIGD RAVSMGLGVC ELRPRCAVWR RVLSGKRCCG KVCVCRGWVC

Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: XM_059098.1
 Coding sequence: 178-618 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 GATGTACACT CTGAAGTGAG CACATTCTCT TTGGCAGGAC ATGACACCTT GGCAGCAAGC 60
 ATCTCCTGGA TCCTTTACTG CTTGGCTCTG AACCTGAGC ATCAAGAGAG ATGCCGGGAG 120
 50 GAGGTACAGG GCATCCTGGG GGATGGGTCT TCTATCACTT GGGACCAGCT GGGTGAGATG 180
 TCGTACACCA CAATGTGCAT CAAGGAGACG TGCCGATTGA TTCTGCAGT CCCGTCCATT 240
 TCCAGAGATC TCAGCAAGCC ACTTACCTTC CCAGATGGAT GCACATTGCC TGCAGGGATC 300
 ACCGTGGTTC TTAGTATTGG GGGTCTTAC CACAACCTCT CTGTCTGGA AAACCCAAAG 360
 55 GTCTTTGACC CCTTGAGGTT CTCTCAGGAG AATTCTGATC AGAGACACCC CTATGCCTAC 420
 TTACCATCTC CAGCTGGATC AAGGAACTGC ATTGGGCAGG AGTTTGCCAT GATTGAGTTA 480
 AAGGTAACCA TTGCCTTGAT TCTGCTCCAC TTCAGAGTGA CTCAGACCC CACCAGGCCT 540
 CTTACTTTCC CCAACCATTT TATCCTCAAG CCCAAGAATG GGATGTATTT GCACCTGAAG 600
 AAACTCTCTG AATGTAGAT CTCAGGGTAC AATGATTAAA CGTACTTTGT TTTTGAAGT 660
 60 TAAATTTACA GCTAATGATC CAAGCAGATA GAAAGGGATC AATGTATGGT GGGAGGATTG 720
 GAGGTGGTGG GGATAGGGGT CTCTGTGAAG AGATCCAAAA TCATTCTAG GTACACAGTG 780
 TTGACAGTAG ATCTGTTTCT ATATACTTT GGGAGATTIT CAGATCTTTT CTGTTAAACT 840
 TTCACTACTA TTAATGCTGT ATACACCAAT AGACTTTCAT ATATTTCTG TTGTTTTTAA 900
 AATAGTTTTC AGAATTATGC AAGTAATAAG TGCATGTATG CTCAGTGTCA AAAATTCCCA 960
 65 ACACAGAAA ATCATGTAGA ATAAAAATTT TAAATCTCAC TTCATTAGC CGACATTCCA 1020
 TGCCCTGACC AATCCTACTG CTTTCTCTAA AAACAGAATA ATTGGGTGTG CATTCTTTCA 1080
 GACTTTTTC TATACATTTT ATATGTAGAA ATGTAGCAAT GTATTGTAT AGATGTGATC 1140
 ATTCTATAT TGTATTGAT TTTTTCCT TAATAAAAAA TCACCTTATT CCTT

70 Seq ID NO: 52 Protein sequence:
 Protein Accession #: XP_059098.1

75 1 11 21 31 41 51
 MSYTMCIKE TCRLIPAVPS ISRDLKPLT FPDGCTLPAG ITVVLISWGL HHNPVWKNP 60
 KVFDPLRFSQ ENSDQRHPYA YLPFSAGSRN CIGQEFAMIE LKVITIALILL HFRVTPDPTR 120
 PLTFPNHFIL KPKNGMYLHL KKLSEC

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_030916
Coding sequence: 1-1533 (underlined sequences correspond to start and stop codons)

5
1 11 21 31 41 51
| | | | |
| | | | |
ATGCCCTGT CCTGGGAGC CGAGATGTGG GGGCCTGAGG CCTGGCTGCT GCTGCTGCTA 60
CTGCTGGCAT CATTTACAGG CCGGTGCCCC GCGGGTGAGC TGGAGACCTC AGACGTGGTA 120
10 ACTGTGGTGC TGGGCCAGGA CGCAAACTG CCCTGCTTCT ACCGAGGGGA CTCCGGCGAG 180
CAAGTGGGGC AAGTGGCATG GGCTCGGGTG GACGCGGGCG AAGGCGCCCA GGAAGTACG 240
CTACTGCACT CCAATACGG GCTTCATGTG AGCCCGGCTT ACGAGGGCCG CGTGGAGCAG 300
CCGCCGCCCC CACGCAACCC CCTGGACGGC TCAGTGCTCC TCGCAACGC AGTGACAGCG 360
GATGAGGGCG AGTACGAGTG CCGGGTCAGC ACCTTCCCG CCGCAGCTT CCAGGCGCGG 420
CTGCGGCTCC GAGTGTGGT GCCTCCCTG CCCTCACTGA ATCTGTGTCC AGCACTAGAA 480
15 GAGGCGCAGG GCCTGACCTT GGCAGCCTCC TGCACAGCTG AGGGCAGCCC AGCCCCAGC 540
GTGACCTGGG ACACGGAGGT CAAAGGCACA ACGTCCAGCC GTTCTTCAA GCACTCCCGC 600
TCTGCTCCCG TCACCTCAGA GTTCCACTTG GTGCTAGGCC GCAGCATGAA TGGGCAGCCA 660
CTGACTTGGT TGGTATCCCA TCCTGGCCTG CTCCAGGACC AAAGGATCAC CCACATCTCT 720
CACGTGTCTT TCCTTGCTGA GGCTCTGTG AGGGGCTTGA AAGACCAAAA TCTGTGGCAC 780
20 ATTGGCAGAG AAGGAGCTAT GCTCAAGTGC CTGAGTGAAG GGCAGCCCC TCCTCATAC 840
AATCGACAC GGCTGGATGG GCCTCTGCCC AGTGGGGTAC GAGTGGATGG GGACACTTTG 900
GGCTTTCCCC CACTGACCAC TGAGCACAGC GGCATCTACG TCTGCCATGT CAGCAATGAG 960
TTCTCTCAA GGGATTCTCA GTCACTGTG GATGTTCTT ACCCCAGGA AGACTCTGGG 1020
AAGCAGGTGG ACCTAGTGC AGCTCGGTG GTGGTGGTGG GTGTGATCGC CGCACTCTTG 1080
25 TTCTGCCTTC TGGTGGTGGT GGTGGTGCTC ATGTCCGAT ACCATCGGCG CAAGGCCAG 1140
CAGATGACCC AGAAATATGA GGAGGAGCTG ACCCTGACCA GGGAGAATC CATCCGGAGG 1200
CTGCATTCCC ATCACACGGA CCCAGGAGC CAGCCGAGG AGAGTGTAGG GCTGAGAGCC 1260
GAGGGCCACC CTGATAGTCT CAAGGACAAC AGTAGCTGCT CTGTGATGAG TGAAGAGCCC 1320
GAGGGCCGCA GTTACTCCAC GCTGACCACG GTGAGGGAGA TAGAAACACA GACTGAACTG 1380
30 CTGTCTCCAG GCTCTGGGGC GGCCGAGGAG GAGGAAGATC AGGATGAAGG CATCAACAG 1440
GCCATGAACC ATTTGTTC GAAGAATGGG ACCCTACGGG CCAAGCCCA GGGCAATGGC 1500
ATCTACATCA ATGGGCGGGG ACACCTGGTC TGA

Seq ID NO: 54 Protein sequence:
Protein Accession #: NP_112178.1

1 11 21 31 41 51
| | | | |
| | | | |
40 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSVTV TVVLGQDAKL PCFYRGDSGE 60
QVGGQVAVAR V DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA 120
DEGEYECRVS TFPAGSFQAR LRLRVLPPL PSINPGPALE EGQGLTAAAS CTAEGSPAPS 180
VTWDTVEVKT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPL LQDQRTHIL 240
HVSFLAEASV RGLDQNLWH IREGAMLKC LSEGQPPSY NWTRLDGRLP SGVRVDGDTL 300
45 GFPLTTEHS GIYVCHVSN FSSRDSQVTV DVLPQEDSG KQVDLVASV VVVGVIALL 360
FCLLVVVVL MSRYHRRKAQ QMTQKYEEL TLTRENSIRR LHSHTDPRS QPEESVGLRA 420
EGHPDSLKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIK 480
AMNHVFQENG TLRKPTGNG IYINGRHLV

Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: AF007170.1
Coding sequence: 73-1725 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
| | | | |
55 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
CTGGACCACT GCATGACCGC CCTGGACCTC TTCCTACCA ACCAGTCTC AGAAGCACTC 120
AGCTACCTCA AGCCAGAAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
ATGAAGGAGG CACAGATGCT GTGTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
60 TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
GAGGTCTGCT ATGCAGAGTG CCTGCTGAGC CGAGCAGCCC TGACCTTCT GCAGGACGAG 420
AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTGCAA ACAGCTACCA GACCTACAAG 480
GAGCTGGACA GCCTTGTTC GTCCTACAA TACTGCAAGG GTGAGAACCA CCCGCACTTT 540
GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
65 AGGATCTCTGA AGCTGTTGGA GTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
CAGCTGGAGG AGGGAGGCTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
CTGTGTCTAC ACACCTTCTT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGGTGCCAT CTTCCTGTTT 840
TTTGACGGGA GGATTGAAGT CATTAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
70 GAGTGTCTGT AGGCCAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
ATGTGTGTCT ACACCTACAA GGGCCAGTGG AAGATGTCCT ACTTCTACGC CGACCTGCTC 1020
AGCAAGGAGA ACTGCTGCTC CAAGGCCACC TACATTTACA TGAAGGCCG CTACCTCAGC 1080
ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGACG AAGTGAAT ATTTCGAGCT 1140
GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
75 CGGAAGTCCC GGGGCTACTT CTCTCCAAC CCTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260
ATGATGTACA TCTGGAACGG CTACGCCGTG ATTGGGAAGC AGCCGAACT CACGGATGGG 1320
ATACTTGAGA TTACTACAA GGCTGAAGAG ATGCTGGAGA AAGGCCAGA GAACGAGTAC 1380

5 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
 CTGTGCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCTGTCTGCT TATGGAGCAA 1560
 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620
 10 TCCATGGAGT CAAGGACACA CTTTGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800
 CCCCCTGCCC TGGCCTGCTT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
 TGTATCCGTG CAGAAGCCGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCAAG 1920
 15 GGCAGAGCAG GTGGAGCCCT CTGCCCTGCC TATCACAT ACGGGTACTT GCTTTTCACT 1980
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040
 CACAGTTGGC TTTAAAAACC AACACAATC AACCACCTGT AAGTCTTTGT CTTACCTAT 2100
 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAATTG CTTTTCAAAT 2160
 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCTGGG 2220
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC 2280
 CCACTACCTT ACTACTACCA CTTCAATTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340
 AAGCAGCTCT TTTTAGTGAG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
 20 AGTAGAAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
 AAATTTGGGG GGCAGGAGGA GGTCTCTAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
 CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580
 CATTGCTTA CTCAGACGAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAAAA 2640
 AA

25 Seq ID NO: 56 Protein sequence:
 Protein Accession #: AAC39582.1

1 11 21 31 41 51
 | | | | |
 30 MTALDLFLTN QFSEALSULK PRKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAECVY AECLLQRAAL TFLQDENMVS 120
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSLMLPTRLR 180
 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEAEKL 240
 LKPYLNRYPK GAIFLFFAGR IEVIGKNIDA AIRRFEECCE AQHWHKQFHH MCYWELMWCF 300
 35 TYKGGQKMSY FYADLLSKEN CWSKATYIYM KAAYLMSFGK EDHKPFGDDE VELFRA VPGL 360
 KLKAGKSLP TEKFAIRKSR RYFSSNPISL PVPALEMMYI WNGYAVIGKQ PKLTDGILEI 420
 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 LIPNALLELA LLLMEQDRNE EAIKLLES AK QNYKNYSMES RTHFRIQAAT LQAKSSLENS 540
 SRSMVSSVSL

40 Seq ID NO: 57 DNA sequence
 Nucleic Acid Accession #: NM_006670.1
 Coding sequence: 1-927 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 45 ATGCTCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCCTCTGCG GCTGGCGCGA 60
 CTAGCGCTGG TACTCTCTGG CTGGGTCTCC TCGTCTTCTC CCACTCTCTC GGCATCTCTC 120
 TTCTCTCTCT CGGCGCCGCT CTTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 50 CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACC GC 240
 AATCTGACCG AGGTGCCAC GGAACCTGCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCAGCTGG CCAGCAACCA CTCCTTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCTGACCTA CGTGTCTTTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTTAC 480
 55 AATGCAACCC TGGCTGAGT GCAAGGTCTA CCCACATTA GGGTTTCTCT GGACAACAAT 540
 CCTGGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAG AAATGAGGAA TCGGGTCTCT 660
 TTGGAACCTA CACAGTGCTGA CTTGGAAGTGT GACCCGATTG TTCCGCCATC CCTGCAAAAC 720
 60 TCTTATGTCT TCCTGGGTAT TGTTTATGCC CTGATAGGCG CTATTTCTCT CTTGGTTTGT 780
 TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTTCTAACT CGGATGTCCT CGAGTGA

65 Seq ID NO: 58 Protein sequence
 Protein Accession #: NP_006661.1

1 11 21 31 41 51
 | | | | |
 70 MPGGCSRGA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKVNR NLTEVPTDLP AYVRNLFTG NQLASNHFLY LPRDVLALQLP 120
 SLRHLDSLNN SLVSLTYVSF RNLTHLES LH LEDNALKVLH NGTLAELOGL PHIRVFLDNN 180
 PWVCDCHMAD MVTWLKETE VQGDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
 75 SYVFLGIVLA LIGAILLV LYLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVL E

Seq ID NO: 59 DNA sequence
 Nucleic Acid Accession #: NM_024022

Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
5      |      |      |      |      |
      |ATGGGGGAAA ATGATCCGCC TGCTGTTGAA GCCCCTTCT CATTCCGATC GCTTTTGGC 60
      |CTTGATGATT TGAATAAAG TCCTGTTGCA CCAGATGCAG ATGCTGTTGC TGCACAGATC 120
      |CTGTCACTGC TGCCATTGAA GTTTTTCCTA ATCATCGTCA TTGGGATCAT TGCATTGATA 180
      |TTAGCACTGG CCATTGGTCT GGGCATCCAC TTCGACTGCT CAGGGAAGTA CAGATGTCGC 240
      |TCATCCTTTA AGTGATATCGA GCTGATAGCT CGATGTGACG GAGTCTCGGA TTGCAAAGAC 300
10     |GGGGAGGACG AGTACCCTG TGTCGGGTG GGTGGTCAGA ATGCCGTGCT CCAGGTGTTT 360
      |ACAGTGTCTT CGTGGAAAGAC CATGTGCTCC GATGACTGGA AGGGTCACTA CGCAAAATGTT 420
      |GCCTGTGCCC AACTGGGTTT CCAAGCTAT GTGAGTTTCA ATAACCTCAG AGTGAGCTCG 480
      |CTGGAGGGGC AGTTCGGGA GGAGTTTGTG TCCATCGATC ACCTTTGCC AGATGACAAAG 540
      |GTGACTGCAT TACACCCTC AGTATATGTG AGGGAGGGAT GTGCCTCTGG CCACGTGGTT 600
15     |ACCTTGCAGT GCACAGCCTG TGGTCATAGA AGGGGTACA GTCACGCAT CGTGGGTGGA 660
      |AACATGTCTT TGCTCTCGCA GTGGCCTGG CAGGCCAGCC TTCAGTTCCA GGGCTACCAC 720
      |CTGTGCGGGG GCTCTGTCTA CAGGCCCTG TGGATCATCA CTGCTGCACA CTGTGTTTAT 780
      |GACTTGTACC TCCTCAAGTC ATGGACCATC CAGGTGGGTC TAGTTTCCCT GTTGACAAT 840
      |CCAGCCCCAT CCCACTTGGT GGAGAAGATT GTCTACCACA GCAAGTACAA GCCAAAGAGG 900
20     |CTGGGCAATG ACATCGCCCT TATGAAGCTG GCCGGGCCAC TCAGTTCAA TGAATGATC 960
      |CAGCCTGTGT GCCTGCCCAA CTCTGAAGAG AACTTCCCGG ATGGAAGAGT GTGCTGGACG 1020
      |TCAGGATGGG GGGCCACAGA GGATGGAGGT GACGCTCCC CTGTCTGAA CCACGCGGCC 1080
      |GTCCCTTTGA TTCCAACAA GATCTGCAAC CACAGGACG TGTACGGTGG CATCATCTCC 1140
      |CCCTCCATGC TCTGCGCGGG CTACCTGACG GGTGGCGTGG ACAGCTGCCA GGGGGACAGC 1200
25     |GGGGGGCCCC TGGTGTGTCA AGAGAGGAGG CTGTGGAAGT TAGTGGGAGC GACCAGCTTT 1260
      |GGCATCGGCT GCGCAGAGGT GAACAAGCCT GGGGTGTACA CCGGTGTAC CTCCTTCTG 1320
      |GACTGGATCC ACGAGCAGAT GGAGAGAGAC CTAACCTGA

```

Seq ID NO: 60 Protein sequence
Protein Accession #: NP_076927

```

1      11      21      31      41      51
35     |      |      |      |      |
      |MGENDPPAVE APFSRSLFG LDDLKISPA PDADAVAAQI LSLPLKFFP IIVIGIALI 60
      |LALAIGLGIH FDCSGKYRCK SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVVLQVF 120
      |TAASWKTMCSD DQWKGYHANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
      |VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFGYH 240
      |LCGGSVITPL WIITAHCYVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
      |LGNDIALMKL AGPLTFNEMI QPVLNPNSEE NFPDQKVCWT SGWGATEDGG DASPVLNHA 360
40     |VPLSNKICN HRDVYGGIIS PSMLCAGYLT GGVDSQCQGS GGPLVCQERR LWKLVGATSF 420
      |GIGCAEVNKP GYVTRVTSFL DWIHEQMERD LKT

```

Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 28-2538 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
50     |      |      |      |      |
      |AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCTTTT TACCATGTT TTCTCTACTA 60
      |TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAAATCATT ATGACAAGAT CTGGGCTCAT 120
      |AGTCGTATCA GGGGTGCGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
      |ACCAAAAAGA AATCTTCAG CACTTGAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
      |AAAAGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
      |TGCCAGCAG TTTTGCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
55     |ACAACGCAGC GTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
      |TTCACTTACT TTGACCGAG TAATGAGGCT TGGGCAAACT TGGATTCTGA TATCCGTAGA 480
      |GGTTTGGAGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
      |AAGAGAATGT TGACCAAGGA CTAAAAAAT GGCATGATTA TTCCTCAAT GTATAACAAT 600
      |TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC 660
60     |ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCATG TCAATGACCG TGTGCTTACA 720
      |CAAATTTGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
      |GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
      |TTTGCTCCCA CCAATGAGGC TTTTGAAGAA CTCCACGAG GTGTCCTAGA AAGGTTTCATG 900
      |GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
65     |TCTGAGTCTA TATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020
      |GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
      |GTGACAAATA ATGGTGTGAT CCATTGTATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140
      |CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200
      |GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
70     |GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAATTAAT TCTGCAGAAT 1320
      |CACATATTGA AAGTAAAAAG TGGCCTTAAT GAGCTTTACA ACGGGCAAACT ACTGGAAACC 1380
      |ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGCTGTCAT TGAATAATCA 1440
      |TGCAATGGGA AAGGGAGTAA GCAAGGGAGA AACGGTGCAG TTCACATATT CCGGAGATC 1500
      |ATCAAGGCCA CAGAGAAATC CCTCCATGAA AAGTAAAAAC AAGATAAGCG CTTTAGCACC 1560
75     |TTCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAAACC TGGAGACTGG 1620
      |ACATTATTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
      |CTGATACGGG ACAAATATGC TCTTCAAAAC ATCATCTTTT ATCACCTGAC ACCAGGAGTT 1740

```

5 TTCATTGGAA AAGGATTGTA ACCTGGTGTT ACTAACATTT TAAAGACCAC ACAAGGAAGC 1800
 AAAATCTTTC TGAAAGAAGT AAATGATACA CTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
 TCTGACATCA TGACAAACAA TGGTGTAATT CATGTTGTAG ATAACTCCT CTATCCAGCA 1920
 GACACACCTG TTGGAATGTA TCAACTGCTG GAAATACCTA ATAAATTAAT CAAATACATC 1980
 CAAATTAAGT TTGTTCTGGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT 2040
 AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAGTGA TTGAAGGCAG TCTCAGCCT 2100
 ATATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTC 2160
 AGACTGATTA AAGAAGGTGA AACAACTAAGT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
 10 AAATACACCA AAATCATTGA TGGAGTGCCT GTGGAAATAA CTGAAAAAGA GACACGAGAA 2280
 GAACGAATCA TTACAGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT 2400
 GAAGGTGGTG ATGGTCATTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460
 ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520
 15 GAAGGTGCGT CTCAGTGA AAATCAAAAAC CAGAAAAAAA TGTTATACA ACCCTAAGTC 2580
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACCTG AAACATCAGC 2640
 ACAAGAAGAC AATCATCAAA TAATTCTGAA CACAAATTA ATATTTTTT TTCTGAATGA 2700
 GAAACATGAG GGAATTTGTG GAGTTAGCCT CCTGTGGTAA AGGAATGAA GAAAAATATA 2760
 CACCTTACAC CCTTTTTCAT CTGACATTA AAAGTTCTGG CTAATTTGG AATCCATTAG 2820
 20 AGAAAAATCC TTGTCAACAG ATTCATTACA ATTCAAAATC AAGAGTTGTG AACTGTTATC 2880
 CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TATTTTTTA 3060
 CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTA 3120
 25 TCTCAAACGT TCAATAAAA CCATTTTTC GATATAAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAAA ACTCAAGATT TAAGTAAAA AGTGGTTGG ACTTGGGAA

Seq ID NO: 62 Protein sequence:

Protein Accession #: NP_006466

30 1 11 21 31 41 51
 | | | | |
 MIPFLPMFSL LLLLVNPN ANNHDKILA HSRIRGRDQG PNVCALQQL GTKKKYFSTC 60
 KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTGLVIGA TTTQRYSDAS 120
 35 KLEIEIEGKG SFTYFAPNSE AWDNLDSDIR RGLSNVNVLE LLNALHSHMI NKRMLTKDLK 180
 NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVDIRVL TQIGTSIQDF 240
 IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL 300
 MKYHILNTLQ CESMGMGA V FETLEGNTIE ICDGDSITV NGIKMVNKKD IVTNNGVIHL 360
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
 40 VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
 RNGAIHFIRE IKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
 FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNIKTTQG SKIFLKEVND 600
 TLLVNELKSK ESDIMTTINGV IHVVDKLLYP ADTPVGNLQL LEILNKLIIY IQIKFVRGST 660
 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
 45 TEVIHGEPII KKYTKIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL 780
 QEEVTKVTKF IEGGDGHLFE DEEIKRLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

Seq ID NO: 63 DNA sequence

Nucleic Acid Accession #: NM_020974

Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 GCGGTCCGCG CACACCTCCC CGCGCCGCGC CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CCGCAACCGC TGAGCCATCC ATGGGGGTCG CCGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120
 55 CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCGTCCCGC 180
 CCGGTCCGGG CCGTGCCGCG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCTACAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360
 TCAATGGAGG CTGTGTCAT CACTGTTTGA ATATTCCAGG CAATTATCGT TGCATTGTT 420
 60 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGCTT TGATGTGGAC GAGTGCCTGG 480
 AGAACATGG CCGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCTG 540
 GCAAGGAGGG GTTTTTCTG AGTGACAATC AGCACACCTG CATTACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 GCAGCGTCCG CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 65 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCGGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGTGCCTTG 840
 AGCGAGAGGA CAATGCTCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960
 ACCGCACTTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACTC 1020
 70 TCCAGTTGGA TGGGAAGACA TGTAAGATA TTGATGAGTG CCAAGCCCGC AATGGAGGTT 1080
 GTGATCATTT CTGCAAAAC ATCGTGGGCA GTTTGACTG CCGCTGCAAG AAAGGATTTA 1140
 AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTGG GATAGGACCT 1200
 GTGACCACAG CTGCATCAAC CACCCTGGCA CATTGCTTGG TGCTGCAAC CGAGGGTACA 1260
 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 75 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CAGTGCCAC CCGGGGTACA 1380
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440
 CACCCCGTGT GTCCTGCAC TCGGTAAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500

5 GTCACTCTGG CATTACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560
 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTCCCGAG GGTCTGCGAC 1620
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680
 GCAGCTCTGG CAGGAAATGC CCAGGAGGCC CTGGCCGACC AAGCACCCTT AAGGAAATGT 1740
 10 TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
 AGGCCGTCCA CAGGGAGCAG TTTACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG 1980
 CAGAAAAACA ATGTGTGAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
 15 GCCCAAGACC AGGAAATTCT GGGGCCCTGA AGACCCAGA AGCTTGAAT ATGTCTGAAT 2160
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT 2220
 GTGCCCTGGG CACGTTCCAG CCTGAAGCTG GTCGAACCTC CTGCTTCCCC TGTGGAGGAG 2280
 GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
 GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA 2400
 CATACCAGCC TGAATTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
 20 GAGATTTCAC TGGGTACATC GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
 AGTGTAAGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA 2640
 TCTTCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700
 CCAATTCGTG GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760
 CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCATGA AGGGAACAGC GCTAGAGGGT 2820
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC 2880
 25 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAACTTA 2940
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCGAGG 3000
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGGTGGG ACAGAGCTGT CTTCCTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC 3180
 30 CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT 3240
 GAACTTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT 3360
 TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAATCTCTC TCAAGGAGTC 3420
 TGTAGTGGA AGGAGGGCAC AGAATAAGCT GCTTATTCG AAACTTCAGC TTCTCTAGC 3480
 35 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGC 3540
 CAAGAGGGGA GGGAGGAGA CCCTGCAGG CTCCCTCCAC CCACCTTGA ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TETCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
 AGTTCTAAGC AGTGCTCGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720
 AGCACTCTG GAGACAT

40 Seq ID NO: 64 Protein sequence:
 Protein Accession #: NP_066025.1

1 11 21 31 41 51
 45 MGVAAGRNRPG AAWAVLLLLL LLPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CCKPGYQGE GRQCEIDEC GNELNGGCVH DCLNIPGNRY CTCFDGFMLA 120
 HDGHNCLDVD ECLNNNGGCG HTCVNVMGYS ECCCKEGFFL SDNQHTCIHR SEGLSCMNK 180
 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGCQHSDD TADGPECSCH 240
 50 PQYKMHDTGR SCLEREDTVL EVTESNTTSV VDGDKRVRKR LLMETCAVNN GGCRTCKDT 300
 STGVHSCSPV GFTLQLDGT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQVQCVN 420
 TVGSEYECQH PGYKLHWKMK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTIIRTS VTFKLNEGKC SLKNAELFPE GLRPALEKH SSVKESFRYV NLTCSGKQV 540
 55 PGAPGRPSTP KEMFIVFEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TFQNEEGQMT CEPCTPRGNS GALKTPEAWN MSECGLCQP GEYSADGFAP CQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSGPHFY NTTTHRCIRC PVGTYPQPEF 780
 60 KNNCVSCPQN TTTDFDGSTN ITQCKNRRCG GELGDFGTGY ESPNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTY ETCQTYERPI AFTSRSKLW 900
 IQFKSNEGNS ARGFPVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

65 Seq ID NO: 65 DNA sequence
 Nucleic Acid Accession #: NM_007210
 Coding sequence: 1-1869 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 ATGAGGCTCC TCCGACAGCG CCACATGCCC CTGCGCCTGG CCATGGTGGG CTGCGCCTTT 60
 GTGCTCTTCC TCTTCTCTCT GCATAGGGAT GTGAGCAGCA GAGAGGAGGC CACAGAGAAG 120
 CCGTGGCTGA AGTCCCTGGT GAGCCGGAAG GATCACGTCC TGGACCTCAT GCTGGAGGCC 180
 ATGAACAACC TTAGAGATTC AATGCCCAAG CTCCAATCA GGGCTCCAGA AGCCAGCAG 240
 75 ACTCTGTTCT CCATAAACA GTCTGCCTC CTTGGGTTCT ATACCCAGC TGAACCTGAAG 300
 CCCTTCTGGG AACGGCCACC ACAGACCCCT AATGCCCTGT GGGCAGATGG AAAAGCATT 360
 CAGAAGAGCA AGTGGAGCCC CTGGAGACC CAGGAAAAGG AAGAAGGCTA TAAGAAGCAC 420
 TGTTTCAATG CCTTGGCAG CGACCGGATC TCCCTGAGA GGTCCCTGGG GCCAGACACC 480
 CGACCACCTG AGTGTGTGGA CCAGAAGTTC CGGCGCTGCC CCCCACTGGC CACCACGAG 540

5 GTGATCATTG TGTTCACAA CGAAGCCTGG TCCACACTGC TGCGAACAGT GTACAGCGTC 600
 CTACACACCA CCCCTGCCAT CTGTCTCAAG GAGATCATAC TGGTGGATGA TGCCAGCACA 660
 GAGGAGCACC TAAAGGAGAA GCTGGAGCAG TACGTGAAGC AGCTGCAGGT GGTGAGGGTG 720
 GTGCGGCGAGG AGGAGGCGGAA GGGGTTGATC ACCGCCCGGC TGCTGGGGGC CAGCGTGGCA 780
 CAGGCGGAGG TGCTCACGTT CCTGGATGCC CACTGTGAGT GCTTCCACGG CTGGCTGGAG 840
 CCCCTCTGG CTCGAATCGC TGAGGACAAG ACAGTGGTGG TGAGCCGAGA CATCGTCACC 900
 ATCGACCTTA ATACTTTTGA GTTCGCCAAG CCCGTCCAGA GGGGCAGAGT CCATAGCCGA 960
 GGCACACTTG ACTGGAGCCT GACCTTCGGC TGGGAAACAC TTCCTCCACA TGAGAAGCAG 1020
 AGGCGCAAGG ATGAAACATA CCCCATCAA TCCCCGACGT TTGCTGGTGG CCTCTTCTCC 1080
 10 ATCCCAAGT CCTACTTGA GCACATCGGT ACCTATGATA ATCAGATGGA GATCTGGGGA 1140
 GGGGAGAACG TGGAAATGTC CTTCGGGTG TGGCAGTGTG GGGGCCAGCT GGAGATCATC 1200
 CCTGTCTGT TGTAGGCCA TGTGTTCCGG ACCAAGAGCC CCCACACCTT CCCCAGGGC 1260
 ACTAGTGTC TGTCTCGAA TCAAGTGGC CTGGCAGAGG TCTGGATGGA CAGCTACAAG 1320
 AAGATTTTCT ATAGGAGAAA TCTGCAGGCA GCAAAGATGG CCAAAGAGAA ATCCTTCGGT 1380
 15 GACATTCGG AACGACTGCA GCTGAGGGAA CAACTGCACT GTCACAACTT TTCTGGTAC 1440
 CTGCACAATG TCTACCCAGA GATGTTTGT CTGACCTGA CGCCACCTT CTATGGTGCC 1500
 ATCAAGAACC TCGGCACCAA CCAATGCCTG GATGTGGGTG AGAACAACCG CGGGGGGAG 1560
 CCCCTCATCA TGTACTCTG CCACGGCCTT GCGGCAACC AGTACTTTGA GTACACAACT 1620
 CAGAGGGACC TTCGCCACAA CATCGCAAAG CAGCTGTGTC TACATGTCAG CAAGGGTGCT 1680
 20 CTGGGCTTGG GGAAGCTGCA CTTCCTGGC AAGAAAGCC AGGTCCCAA GGACGAGGAA 1740
 TGGGAATTGG CCCAGGATCA GTCATCAGG AACTCAGGAT CTGGTACCTG CCTGACATCC 1800
 CAGGACAAAA AGCCAGCCAT GGCCCCCTGC AATCCCAAGT ACCCCCATCA GTTGTGGCTC 1860
 TTTGTCTAGG ACCCAGATCA TCCCAGAGA GAGCCCCAC AAGCTCTCA GGAAACAGGA 1920
 25 TTGCTGATGT CTGGGAACCT GATCACCAGC TTCTCTGGAG GCCGTAAGA TGGATTCTA 1980
 AACCCTCTGG GTGGCAAGGC AGGACCTTCC TAATCTTGC AACACATTTG GGCCCATTTT 2040
 CTTTCTCTCA CACCGATGGA AGAGACCAAT AGGACATATA TTAGCCTAG CGTTTCTCTG 2100
 TTCTAGAAAT AGAGGCTCCC AAAGTAGGGA AGGCAGCTGG GGGAGGGTTC AGGGCAGCAA 2160
 TGCTGAGTTC AAGAAAAAGTA CTTCAGGCTG GGCACAGTGG CTCATGCTG AAATCTTAGC 2220
 30 ACTTTGGGAA GACAAATGTTG GAGAATGGCT TGAGCCAGG AGTTCAAGAC CGGCTGAGC 2280
 AACATAGTGA GGATCCCATC TCTACGCCCA CCCTCCCCCG GGCACAAAAA AAGCTGGGT 2340
 ATGGTGGCT ATGCTGTAG TCGCAGCTAC TCAAGAGGCT GAGGTGGGAG GATTGCTTGT 2400
 TCCCGGAGG TTGAAGCTAC AGTGAGCCTT GATTGTGTC CTGCACTCA GCCTGGGCAA 2460
 CAGGTAAAGC TCTGTCTCAA AAAAAAACA AAAAAAGA AGAAAAAGTAC TTCTACAGCC 2520
 35 ATGTCTATT CCTTGATCAT CCAAAGCAC TGCAGAGTCC AGTGAAATGA TATATTCTGG 2580
 CTGGGCACAG TGGCTCACAC CTGTAATCTC AGCACTTTGG GAGGCCAAGG CAGGTGGATC 2640
 AACTGAGGTC AGAAGTTTGA AACCAAGCTG GACTACATGG TGAAGTCCA TCTCTACTAA 2700
 AAGTACAAAA ATTAGCTGGG CATGATGGCA CGCACCTGCA GTCCAGCTA CTGGGAGGC 2760
 TGAGGCAGGA GAATCACTCG AACCCAGGAG GCAGAGGTTG CAGTGAGCCA AGACAGCACC 2820
 40 ATTGCACCCC AGCCTGAGCA ACAAGAGCGA AACTCCATCT CAGGAAAAAA AAAAAAAA 2880
 A

Seq ID NO: 66 Protein sequence:

Protein Accession #: NP_009141

45 1 11 21 31 41 51
 | | | | |
 MRLLRRRHMP LRLAMVGCFA VLFLFLHRD VSSREEATEK PWLKLVSRR DHVLDLMLA 60
 MNNLRDSMPK LQIRAPEAQ TLFSINQSL PGFYTPAELK PFWERPPQDP NAPGADGKAF 120
 QKSWTPLET QEKEEGYKHH CFNAFASDRI SLQSLGPDRT RPPECVDQKF RRCPLATTS 180
 50 VIIVFHNEAW STLLRTVYSV LHTTPAILLK EILVDDAST EEHLKEKLEQ YVKQLQVVRV 240
 VRQEERKGLI TARLLGASVA QAEVLTFLDA HCECFHGWLE PLLARIAEDK TVVVSPIVIT 300
 IDLNTFEFAK PVQGRVHSR GNFDWSLTFG WETLPHEKQ RRDDETYPIK SPTFAGGLFS 360
 IPKSYFEHIG TYDNQMEIWG GENVMSFRV WQCGGQLEII PCSVVGHVFR TKSPTFPKG 420
 55 TSVIARNQVR LAEVMDSYK KIFYRRNLQA AKMAQEKSFG DISERLQRL QHCHNFSWY 480
 LHNVPYEMFV PDLTPFYGA IKNLGTNQL DVGENNRGGK PLIMYSCHGL GGNQYFEYTT 540
 QRDRLHNIK QLCLHYSKGA LGLGSCFTG KNSQVFKDEE WELAQDQLR NSGSGTCLTS 600
 QDKKPAAPC NPSPHQLWL FV

Seq ID NO: 67 DNA sequence

Nucleic Acid Accession #: NM_014112

Coding sequence: 600-4484 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 65 TTCTCCGCG AAGGCTCCTT TGATATTAAT AGTGTGGTG TCTTGAACG GACGTAATGC 60
 GCGGAGACTG AGGTCTGAC AAGCGATAAC ATTTCTGATA AAGACCCGAT CTACTGCAA 120
 TCTTAGCGT CCTTCTTTT GTTGCTGCTG GTTCTCCAG ACCTCGCTC CTCTCGATTG 180
 CTCTCTCGCC TTCTATTTC TTTTCTTTT TTTTAAACAA AAAACAACAC CCCCTCCCT 240
 70 CTCCACCCCG GCACCGGGA CATCCTTGCT CTATTTCTCT TCTCTTCTC TCTCTCTCTC 300
 TCTCTTTT TATAAGGGTG GGGAGGGAA AGGGGGGGA GGCAGGAAAG ACCTTTTCT 360
 CTCCCCCGG CAATAATCCA AGATCAACTC TGCAACAAC AGAAGACGGT TCATGGCTTT 420
 GGCCGCCGCG CCACCATCTT TCGGGCTGCC GAGGGTGTTC TTGACGATTA ATCAACAGAT 480
 GTACAGATCA GCTCTCAAAA TGTCTTCTGT GTCTTCTGAG CGTCTCTAA GACAATTGCA 540
 75 TTAGCTCTCT GCTAGTTGAC TAATAGAATT AATAATTGTA AAAAGCACTT TAAAGCCACA 600
 TGCCTTATGA AGTCAATGCT GGGTATGATT TTACAAATAT GGTCCGGA AAGAACCC 660
 CTCTGAGAAA CGTTGCAAGT GAAGGCGAGG GCCAGATCCT GGAGCCTATA GGTACAGAAA 720
 GCAAGGTATC TGGAAAGAAC AAAGAATTCT CTGCAGATCA GATGTCAGAA AATACGGATC 780

5 AGAGTGTATGC TGCAGAACTA AATCATAAGG AGGAACATAG CTGTGATGTT CAAGATCCAT 840
 CTCTAGCAG TAAGAAGGAC TTGAAAAGCG CAGTTCTGAG TGAGAAGGCT GGCTTCAATT 900
 ATGAAAGCCC CAGTAAGGGA GGAAACTTTC CCTCCTTTC GCATGATGAG GTGACAGACA 960
 GAAATATGTT GGCTTTCTCA TTTCAGCTG CTGGGGGAGT CTGTGAGCCC TTGAAGTCTC 1020
 CGCAAAGAGC AGAGGCAGAT GACCCCTCAAG ATATGGCCTG CACCCCTCA GGGGACTCAC 1080
 TGGAGACAAA GGAAGATCAG AAGATGTCAC CAAAGGCTAC AGAGGAAACA GGCAAGCAC 1140
 10 AGAGTGGTCA AGCCAATTGT CAAGGTTTGA GCCCAGTTTC AGTGGCCTCA AAAAACCAC 1200
 AAGTGCCTTC AGATGGGGGT GTAAGACTGA ATAAATCCAA AACTGACTTA CTGGTGAATG 1260
 ACAACCCAGA CCCGGCACCT CTGTCTCCAG AGCTTCAGGA CTTTAAATGC AATATCTGTG 1320
 GATATGGTTA CTACGGCAAC GACCCACAG ATCTGATTAA GCACTCCGA AAGTATCACT 1380
 TAGGACTGCA TAACCGCAC AGGCAAGATG CTGAGCTGGA CAGCAAAATC TTGGCCCTTC 1440
 ATAACATGGT GCAGTTCAGC CATTCCAAAG ACTTCAGAA GGTCAACCGT TCTGTGTTTT 1500
 CTGGTGTGCT GCAGGACATC AATTCTTCAA GGCCTGTTTT ACTAAATGGG ACCTATGATG 1560
 TGCAGGTGAC TTCAGGTGGA ACATTCACTG GCATTGGACG GAAAACACCA GATTGCCAAG 1620
 15 GGAACACCAA GTATTTCCCG GTAAATTTCT GCAATTTTCA TTATATGGGC AACTCATCCA 1680
 CCGAATTAGA ACAAACTTTT CTTCAGACTC ACCCAAACAA AATAAAAGCT TCTCTCCCCT 1740
 CCTCTGAGGT TGAAAACTCT TCAGAGAAAA ACTCTAACAA GTCCATCCCT GCACITCAAT 1800
 CCAGTGATTC TGGAGACTTG GGAATAATGGC AGGACAAGAT AACAGTCAAA GCAGGAGATG 1860
 ACCTCTCTGT TGGGTACTCA GTGCCATAA AGCCCTCTGA TTCTCTAGA CAAATGGTA 1920
 20 CAGAGGCCAC CAGTTACTAC TGGTGTAAT TTTGTAGTTT CAGCTGTGAG TCATCTAGCT 1980
 CACTTAACT GCTAGAACAT TATGGCAAGC AGCAGGAGC AGTGCAGTCA GCGGCCCTTA 2040
 ATCCAGAGTT AAATGATAAG CTTTCCAGGG GCTCTGTCTA TAATCAGAAT GATCTAGCCA 2100
 AAAGTTCAGA AGGAGAGACA ATGACCAAGA CAGACAAGAG CTCGAGTGGG GCTAAAAAGA 2160
 25 AGGACTTCTC CAGCAAGGGA GCCGAGGATA ATATGGTAAC GAGCTATAAT TGTCACTTCT 2220
 GTGACTTCGG ATATTCCAAA AGCCATGGCC CTGATGTAAT TGTAGTGGGG CCACTTCTCC 2280
 GTCAATTACA ACAGCTCCAT AACATTACCA AGTGATCCAT TAAACACTGT CCATTCTGTC 2340
 CCAGAGGACT TTGACGCCCA GAAAAGCAC TTGGAGAAAT TACTTATCCG TTTGCTTGTA 2400
 GAAAAAGTAA TTGTCCAC TGTCACCTCT TGCTTCTGCA CTGTCTCCT GGGCGGCTG 2460
 30 GAAAGTGGCG AGTCAACAT CAGTGCCATC AGTGTTTCACT CACCACCCT GACGTAGATG 2520
 TACTCTCTT TCACTAGTAA AGTGTGCATG AGTCCCAAGC ATCGGATGTC AAACAAGAAG 2580
 CAAATCACT CCAAGGATCG GATGGGCAGC AGTCTGTCAA GAAAAGCAAA GAACACTCAT 2640
 GTACCAATG TGATTTTATT ACCCAAGTGG AAGAAGAGAT TTCCGACAC TACAGGAGAG 2700
 CACACAGCTG CTACAAATGC CGTCAGTGCA GTTTTACAGC TGCCGATACT CAGTCACTAC 2760
 35 TGGAGCACTT CAAGACTGTT CACTGCCAGG AACAGGACAT CACTACAGCC AACGGCGAAG 2820
 AGGAGCGTGA TGCCATATCC ACCATCAAG AGGAGCCCAA AATTGACTTC AGGGTCTACA 2880
 ATCTGTAAC TCAAGACTCT AAAATGGGAG AGCCAGTTTC TGAGAGTGTG GTGAAGAGAG 2940
 AGAAGCTGGA AGAGAAGGAC GGGCTCAAAG AGAAAGTTTG GACCGAGAGT TCCAGTGATG 3000
 ACCTTCGCAA TGTGACTTGG AGAGGGGCGAG ACATCCTGCG GGGGAGTCCG TCATACACCC 3060
 40 AAGCAAGCTC GGGGCTGCTG ACGCCTGTGT CTGGCACCCA AGAGCAGACA AAGACTCTAA 3120
 GGGATAGTCC CAATGTGGAG GCGGCCCATC TGCGCGGACC TATTATGGC TTGGCTGTGG 3180
 AAACCAAGG ATTTCTGCG GGGGCGCCAG CTGGCGGAGA GAAGTCTGGG GCCCTCCCC 3240
 AGCAGTATCC TGCACTGGGA GAAAACAAGT CCAAGGATGA ATCCAGTCC CTGTTACGGA 3300
 GCGGTAGAGG CTCCGGTGT TTTTGTGCCA ATTGCCTGAC CACAAAGACC TCTCTCTGGC 3360
 45 GAAAGAAATG AAATGGCGGA TATGTATGCA ACGCGTGTGG CCTCTACCA AGACTTCACT 3420
 CGACTCCAG GCCTTTAAAC ATCATTAAAC AAAACAACCG TGAGCAGATT ATTAGGAGGA 3480
 GAACAAGAAA GCGCCTTAAC CCAGAGGCAC TTCAGGCTGA GCAGTCAAC AAACAGCAGA 3540
 GGGGCAAGCA TGAGGAGCAA GTCAATGGAA GCCCGTTAGA GAGGAGGTCA GAAGATCATC 3600
 TAACTGAAAG TCACCAAGAGA GAAATTCAC TCCCCAGCCT AAGTAAATAC GAAGCCAGG 3660
 50 GTTCATTGAC TAAAGCCAT TCTGCTCAGC AGCCAGTCTCT GTTCAGCCAA ACTCTGGATA 3720
 TTCACAAAAG GATGCAACCT TTGCACATTC AGATAAAAG TCCTCAGGAA AGTACTGGAG 3780
 ATCCAGGAAA TAGTTTATCC GTATCTGAAG GGAAGGGAAG TTCTGAGAGA GGCAGTCTCA 3840
 TAGAAAAGTA CATGAGACTT GCGAAACACC CAAATTATTC ACCACAGGC AGCCATTG 3900
 AAAAGTACCA GTACCAACTT TTGGACTTC CCTTTGTACA TAATGACTTC CAGAGTGAAG 3960
 55 CTGATTGGCT GCGGTCTCG AGTAAATATA AGCTCTCCGT TCTGGGAAT CCGCACTACT 4020
 TGAGTCACGT GCCTGGCCTA CCAAATCCTT GCCAAAACCTA TGTGCCTTAT CCCACCTTCA 4080
 ATCTGCCTCC TCAATTTTCA GCTGTGGAT CAGACAATGA CATTCTCTA GATTGGCGA 4140
 TCAAGCATTC CAGACCTGGG CCAACTGCAA ACGGTGCCTC CAAGGAGAAA ACGAAGGCAC 4200
 CACCAATGT AAAAAATGAA GGTCCCTTGA ATGTAGTAAA AACAGAGAAA GTTGATAGAA 4260
 60 GTACTCAAGA TGAACCTTCA ACAAATGTG TGCAGTGTGG CATGTCTTT CTGGATGAAG 4320
 TGATGTATGC TTTGCATATG AGTIGCCATG GTGACAGTGG ACCTTCCAG TGCAGCATAT 4380
 GCCAGCATCT TTGCACGGAC AAATATGACT TCACAACACA TATCCAGAGG GGCCTGCATA 4440
 GGAACAATGC ACAAGTGGA AAAAAATGGA AACCTAAAGA GTAAACCTT AGCACTTAGC 4500
 ACAATTAAT AGAAATAGGT TTTCTTGATG GGAATTCAAT AGCTTGTAA GTCTTATGAA 4560
 65 GACCTATTA AAAAACTT CATAGAGCCT GCCTTATCCA ACATGAAAT CCCTTCTTT 4620
 GTTATCTTT CTTTGTATGA GTAGGTTACC AAGATTAAAA AGTGAGATA ATGGTCAATG 4680
 AGAAGAAATG GAAGATGGTA AACAATCACT TTTTAAACC TGTTAAGTCA AAACCATCTT 4740
 GGCTAATCT TACTGGGGA AATATCCATA AGAGATATCA CCAGACTAGA ATTAATATAT 4800
 TTATAAGAA AGAGACCAAA ACTGTCTAGA ATTTGAAAG GTTACATAT TATTACTA 4860
 70 AAGCAGTACT GGACTGGCCA TTGGACCAT TGTTCAAAA CCCATAAAT GTTGCCTAAA 4920
 TTTATAATG CATGAAACC CTAGGCAGAG GAGGAGAAAT TGAAGGTCCA GGGCAATGAA 4980
 AGAAAAATGG CGCCCTCTCA ATTTAGTCTT CTCTCATTTG CCATGTTTCA GATTTTGACC 5040
 TAGAAATGCG AGCTGTGGT AGGCTTGGT AGAGTGCAGC AAGCAACATG ACAGATGGTG 5100
 GCACGCTGTT TTTACCCAGC CCGCTGTGTA CATACACATG CACACCTCT CTGATATTTT 5160
 75 TGTCTTTAG ATGTTCAAA ACTCAGTAGT CCTTTGTTT GCGGTTTAGA TTCATTTTGT 5220
 CCACACATGT ACCCATTTTA AAAACAATG TCCTCGATGC TTCTGTAGTG ATTTTCAATTT 5280
 AGCCAGGTAT TTTCTTCTG TGTGTGATGA ACCAGTATGG ATTTGCTTTT CTAAGCCTCC 5340
 TGTGTGTTAC TAATCTCAT TGGCACATTA TAACTAAAGG AATCCCTCA ATTCAAAAGC 5400

5 ATAGATGGAT ACAAATGTCA GACCGTGGGT TTAATTTGTT TAGAACACAT GGCATTTCTT 5460
 CACAAGGTAA CCTGCTGTAT TTATTTATTT TCTTTTGTTT AAATATAATT TCCAACTTTT 5520
 GTGGTCAGGC AGCGCTAAG GTTACGTTAC CACAGACTGA CAGTTGGTAT ATGTACCAGC 5580
 CAATCCCTTC ATTAAATGTA TACAGATTAA GTTAAGTAGC ATTAATAGG ATTCTTAGAA 5640
 10 GTATGTCCTC ATAGAACTTT TAATACTTAA GGCTTTGTAA AAACATATCCA TGAAGGGAAA 5700
 GCTCCTCAGC ATAACGTCTC AGGGAAATAG GGCTAAATAA CTGAACATTA AATAATTGGT 5760
 TAAAGGTGCT GTTAGTCGAG CCTCAATGCT TGCTACAAGG ATGTATGTAC AAGGACTGAC 5820
 TTTAATAATT TGCATTATAT TGCCCAACC AGTAGTTTAT TTTTGGCCAC GGAGATGTAG 5880
 AAGATATTAC AAGCTACTGG ATGCACGTGC AGATTAACTT ATTTCAATTA AGAAGTTGGG 5940
 15 AGAACAAATA GGAAAAAATA AACTTATTTT TCTAGTAAAT ATTAATGTAT TACATTTCAA 6000
 ATAATGGTGC CTGACATATT GAATAATTAT TTTCTACAGT GTACGTATGC AACAAAGATA 6060
 TTCCATCATG CATTAGATGC AGTTCTGGCT CTGCTAGCT GTTACATTT GCAAAATGTAG 6120
 CAAACAAGGT AATGAAGCAA CTATTTCTAT TGCAGTAGAT ATCCTTTTGT GTGTGTGTGT 6180
 GTGCATTAAT GTTGTAAACG GTAACATGAA ACAAATGAAA GTTCTTGCTA TAATGGTATG 6240
 20 GAAAAAAGA AGGAATGAA AATATTTTAA TGCCTACTTA GGAAAAAAG GGTAGCACTT 6300
 ATTCATTCCA AGTACTTTTT TTTTITTAAT TTTAAGCTC TTAACTCACA TTGTTATGCT 6360
 TAAGATGATA AACATATATC CTCTTTTAT TGCTTTGTCT ATGTTTCATA TGAACATTT 6420
 CAGAAATTA TTGTATAAGT GTTGCTGGA TCTGCAACGC TGATTTTTTT TTGCATTCTG 6480
 TAGTCGCATT TGCACTCCAT TTTTACATTA ATTCGCAGTT GCTTTGTATC ATTGTTTTGT 6540
 25 TIGGGTTTTG TTCTTTTTC ACAGTGCCGC GTCTTCGTTT CTAAAGTTG GATGGCAGGT 6600
 AGAGTTCAAC CAGTTCGTGA CTGTTGTAGC GAATGAAGTT AAAAAAATGT CTTTCTGATG 6660
 TTGTGTTGTC ATTTTCATTT TTGCATTTTT TTGTTTGCAT ATAAAAAAA GAGAAAAAGAG 6720
 AAAGCAAGAG ACAGAAATCA GGACTAAGTC CTCTGCTTCA GTTTCATTGT TAACGGGCT 6780
 TATTCTGATC TCACCTGTGC CGTAGCTCTA ATATTCACAT AAAGTAAAT AAAGAAGTGG 6840
 30 AATGAGGAGC TTGACATTC AAATTATGTG ATGTAATTTA TCTTCCITAG GAATTTTGAT 6900
 GGATGCATCT CAAAATGTAT AGCCAGACTT GAGAGGTGAC AATTAAGAT CTAAGAAAAA 6960
 GAGGAGATTC CCCCACAA CAATATTTAA TTTTCTAGT AAAAGAATA ACAGAAATGCA 7020
 TCGTGGCAAT CCTTAAGCAA CATTATCTAT GTGGACTGCT TAAATCAGCA AACACCAGA 7080
 AGTTTGGTCA ACTTGGGCAA TATGACAAGT ATTACTTTTT GGGCAAAACT ACTCATTAAG 7140
 35 CAATTTCTCT AGTGTGTCGG ACACAAATAG GTTCTTTAT TTTGGCATGT ATGCCTTTTT 7200
 ATTTTCATTC AATTTTTTTT TTTTCTCAGA CAGACATAGT AGTATCAACT AGCATTGGAA 7260
 AATACATATC ACTATTCTTG GAATATTTAT GGTCACTCTA CTTTITAGTA AAATATTTT 7320
 GGATAGCGTT GACACGATAG ATCTTATTC ATACTTCTTT ATTATTGATA ATTTTATTTT 7380
 CATTTTTTGC TTCAATTAT ATACATATTT TGGTGGAGAA GAGGTTGGGC TTTTTTGAAA 7440
 40 GAGACAAAAA TTTATTATA CACTAACAC TCCTTTTTTG ACATATTAAT GCCTTTATTC 7500
 CATCTCTCAA GATATATTAT AAAATTTATT TTTTAAATTT AAGATTCTG AATTATTTTA 7560
 TCTTAAATTT TGATTTTAAA CGAGCTATTA TGGTACGGAA CTTTTTTTAA TGAGGAATTT 7620
 CATGATGATT TAGGAATTTT CTCTCTTGA AAAGGCTTCC CCTGTGATGA AAATGATGTG 7680
 CCAGCTAAA TTTGTGTGCA TTTAAAAACT GAAAATATTT TAAATTTATT TGTCTATATT 7740
 45 CTAAATTGAG CTTTGGATCA AACTTTAGGC CAGGACCAGC TCATGCGTTC TCATTCTTCC 7800
 TTTTCTCACT CTTTCTCTCA TCACCTACCT CTGTATTCAT TCTGTTGTTT GGGATAGAAA 7860
 AATCATAAAG AGCCAACCCA TCTCAGAACG TGTGGATTG AGAGAGACAC TACATGACTC 7920
 CAAGTATATG AGAAAGGAGC AGAGCTCTAA TTGATAACTC TGATGTTCAA AAGGAAAAA 7980
 50 GTATGCCCAA TTCTCTCTAC ATGACATATT GAGATTTTT TTAATCAACT TTTAAGATAG 8040
 TGATGTTCTG TTCTAAACCTG TTCTGTTTT GTGAAGGTAG ATTTTTATAA AACAAGCATG 8100
 GGGATTCTTT TCTAAGGTAA TATTAATGAG AAGGGAAAAA AGTATCTTTA ACAGCTCTTT 8160
 GTTGAAGCCT GTGGTAGCAC ATTATGTTA TAATTGCACA TGTGCACATA ATCTATTATG 8220
 ATCCAAATGCA AATACAGCTC CAAAAATATT AAATGTATAT ATATTTTAAA ATGCCTGAGG 8280
 AAATACATTT TTCTTAATAA ACTGAAGAGT CTCAGTATGG CTATTAATAA AATTATTAGC 8340
 55 CTCTGTTTGT GTGGCTGCAA AACATCACA AGTGACCGGT CTTGAGACCT GTGAACGTGC 8400
 GCCCTGTGTA GTAAATAAAA TTAATGCATT TCTAGAGGGG GAATATCTGC CATCCAGTGG 8460
 TGGAAATGTG GATGTAAGAA GCTGGTGGTC TGCTTCTGTG CTGTATGCCA GCCTTTTGCC 8520
 TTAAGTTGAG AGGAGGTCAA CTTTAGCTAC TGCTTTGGT TTGAGAGCCA TGGCAAAAAA 8580
 AAAAAAGAAA AAAAAATCA AGTCGTCTTT GGTGAGCCAG TAAAGTGAAA GCTTGCTGAC 8640
 60 TGTCACAGGC ACAAGAGAAA ATTGAGGAAT TGAAATGCAA CCTGAGTATC AAACATAATA 8700
 TTCTAATCAA AGGTAGGTAC TGTTAGGTGG AATTCTATCA GCAGGCAACT GCAATGAGA 8760
 AGAAGATAGA AGGACGCCCG TCGGACTTT GGAGGGCATT GTTATTTTCC CAAAGAAAAA 8820
 CGGCCAAGGG CAGAGGCATG GATTCTTTC AGAGCACTTC CTTTGGGTTT TTCAGTACTG 8880
 TTTTCATAGC AGTGGGCTCA CATGTTCTG ATAGTGCTGC AGTTGCTTAG AAAGCATCCC 8940
 65 AGTTAATTGC AGTAATTAGA ACTTCTGGAA TATGCTAGGG CAGAAATATG TCAAGTATGT 9000
 CACATGAAGA AAATGTGAAA TTCAAGAGTA ATCCACACGT GAGAACTAG ACAATGTACA 9060
 TTCATGTGTT CTCTGAAAG GAAAGGGAGA GCTGTAAGCT TCACTCTGTC CTACACCGGA 9120
 GAAAAAGCAGG AATAACTTTA CCGTGGAAAT AATGTTTAGC TTTTATCAGA GAAAAATTGC 9180
 CTTCTAGAGC ATAGAGTCCC AAAAATCAAT TCTGGTTTTT CCCTGTTTTT TTTTITTTTT 9240
 70 TTTTCCCAA CATATGAAT GCAGCATATC ACTTTTCTT TTTGTGCTC AAGTTCTCTCA 9300
 CCTGTAATAA TGAAAAATAT ATGTATTAAT AATATTATTA ATAATAATAA TGGTAATGTA 9360
 GTACTTGTTT GTAAAGCACT TTGAGATCCT TGGTTGAAAG GCACCATAGG AGTGCCAAAT 9420
 ATATTATGT GGCCAAAGGG GTTATTTAAA CTGTCAGTTC CCAAAGGCCA GGAAAGGTTG 9480
 GGGTCATTTT TCTTAAAGC GAGCTGTAAA TATCAACTAG GCAGCCAATA GTGTGACTA 9540
 75 TGAAGATGCA AAATATTAC TAGGCTGATA AAATCATAGT TTCTTAATGG CTACCAATAA 9600
 GGCAAAATAT ACAATAATA ACGCCAAAT CCTTAGGGCG GACTATTGA CAACCATATG 9660
 GAAAACTTG GGGGAGGCAT GAGGGGGGAA CATCTCAAAA TGCCAATGTA AAATTTAACT 9720
 TACAGCAAT TTACACGACA GAAAAATGCT TCCATATGGA ATGATTTCAT GTTGCTAAGA 9780
 AAAAGAATTC AATTGTAGT CCTGATTGA ATACTAGAAT GTTGCTATA ATAGTTCTGT 9840
 TCTTACAAC CATGAAATTT TTTGTTTTT TTTTATTTT TTTTCAATG GCATGTTTAT 9900
 TTCTACTAC AAACATGTT TGGGTGATT TCTTATGCAA ACAATCTTCA GGCAGCAAA 9960
 ATGCTGTGTA CATCTAACT TGAATAATA AGTTTACCA CCAGTTACAC A

Seq ID NO: 68 Protein sequence:

Protein Accession #: NP_054831

5
1 11 21 31 41 51
| | | | |
MPYEVNAGYD FTNMVRKKNP PLRNVA SEGE GQILEPIGTE SKVSGKNKEF SADQMSENTD 60
QSDAAELNHK EEHSLHVQDP SSSSKDLKS AVLSEKAGFN YESPSKGGNF PSFPHDEVTD 120
10 RNMLAFSPPA AGGVCEPLKS PQRAEADDPQ DMACTPSGDS LETKEDQKMS PKATEETGQA 180
QSGQANCOGL SPVSVASKNP QVPSDGGVRL NKSKTDLN DNDPAPLSP ELQDFKCNIC 240
GYGYGNDPT DLKHFYKYL LGLHNRTRQD AELDSKILAL HNMVQFHSK DFQKVNRSVF 300
SGVLQDINSS RPVLLNGTYD VQVTSGGTFI GIGRKTDPDCQ GNTKYFRCKF CNFTYMGNSS 360
TELEQHFLQT HPNKKASLP SSEVAKPSEK NSNKSIPALQ SSDSGDLGW QDKITVKAGD 420
15 DTPVGYSVPI KPLDSSRQNG TEATSYWCK FCSFSCSSS SLKLEHYGK QHGA VQSGGL 480
NPENLNDLSR GSVINQNDLA KSEGETMTK TDKSSSGAKK KDFSSKGAED NMVTSYNCQF 540
CDFRYKSHG PDVIVVGPLL RHYQLHNIH KCTIKHCPFC PRGLCSPEKH LGEITYPFAC 600
RKSNCSCAL LLLHLSPGA GSSRVKHQCH QCSFTTPDVD VLLFHYESVH ESQASDVKQE 660
ANHLOGSDGQ QSVKESKEHS CTKCDFITQV EEEISRHYRR AHSCYKCRQC SFTAADTQSL 720
20 LEHFNTHCQ EQDITANGE EDGHAISTIK EEPKIDFRVY NLLTPDSKMG EPVSESVVKR 780
EKLEEKDGLK EKVWTESSSD DLNRVTWRGA DILRGSPSYT QASLGLLTPV SGTQEQTTL 840
RDSFNVEAAH LARPYGLAV ETKGFLQGAP AGGEKSGALP QQYPASGENK SKDESQSLR 900
RRRGSGVFCA NCLTKTSLW RKNANGGYVC NACGLYQLKH STPRPLNIK QNNGEQIIR 960
RTRRLNPEA LQAEQLNKQK RGSNEEQVNG SPLRRSEDH LTESHQREIP LPSLSKYEAQ 1020
25 GSLTKSHSAQ QPVLVSQTL D IHKRMQPLHI QKSPQESTG DPGNSSSVSE KGKSSERGS 1080
IEKYMRAKPH PNYSPGSP EKYQYPLFGL PFVHNDQFSE ADWLRFWSKY KLSVPGNPHY 1140
LSHVPGLPNP QONYVPYPTF NLPFHFAVG SDNDIPLDLA IKHSRPGPTA NGASKEKTKA 1200
PPNVKNEGPL NVVKTEKVD R STQDELSTKC VHCIVFLDE VMYALHMSCH GDSGPFQCSI 1260
CQHLCTDKYD FTTHIQRGLH RNNAQVEKNG KPKE

Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: XM_073879

Coding sequence: 1-387 (underlined sequences correspond to start and stop codons)

35
1 11 21 31 41 51
| | | | |
ATGGGGTTTG GAGACCAGG AACGGTGGAA GGGAGCCTAG GAACGTCGAA AAAACCACT 60
GAAGTGAAAA TGTTTGAGC CAGTCAAGGT TTGCTGACAA TGGAAACAAA CCAGTCCCTG 120
GCACAAGGCA CAGGCTGCTC AGTAGTAAAG GTAGACACTG TTCTCTCGA GAGTTTATAC 180
CACTGGCGGT TTGAACACGG GAGCGTGATG CACTGCCTTG GGGATGATCA CCCCAGGAA 240
40 GACAGGAAGG CTCACCTCTC TGCCCCAGT GCAGCCATCG CCTCTCCAGC ACCGACTCCT 300
GTCTGTCTG TCACCACTC AACACAGAGC ATCTGCCAGT TTCTACAGCA CTGCAGGCAG 360
AACACTCACT GACAGGCTGC TAACTA

Seq ID NO: 70 Protein sequence:

Protein Accession #: XP_073879

45
1 11 21 31 41 51
| | | | |
MGFGDQGTVE GSLGTSKPP EVKMFGASQG LLTMTNQSL AQGTGCSVVK VDTVLFESLY 60
50 HCGFEHGSVM HCLGDDHPQE DRKAHFSAPV AAIASPAPT VCPAHSTQS ICQLQHCRQ 120
NTHLQAAN

Seq ID NO: 71 DNA sequence

Nucleic Acid Accession #: AB033064

Coding sequence: 826-1986 (underlined sequences correspond to start and stop codons)

55
1 11 21 31 41 51
| | | | |
GGGGAACAGC AAATTCAGTC ACAGACAATC CTCCACTCGG TCAAGAGCCA CTTTCTCTT 60
CCTGCCTTGC CCCCCGCGAG GGGGTAAGGA ACTGAGCGTT TAATCTTTAG CCGGTTGGCT 120
60 ACCAGCTAAA ATTCTACTTA TCTTAGTTTC TAGTGGATAG CTTCCTTATT TTGCCATGT 180
TTTCTTAGAA TCCCTGTTTA ATATACTTT GTCACTAGTA GTATCTAGGA GTAGCAGGGA 240
GAGTGACAAAT AAATTAGCCC CTCTTTTTT CCCCTGTCAT TCAGGCGCCT TTTCTCTCC 300
AGAGGGAAT TACCAGTAAA CTCTCTAAA TCTTCCACCC CTCTCAGTC ATACTGTGAA 360
65 GAAACACACT AAAGTGGACA TTATTTGACC AGTGAACACG AACCCAGCTT CAGGCATTGG 420
TTTGTGTGG CACATGGAGA AACATCTCTT TTAATAATC TCCCAATTAC CCTTTTCACA 480
ATTGTATCC ACCTAGGATT TGCTGCTGGG GTAAGTCACT AGAATTATTT CTCAAAGCTC 540
CCCTCTCTAT GAGCTGAAAG ACTGACCAAC CATGAACACT AGTAGGGAT GGGGAAAGGG 600
70 GACAGAGCAG AGCAGTTGT TCCACACTT GGGAAAGCAG AGTAGCTTTT ATCATCTTCC 660
TCTGGGGAGC AGGCATAGAG ACATAACTG AGTGAATAAG GGTGGAGGAA GAACCTCTAT 720
ACCCACGAAC AACATGTGAA GAGAGAGAAC CAAACATAAA GTAAGGAGGG TAGACGTTAC 780
ATCCAAGAGG AAATAATCCA GGCAAGGAAG CACAAGCTGA TCAAGATGTG TAGTCTGTG 840
75 GCTGCCAAGT TGTGTTTTT GACAGATCGT CGCATCAGGG AAGACTATCC TCAAAAAGAG 900
ATTTTACGAG CATTGAAGGC CAAATGTTGT GAGGAGGAAC TGGACTTTAG GGCTGTGGTG 960
ATGGATGAGG TGGTGCTGAC AATCGAGCAA GGAAACCTGG GTCTGCGGAT CAATGGAGAG 1020
CTAATCACTG CCTACCCACA AGTGGTGGTA GTCAGAGTAC CAACCCCTTG GGTGCAAAAGT 1080
GATAGTGACA TCACTGTTTT GCGCCATCTA GAGAAGATGG GATGTCGGTT AATGAACCGA 1140

CCTCAAGCCA TCCTGAAGCTG CGTTAATAAG TTCTGGACAT TTCAAGAGTT GGCTGGCCAT 1200
 GGTGTTCCCT TGCCGGATAC TTCTCTTAT GGTGGCCACG AAAATTTTGC TAAATGATT 1260
 GATGAGGCTG AAGTTCTGGA GTTCCCAATG GTAGTAAAGA ATACGCGGGG TCACAGAGGT 1320
 AAAGCTGTTT TCTTGGCTCG AGATAAGCAC CATTTGGCTG ATCTAAGCCA TCTTATTCGC 1380
 5 CATGAAGCGC CATACCTGTT CCAGAAAGTAT GTTAAAGAGT CTCTGGACG GGATGTACGT 1440
 GTCATTGTCG TGGGAGGCCG TGTGGTTGGC ACCATGTTAC GTTGTTCAC AGATGGGAGA 1500
 ATGCAAAGCA ACTGCTCATT AGGTGGTGTG GGGATGATGT GCTCATTTAG TGAACAAGGG 1560
 AAGCAGCTAG CTATCCAGGT GTCTAATATC CTGGGGATGG ATGTGTGTGG CATTGACCTG 1620
 10 CTGATGAAAG ATGACGGCTC CTCTGCGTC TGTGAGGCCA ATGCAAATGT AGGTTTCATC 1680
 GCCTTTGATA AGGCTTGTA TCTAGATGTA GCTGGTATCA TAGCAGACTA TGCCGCTCC 1740
 CTCTACCTT CTGGCCGGCT CACCGGGCT ATGTCCCTGC TCTCCGTGGT GTCCACTGCC 1800
 AGTGAGACTA GTGAGCCGGA GCTGGGTCCC CCAGCCAGCA CTGCTGTTGA CAACATGAGT 1860
 GCAAGTTCCA GCTCTGTTGA CAGGACCTT GAAAGCACGG AGCGAGAGCT GCTCACCAG 1920
 15 CTCCAGGGG GCCTGTTCAC CATGAACCAG CTGCTAGCCA ATGAAATCAA ACTACTGGTG 1980
 GACTGATCC ACTGGTAATT AACCAACAAA ACCCTTGTA AACCTTCTTT CTCTTTTCT 2040
 ATTTTAAAA CCAACTGCA ATGCTGTTCA TGGAGGATGC TCAGGAAGAT GAGAGAAAA 2100
 TAGTAGGATT AGTTGGAGAG AGTGGGAGAT AGATGAGACC TCTGCTAGTA AGATGTTACT 2160
 TTCATTACA AATCCTACAA ATAGAGAGGC AGAATAGGTG GGTATAGAA AAATGTCAGG 2220
 20 CTCTCATAGT TACCCTTTA AATTGCTAAA AAATGTGTAT GCTCATAGGC CATGAGAAC 2280
 AAATACTTTT TTTTTCAT GGTCCCTTGC TTTTGTGTT GTACAAAAAA AAATGGTTTT 2340
 GCTACAAATA TCCAAGTAGC ATAACCTCAC ATGTGTGTTG AAGATTGTG ATCAGTGAGG 2400
 AAAACATCTG CTAAATATC AGGAATTTT GTATTATACA GCTCTGAAAA TTCTGCCATT 2460
 TCCTTATTA CTAGCAGCTT TAGTTGTAG TTTATGAAAT CTGAGGGGG TCTTTTACTG 2520
 25 GGATTCTTTA TTTTGTGTT TTTTCCGCT TAATTGGTG GGAGGTCAA TTGAATATA 2580
 CCCAATAAAG GCTCTTAAT GACAAAATTG GCATGTTTGC ATGATGAAAT GGAATGAAC 2640
 AGTATTGCAA TGTCGGTAT ACAAAATAAC ATTAATTCAA TGTAGATAAA ATTACACTAG 2700
 TTTAAATAT GTGCATTAC TTGTATTGT TAGTGTGTTA GTCTTTTGG AAAGATGTGC 2760
 TCTGTTAATG TTGCTTTTTT TTTTTCAT TAATACATGC TAGTCTAACA TTCTCTGCTC 2820
 30 TAGCGCTGTA TCTTTAACA TGGCCAAAGT GAAGAAAATG CTACCTTTT TGTAAACAAG 2880
 ACACGACTT GAAACATGTA CATTTAAAGC CTTTATTTT TTCCCTTTT GTTTGGTAG 2940
 TTGGGCTTT AAATAAGGAC AAGGAAAAAT ATTTTGGGG GCAAAATCAAG AGCCTATGAG 3000
 TTCTAAGTAT AAAGCTGAAG TGATTTCGAA TGCCAGCTT ATATATTGCT ATTTTTCACA 3060
 TTTTACGAGG GAGTATATGT GTATGTGTG GCACGCTATG ATGTGATGT GTTTTGCTTT 3120
 35 TTGTTTCCAT CACTAATCA AAAAGGATAA TTTAGAAAAA GGAGCATGAT GGGAAACAGA 3180
 GTTTTGAAT TAAAAACA GATGAGTGT TTTCTAAGT AGACTCCACT GGGGTAGAGG 3240
 TATTCACCTT AAAACATAGG GTGAGTAGAT GCTTTTTAG GCCTTTTGT GTATATGTAC 3300
 GTTGTGTTG TTGTTCTTT TTGTTCTAGC CTGTTCAAGT TACAGTTAT TCAAGGCTAC 3360
 ATGCTTTTCT TTAATGCTTC TGCTATGCA TTTTCTTTT TTACATATAG GATTGGGGAT 3420
 40 TGGGGGTGGG TTGATGTTT TTGTTGGGG ACTTATTAG TAGTATTGAG TCTCTTATAG 3480
 CCCTACTCTT AAGCCTTCAA TACTGTCCAC TCTTATATT CCTTACTTG CAGAAATTAT 3540
 AAAAGCCCCC AAATGCTATA TAATATGAGC CTTTAAAAA TGGGTAAAA TAATCCCAT 3600
 GATGGGTTTG GATGGTTATG TAAGAAATGG AGATGCTGCA GAGCCCAACG TAATTTTFTA 3660
 AACAGCAAGT TTTCATCTC CTACGAATC CTCTGAAGCT TTTACCCAAG CCCTTTCTTG 3720
 45 CCTCTCAGT GCTATTTTCC TTCAGATGGA CCTTAAACAT AATTCTTGG AACTACTAG 3780
 AGAGACTTCG AGGCAATAA AAAAGATCAG TATTAACCAG CTATAACAGA GGTTTGATCA 3840
 TGCTTACTTG TACAGTTTTT CCCCCGTTT AAAAAGGAAT GTAATAAAAT TTGTTTTTTC 3900
 CATAGAATTA AATAATATTA AAATTGAGTG AAAGGTTGAT TGTGATGAA TAGAATAGTA 3960
 CCTCTCATCT GTGCACTGTC TCATTTCACC TCAGAGAAAA GGATACATAA GAGGAGTTTG 4020
 50 TAATTTATCT TAGGATATTC TAATTGCATT TAAAAAGACT TATCTTGGCG AGGGTAAATG 4080
 GGGGACTCAC ATACATATAT TAATACCTCT GACTCATTAA CAGAAAGAAA TACTTGGTAC 4140
 TTCTTTGCTG GAATGACCAT ACTGTGGAGG ATGCATACTA TTTGATATAG AGAAATAAAT 4200
 GAGGAAGAAA GAATGCTTA ATTAATATTA CATTATATG TTCATATAGA GACCATCTGG 4260
 TTGCCATGTG TATTATGACA CATACACTTT GAATAGTTAC ATATCACAAG TATGTAGTTC 4320
 55 ATGTTTGTGT TGGTGGGTA AGGCATCAGG AAAAATGTAG TTAGTCTTTT CTTAACTTAT 4380
 ACCAAATTA CCAACTATAT TATAGGAAAT ATGTGAAAT AGTTTATTAG CTTTATTAC 4440
 TATTATGAT TCACATGATA TTAACACGTA CACTCAGATG TTAGAATGAA AAGAGCAGTA 4500
 GTTATCTTAG ATTTTAAAAA CATGGATATC TTCTTGAAT CCTTCAAGT TGAGGTAGAG 4560
 AATAAGAGCA AATCATCTG GAAGTACCTT AAGGAAACAA ACAGCAGCAG ATATTTAGGT 4620
 60 TAAACTTATT TTCATAATTG TTTAATAACT TTTGTATAAT CTTCATTGCT ATTATGAGAG 4680
 AGAATGTATA TATCAAAATAT GTGTAATGAT AAAATCTGAA TTGTAAAAAT TTTGTATATT 4740
 GTTAAAAATT TAATTCTAAA TTGTATTCA AAAATGATTA TTCTGATAT TGTTTTATG 4800
 TCACCAATGA TGAAGACTG ACTTTATATA TCTAAACATA CAAGTATGAA CTATTCTATT 4860
 TAAAAATTTT AATGTTTTT TTCTTTTGG GTGCTTATAA TTGATTGGTC ATTTCTGCTG 4920
 65 GCITTTCTCC AATGAACATT GAAATCTTCC TGTATATGTT ACCAATAAGA AAACCTACCT 4980
 GGAACAGTAG AAAAACCCTA CAAGAGACTT GGCACTCATC AAGCACATTA TCAGACTTTG 5040
 AGAACATATT GAAGGCATTG ACTTTGAAAA TCATCTCTTT TTCTCAAGAA GAAAGCAATG 5100
 GAGAAGCAAA TTTGTTTCAT TCAGTGAATC CCCAGTTTGG GGCTTGTGGG GCTTAGAGAC 5160
 ATTGTGAAT CAAATCTTGT GTTACTTTT TCTCTGGCT CACTTTTTT GAGAAGGTTT 5220
 70 ATGGGCTATT TGGCTGGTGA GACACGATCC CCTCCTAAGA AAATGTAGGT GCTCAGACAG 5280
 GTAAACCCTG CTGCTACTGT TTTTATTGT TTGTTGTTT AATTTATTT AAGATTGTTT 5340
 TTTGTTGATC TAGGATTTTA AAAATGTAA TATATTGAG GATTATAAC CAG

Seq ID NO: 72 Protein sequence:

Protein Accession #: BAA86552

75

| | | | | | |
|---|----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
| | | | | | |

MCSSVAAKLW FLTDRIRED YPQKEILRAL KAKCCEELD FRVVMDEVV LTIEQGNLGL 60
 RINGELITAY PQVVVVRVPT PWVQSDSDIT VLRHLEKMG C RLMNRPQAIL NCVNKFWTFQ 120
 ELAGHGVLPL DTFSYGGHEN FAKMIDEAEV LEPPMVVKNT RGHGRKAVFL ARDKHHLADL 180
 SHLIRHEAPY LFQKYVKESH GRDVRVIVVG GRVVGTM LRC STDGRMQSNC SLGGVGM MCS 240
 LSEQGKQLAI QVSNILGMDV GIDLLMKDD GSFVCEANA NVGFIAFDKA CNLDVAGIIA 300
 DYASLLPSG RLTRMSLLS VVSTASETSE PELGPPASTA VDNMSASSSS VSDPESTER 360
 ELLTKLPGGL FMNQLLANE IKLLVD

Seq ID NO: 73 DNA sequence
 Nucleic Acid Accession #: XM_040080.2
 Coding sequence: 159-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 15 CTGAGTGGGG GCGGGGACTG CTGGAGTTGC GGGGCTGCC TGGGGTAGGG CGGGGCAGGA 60
 CAGCTTGGAG ATAGGGCCCG GAATTGCGGG CGTCACTCTG CTCCTGCGAC CTAGCCAGGC 120
 GTGAGGGAGT GACAGCAGCG CATTGCGGGG ACGAGAGCGA TGAGTGAGAA CGCCGCACCA 180
 GGTCTGATCT CAGAGCTGAA GCTGGCTGTG CCTGGGGGCC ACATCGCAGC CAAAGCCTGG 240
 GGCTCCCTGC AGGGCCCTCC AGTTCTCTGC CTGCACGGCT GGCTGGACAA TGCCAGCTCC 300
 20 TTCCAGAGAC TCATCCTCT TCTCCCGCAA GACTTTTATT ACGTTGCCAT GGATTTCGGA 360
 GGTCTATGGG TCTCGTCCA TTACAGCCCA GGTGTCCCAT ATTACCTCCA GACTTTTGTG 420
 AGTGAGATCC GAAGAGTTGT GGCAGCCTTG AAATGGAATC GATTCTCCAT TCTGGGCCAC 480
 AGCTTCGGTG GCGTCGTGGG CGGAATGTTT TTCTGTACCT TCCCGAGAT GGTGGATAAA 540
 25 CTATCTTGC TGGACACGCC GCTCTTCTC CTGGAATCAG ATGAAATGGA GAACCTGCTG 600
 ACCTACAAGC GGAGAGCCAT AGAGCAGCTG CTGCAGGTAG AGGCCTCCCA GGAGCCCTCG 660
 CAGCTGTTC GCTGAAGCA GCTGCTGCAG AGGTTACTGA AGAGCAATAG CCACCTGAGT 720
 GAGGAGTGC GGGAGCTTCT CTTGCAAAGA GGAACCACGA AGGTGGCCAC AGGTCTGGTT 780
 CTGAACAGAG ACCAGAGGCT CGCTGGGCA GAGAACAGCA TTGACTTCAT CAGCAGGGAG 840
 30 CTGTGTGGCG ATTCCATCAG GAAGCTGCAG GCCCATGTCC TGTGTATCAA AGCAGTCCAC 900
 GGATATTTTG ATTCAAGACA GAATTACTCT GAGAAAGGAGT CCCTGTGCTT CATGATAGAC 960
 ACGATGAAAT CCACCTCAA AGAGCAGTTC CAGTTGTGG AAGTCCAGG CAATCACTGT 1020
 GTCCACATGA GCGAACCCCA GCACGTGGCC AGTATCATCA GCTCCTTCTT ACAGTGCACA 1080
 CACATGCTCC CAGCCAGCT GTAGCTCTGG GCCTGGAAC ATGAAGACCT AGTGCTCCCA 1140
 35 GACTCAACAC TGGGACTCTG AGTTCTGTAG CCCCAACAAG AGGCCAGGGA TGGTGGGGAC 1200
 AGGCCTCACT AGTCTTGAAG CCCAGCCTAG GATGTTAGTC AGGGGAAGGA GCGAGATTCC 1260
 AACTTCAACA TCTGTGACCT CAAGGGGGAG ACAGAGTCTG GGTTCAGGG CTGCTTCTC 1320
 CTGGCTAATA ATAAATATCC AGCCAGCTGG AGGAAGGAAG GGCAGGCTGG GCCCACCTAG 1380
 CCTTCCCTG CTGCCCAACT GGATGAAAA TAAAAGGTTT TTGATTCTC A

Seq ID NO: 74 Protein sequence:
 Protein Accession #: XP_040080.1

1 11 21 31 41 51
 | | | | |
 45 MSENAPGLI SELKLAVPWG HIAAKAWGSL QGPPVLC LHG WLDNASSFDR LIPLLPQDFY 60
 YYAMDFGGHG LSSHYSGVP YYLQTFVSEI RRVVAALKWN RFSILGHSFG GVVGMFFCT 120
 FPEMVDKLIL LDTPLFLES DEMENLLTYK RRAIEHV LQV EASQEP SHV SLKQLLRLL 180
 KSNSHLSEEC GELLQRTGT KVATGLVLNR DQRLAWAENS IDFISRELCA HSIRKLQAHV 240
 50 LLKAVHGVF DSRQNYSEKE SLFSMIDTMK STLKEQFQV EVPGNHCVHM SEPQHVASII 300
 SSFLQCTHML PAQL

Seq ID NO: 75 DNA sequence
 Nucleic Acid Accession #: NM_005794
 Coding sequence: 434-1276 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 55 GGTTCCTTC CACGCTGTA AGCTTTGTC TTTTGGTCTT CATGATAAT CTGTGCTG 60
 CTCACCTCGT GGTTCCTGTC CACCTTAAAG AGCTGTAAAC CTCACCGCGA AGGTCTGCAA 120
 60 CTTCACTCCT GGGGCCAGCA AGACCAAGAA TGCACCGAGA GGAATGAACA ACTCTGGACA 180
 CACCATCTTT AAGAACCGTA ATACTCACCG CAAGGGTCTG CAACTTCATT CTTGAAGTCA 240
 GTGAGGCCAA GAACCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTCAAC 300
 TATCAACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360
 CACCAAGCGG TGAGACTATC ACCTATCGCC AAGTGGCCTG ATTCAAGCAGG AAGCATCTCA 420
 65 GACACCAACC ACTATGCTGT CAGCAGTTGC CCGGGGCTAC CAGGGCTGGT TTCACTCCTG 480
 TGCTAGGCTT TCTGTGAGGA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA 540
 CCGGGTAGCC GTGGTCAAGG GGTCCACCAG TGGATCGGC TTTGCCATCG CCCGACGTCT 600
 GGCCTGGGAC GGGGCCACG TGGTCATCAG CAGCCGGAAG CAGCAGAAAG TGGACCGGGC 660
 CATGGCCAAG CTGAGGGGGG AGGGGCTGAG TGTGCGGGG ATTGTGTGCC ACGTGGGGAA 720
 70 GGCTGAGGAC CGGGAGCAGC TGGTGGCCAA GGCCTGGAG CACTGTGGGG GCGTCGACTT 780
 CCTGGTGTGC AGCGCAGGGG TCAACCTCTT GGTAGGGAGC ACTCTGGGGA CCAGTGAGCA 840
 GATCTGGGAC AAGATCCTAA GTGTGAACGT GAAGTCCCA GCCCTGTGTC TGAGCCAGTT 900
 GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTATCCTG GTCTCTTCCA TTGAGCTTA 960
 75 TAATCAGTA GTGGCGCTGG GTGTCTACAA TGTCAGCAAG ACAGCGCTGC TGGGTCTCAC 1020
 TAGAACACTG GCAATTGGAGC TGGCCCCAA GGACATCCCG GTAAACTGCG TGGTCCAGG 1080
 AATTATAAAA ACTGACTCA GCAAAGTGT TTATGGGAAT GAGTCTCTCT GGAAGAAGTT 1140
 CAAGGAACAT CATCAGTGC AGAGGATTGG GGAGTCAGAG GACTGTGCAG GAATCGTGTG 1200

CTTCTGTGC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA 1260
 CTCCTCTCGG CTCTGAGAGG AGTGGGGGCG GCTGCGTAGC TGTGGTCCA GCCCAGGAGC 1320
 CTGAGGGGGT GTCTAGGTGA TCATTGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT 1380
 AGCAATTTGG GGGCTTACTC ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGGCATTCT 1440
 CC

Seq ID NO: 76 Protein sequence:
 Protein Accession #: NP_005785

1 11 21 31 41 51
 | | | | |
 ML SAVARGVQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLRDGD 60
 AHVVISSRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGGVDFLVCS 120
 AGVNPLVGGT LGTSEQIWDK ILSVNVKSPA LLSQLLPYM ENRRGAVILV SSIAAYNPVV 180
 ALGVYVNSKT ALLGLTRTLA LELAPKDIRV NCVVPGIIKT DFSKVFGHNE SLWNKFEHH 240
 QLQRIGESD CAGIVSFLCS PDASYVNGEN IAVAGYSTRL

Seq ID NO: 77 DNA sequence
 Nucleic Acid Accession #: NM_002425
 Coding sequence: 26-1453 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGTCTGCC 60
 AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
 TGCCACAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
 AAAGGACAGT AATCTCATTG TTAATAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
 GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG GCCAAGCCCA GGTGTGGAGT 300
 TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
 TACATACAGG ATTGTGAATT ATACACCAGA TTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
 TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
 AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
 TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
 TATTCATTTT GATGATGATG AAAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
 CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGAAGC 720
 TTTGATGTAC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTTCGCC TTTGCAAGA 780
 TGATGTGAAT GGCACTCAGT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
 GGTGGCCACA AAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
 GTCTTCCTG GGCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
 TTGGGAAGA TCCCACTGGA ACCCTGAACC TGAATTCAT TTGATTCTG CATTTGGCC 1020
 CTCTCTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT 1080
 TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAATGAG GTACAAGCAG GTTATCCAAG 1140
 AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCA CTGTTTCTGA 1200
 CAAGGAAAAG AAGAAACAT ACTTCTTTC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
 TAGCCAGTCC ATGGAGCAAG GCTTCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
 GCCTAAGGTT GATGCTGAT TACAGGCATT TGGATTTTTT TACTTCTCA GTGGATCATC 1380
 ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
 GTTACATTGC TAGGCGAGAT AGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA 1500
 ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGTCATG TTCTGTGACT 1560
 GAAGAAGATG AGCCTTGAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTTCTC 1620
 ACTTGCTTTT GAATGCTACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
 ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
 CTT

Seq ID NO: 78 Protein sequence:
 Protein Accession #: NP_002416

1 11 21 31 41 51
 | | | | |
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQF RRKDSNLIVK 60
 KIQGMOKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGFY SFDGPGHSLA 180
 HAYPPGPGLY GDIHFDDEK WTEDASGTNL FLVAAHELGH SIGLFHSANT EALMYPLVNS 240
 FTELAQFRLS QDDVNGIQL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
 RGEYLFFKDR YFWRRSHWNP EPEFHLISAF WFLPSYLD AYEVSRTDTV FIFKGNFWFA 360
 IRGNEVQAGY PRGIHTLGF PTKRIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
 PRLIADDFPG VEPKVDAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 79 DNA sequence
 Nucleic Acid Accession #: NM_000493.1
 Coding sequence: 1-2043 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGCTGCCAC AAATACCCCT TTTGCTGCTA GTATCCTTGA ACTTGGTTCA TGGAGTGTTC 60
 TACGCTGAAC GATACCAAC GCCCAGAGGC ATAAAAGGCC CACTACCCAA CACCAAGACA 120

CAGTTCCTTCA TTCCCTACAC CATAAAGAGT AAAGGTATAG CAGTAAGAGG AGAGCAAGGT 180
 ACTCCTGGTC CACCAGGCCC TGCTGGACCT CGAGGGCACC CAGGTCTTC TGGACCAACA 240
 GGAAAACCCAG GCTACGGGAG TCCTGGACTC CAAGGAGAGC CAGGGTTGCC AGGACCAOCC 300
 5 GGACCATCAG CTGTAGGGAA ACCAGGTGTG CCAGGACTCC CAGGAAAAAC AGGAGAGAGA 360
 GGACCATATG GACCAAAAGG AGATGTTGGA CCAGCTGGCC TACCAGGACC CCGGGGCCCA 420
 CCAGGACATC CTGGAATCCC TGGACCGGCT GGAATTTCTG TGCCAGGAAA ACCTGGACAA 480
 CAGGGACCCA CAGGAGCCCC AGGACCCAGG GGCTTTCTCTG GAGAAAAAGG TGCACCAAGGA 540
 GTCCCTGGTA TGAATGGACA GAAAGGGGAA ATGGGATATG GTGCTCCTGG TCGTCCAGGT 600
 10 GAGAGGGGTC TTCCAGGCCC TCAGGGTCCC ACAGGACCAT CTGGCCCTCC TGGAGTGGGA 660
 AAAAGAGGTG AAAATGGGGT TCCAGGACAG CCAGGCATCA AAGGTGATAG AGGTTTTCG 720
 GGAGAAATGG GACCAATTTG CCCACCAAGT CCCCAAGGCC CTCCTGGGGA ACGAGGGCCA 780
 GAAGGCATTG GAAAGCCAGG AGCTGCTGGA GCCCAGGCC AGCCAGGGAT TCCAGGAACA 840
 AAAGGTCTCC CTGGGGCTCC AGGAATAGCT GGGCCCCCAG GGCCTCCTGG CTTTGGGAAA 900
 15 CCAGGCTTGC CAGGCTGAA GGGAGAAAGA GGACCTGCTG GCCTTCCTGG GGGTCCAGGT 960
 GCCAAAGGGG AACAAGGGCC AGCAGGTCTT CTGGGAAGC CAGGTCTGAC TGGACCCOCT 1020
 GGAATATGG GACCCCAAGG ACCAAAGGC ATCCCGGTA GCCATGGTCT CCCAGGCCCT 1080
 AAAGGTGAGA CAGGCCCAGC TGGGCTGCA GGATACCTG GGGCTAAGGG TGAAGGGGT 1140
 TCCCTGGGT CAGATGAAAA ACCAGGTAC CCAGGAAAAC CAGGTCTCGA TGGTCTAAG 1200
 20 GGTAACCCAG GGTACCCAGG TCCAAAAGGT GATCCTGGAG TTGGAGGACC TCCTGGTCTC 1260
 CCAGGCCCTG TGGGCCCAGC AGGAGCAAAAG GGAATGCCCG GACACAATGG AGAGGCTGCG 1320
 CCAAGAGGTG CCCTCTGAA ACCAGTACT AGAGGCCCTA TTGGGCCACC AGGCATTCCA 1380
 GGATTCCTG GTCTAAAGG GGATCCAGGA AGTCCCGTC CTCCTGGCCC AGCTGGCATA 1440
 GCAACTAAGG GCCTCAATGG ACCCACCAGG CCACCCAGGC CTCACAGTCC AAGAGGCCCC 1500
 25 TCTGGAGAGC CTGGTCTTCC AGGGCCCCCT GGGCCTCCAG GCCCACCAGG TCAAGCAGTC 1560
 ATGCTGAGG GTTTTATAAA GGCAGGCCAA AGGCCAGTC TTCTGGGAC CCCTCTTGT 1620
 AGTCCAAACC AGGGGGTAA AGGAATGCCT GTGTCTGCTT TTAAGTTAT TCTCTCCAAA 1680
 GCTTACCCAG CAATAGGAAC TCCCATACCA TTTGATAAAA TTTGTATAA CAGGCAACAG 1740
 CATTATGACC CAAGGACTGG AATCTTTACT TGTACAGATC CAGGAATATA CTATTTTCA 1800
 30 TACCACGTG ATGTGAAAGG GACTCATGTT TGGGTAGGCC TGTATAAGAA TGGCACCCCT 1860
 GTAATGTACA CCTATGATGA ATACACCAA GGCTACCTGG ATCAGGCTTC AGGGAGTGCC 1920
 ATCATCGATC TCACAGAAAA TGACCAGGTG TGGCTCCAGC TTCCAATGC CGAGTCAAAT 1980
 GGCCTATACT CTTCTGAGTA TGTCCACTCC TCTTCTCAG GATTCTAGT GGCTCCAAAT 2040
 TGAATACACC CCACAGAGCT AATCTAAATC TTGTGCTAGA AAAAGCATTC TCTAACTCTA 2100
 35 CCCACCCATC CAAATTTTCC ATGGAGGTAG GCTGAAAAAG ATGTAATTTT TATTTTCTGA 2160
 AATACAGATT TGAGCTATCA GACCAACAAA CCTTCCCCT GAAAAGTGAG CAGCAACGTA 2220
 AAAACGTATG TGAAGCCTCT CTGAATTTT TAGTTAGCAA TCTTAAGGCT CTTAAGGTT 2280
 TTCTCCAATA TAAAAAATA TCACCAAGA AGTCCTGCTA TGTAAAAAAC AAACAACAAA 2340
 AAACAAAGCA AAAAAAATA AAATTAATAA AAAAAACAGA AATAGAGCTC TAAGTTATGT 2400
 40 GAAATTTGAT TTGAGAAACT CGGCATTTC TTTTAAAAA AGCCTGTTT TAACATGAA 2460
 TATGAGAACT TCTAGGAAAC ATCCAGGAGG TATCATATAA CTTTGTAGAA CTTAAATACT 2520
 TGAATATCA AATTTAAAG ACATGTATC CCTTAAATA TTCTGATGG TGCACACTC 2580
 TGAGGCCCTG ATGGCCCCCT TCATCAATAT CTATTCAAAT ATACAGGTGC ATATATACT 2640
 GTTAAGCTC TTATATAAAA AAGCCCCAAA ATATTGAAGT TCATCTGAAA TGCAAGGTGC 2700
 45 TTTCATCAAT GAACCTTTT AAACTTTT TATGATTGCA GAGAAGCTT TTATATACCC 2760
 AGCATAACTT GGAACAGGT ATCTGACCTA TTCTTATTTA GTTAACACAA GTGTGATTAA 2820
 TTTGATTTCT TTAATTCCT ATTGAATCTT ATGTGATATG ATTTTCTGGA TTACAGAAC 2880
 ATTACCAT GTACCTTGTG CCTCCATT CAGTGAAGTT ATAATTTACA CTGAGGGTTT 2940
 CAAAATTCGA CTAGAAGTGG AGATATATTA TTTATTTATG CACTGTACTG TATTTTATA 3000
 50 TTGCTGTTA AAACTTTAA GCTGTGCTC ACTTATTTAA GCACAAAATG TTTTACCTAC 3060
 TCCTTATTTA CGACACAATA AAATAACATC AATAGATTTT TAGGCTGAAT TAATTTGAAA 3120
 GCAGCAATTT GCTGTCTCA ACCATTCTT CAAGGCTTTT CATTCGACAC AATAAAATAA 3180
 CATCAATAGA TTTTTAGG

Seq ID NO: 80 Protein sequence:

Protein Accession #: NP_000484.1

1 11 21 31 41 51
 | | | | |
 60 MLPQIPFLLL VSLNLVHGVF YAERYQPTPTG IKGPLPNTKT QFFIPYTIKS KGI AVRGEQG 60
 TPGPPGAPG RHHPGPGSPG GKPGYGSPL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
 GPYGPKG DVG PAGLPGRPG PPGPIGPA GISVPGKPGQ QGPTGAPGR GFPGEKAPG 180
 VPMNGQKGE MGYGAPGRPG ERGLPGQPG TPGSGPPGVG KRGENGVPQG PGIKGDRGFP 240
 65 GEMGPIPPG PQGPPGERP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
 PGLPLGKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGP GNMGPQGPKG IPGSHGLPGP 360
 KGETGPAGPA GYPGAKGERG SPGSDGKPG Y PGKPLDGP K GNPGLPGPK DPGVGGPPGL 420
 PGVPGPAGAK GMPGHNGEAG PRGAPGIPGT RGPIGPPGIF GPPGSKODPG SPGPPGPAI 480
 ATKGLNGPTG PPGPPGPRG SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
 70 SANQGVGTGP VSAFTVILSK AYPAGTPIP FDKILYNRQQ HYDPRTGIFT CQIPGIYYS 600
 YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
 GLYSSEYVHS SFSGFLVAPM

Seq ID NO: 81 DNA sequence

Nucleic Acid Accession #: NM_000786

Coding sequence: 332-1861 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |

CGCGATTCTC AGGGAATTGAT CGGCCTCTTC AGGTAAGTTA TCTTCGGGCC CCGTACCACT 60
 GTGCCACAGG CGCAGCCCGC TTCCTCAGGT GCCCTATCCC GCGCAGAAGA CCACGGCTTC 120
 ACAGAGTGTG ATTTAAGGGC GTGGCCAGCG GAACATCCCG CCCCATTTCTG TGAOCGACGG 180
 GGTGGGCGCG GTGGGACCCG AGGGGTGGGG CTGGGTTTAG TAGGAGACCT GGGGCAAGGC 240
 CCCCTGTGGA CGACCATCTG CCAGCTTCTC TCGTTCGTC GATTGGGAGG AGCGGTGGCG 300
 ACCTGGCCTC TCAGTGTTC CGACGGAGTG AATGGCGGCG GCGGCTGGGA TGCTGCTGCT 360
 GGGCTTGCTG CAGGCGGGTG GGTGGGTGCT GGGCCAGGCG ATGGAGAAGG TGACAGGCGG 420
 CAACCTCTTG TCCATGCTGC TGATCGCCTG CGCCTTCACC CTCAGCCTGG TCTACCTGAT 480
 CCGTCTGGCC GCCGGCCACC TGGTCCAGCT GCCGCGAGGG GTGAAAAGTC TCCTATACAT 540
 TTTCCTCCCA ATTCATTCC TTGGGCATGC CATAGCATTT GGGAAAAAGT CAATTGAATT 600
 TCTAGAAAA GCATATGAGA AGTATGGACC TGATTTAGT TTTACCATGG TAGGCAAGAC 660
 ATTTACTTAC CTTCGGGGA GTGATGCTGC TGCACTGCTT TTTAATAGTA AAAATGAAGA 720
 CCTGAATGCA GAAGATGCT ACAGTGGCCT GACAACACCT GTGTTTGGGA AGGGAGTTGC 780
 ATACGATGTG CCTAATCCAG TTTCTTGGG GCAGAAGAAA ATGTTAAAA GTGGCCTTAA 840
 CATAGCCCACT TTTAAACAGC ATGTTTCTAT AATTGAAAAA GAAACAAAGG AATACTTTGA 900
 GAGTTGGGGA GAAAGTGGAG AAAAAATGT GTTTGAAGCT CTTTCTGAGC TCATAATTTT 960
 AACAGCTAGC CATTTGTTTG ATGGAAAGGA AATCAGAAGT CAACTCAATG AAAAGGTAGC 1020
 ACAGCTGTAT GCAGATTGG ATGGAGGTTT CAGCCATGCA GCCTGGCTCT TACCAGGTTG 1080
 GCTGCCCTTG CCTAGTTTCA GACGCGAGGA CAGAGCTCAT CGGGAATCA AGGATATTTT 1140
 CTATAAGGCA ATCCAGAAAC GCAGACAGTC TCAAGAAAAA ATTGATGACA TTCTCCAAAC 1200
 TTTACTAGAT GCTACATACA AGGATGGGCG TCCTTTGACT GATGATGAAG TAGCAGGGAT 1260
 GCTTATTGGA TTACTCTTGG CAGGCGAGCA TACATCTCA ACTACTAGTG CTGGGATGGG 1320
 CTCTTTTGG GCCAGAGACA AAACACTTCA AAAAAATGT TATTAGAAC AGAAACAGT 1380
 CTGTGGAGAG AATCTGCTC CTTTAACTTA TGACCACTC AAGGATCTAA ATTTACTTGA 1440
 TCGCTGTATA AAAGAAACAT TAAGACTTAG ACCTCCTATA ATGATCATGA TGAGAATGGC 1500
 CAGAACTCCT CAGACTGTGG CAGGGTATAC CATTCCTCCA GGACATCAGG TGTGTGTTTC 1560
 TCCCACTGTC AATCAAGAC TTAAGACTC ATGGGTAGAA CGCTGGACT TTAATCTGA 1620
 TCGTACTTCA CAGGATAACC CAGCATCAGG GGAAGGTTT GCCTATGTGC CATTGGAGC 1680
 TGGGCGTAT CGTTGTATTG GGGAAAAATT TGCCTATGTT CAAATTAAGA CAATTTGGTC 1740
 CACTATGCTT CGTTTATAGT AATTGTATCT CATTGATGGA TACTTTCCA CTGTGAATTA 1800
 TACAATATG ATTCACACCC CTGAGAACCC AGTTATCGT TACAAACGAA GATCAAAATG 1860
 AAAAAAGTTG CAAGGAACGA ATATATGTGA TTATCACTGT AAGCCACAAA GGCATTGCAA 1920
 GAGAAATGAAG TGTACAAAAA AACTCTTGTG GTTACTGTT TTTTAAAGTG TGTAAATCTA 1980
 AAAGCCAGTT TATGATTTAG GATTTTGTTA ACTGAATGGT TCTATCAAA ATAATAGCAT 2040
 TTGACACATT TTCTAATAGT TATGATACTT ATACATGTGC TTTCAGGAAG TTCCTTGGTG 2100
 AAACAATGTT TGAGGGGGGA TCTAGGTAAT TGGCAGATTC TAAATAATAT AATTCCAGA 2160
 TAGTAATTTT AAGAGTACT ATCGCTCTTG CCAATAAAGT TCAGGGTATT CAAATCTTGG 2220
 ACTAGTCTG CAAGGTATAA AGAATAAAAA TCCCAAGTGA ATACTTGGAA ACCACAGTTT 2280
 ATTATATTT ATCTGGGCAA TTATTGTGTG TGTGAGGATG GAAGGGTAGG GAATAATCGA 2340
 ACATCAAAAG CCTTGAATAA GAGAATACTA ATTGTTTGG TATGATGATA CTCAGAAATG 2400
 GAGATATTAT AGGAAAAAGA AATCCTTTGG AATTTAACT AAAATCACTG CATATGGGAA 2460
 ATTAAGAGAT CCAGGACCAT ATTTGATAAG AGTTCCTAAA AATAATGTAA TTATTAATGC 2520
 TAAAGACTGC TCATGTATCT TGA TCTAATT ACTAAATAA TTACATATTT ATTTACCTGA 2580
 TAAATATGTA TCTAGTTCTA CAAGGTGACA TTTATGTGGA AGTCCAAAGT CAAGTCTTA 2640
 GGGGATAATT TTGTTTGGG CTCAGTTGTT CCCTGCTTCC TTTTITTTT TTTTITTTT 2700
 TTGAGATGGA GTCTCGCTCT GTTGCCGAGG CTGGAGTGCA GTGGTGCGAT CTCAGCTCAC 2760
 TGCATCTCT GCCTCCCGGG TTCAAGCAAT TCTTGCCTC AGCTCCCAA GTAGTTGGGA 2820
 TTACAGGCAC CTGGCACCAT GCCTGGCTAA TTTTGTAT TTTTAGTGA GACGGGGGTT 2880
 TCACTATGTT GGCTAGGCTG GTCTTGAAC CTGAGCCTC GTGAGTCCAC CCGCCTTGGC 2940
 CTCCAAAGT GCTGGGATTA CAGGCATGAG CCACCGCACC TGGCCTTCCC TGCTTCTCT 3000
 CTAGAAATCCA ATTAGGATG TTTGTTACTA CTCATATTGA TTAACACAGT TAACAAACTT 3060
 TTTTCTTTT AAAATGTGAG ATCAGTGAAC TCTGGTTTAA AGATAATCTG AAACAAGGTC 3120
 CTGGGAGTA ATAAATTTGG TCACATTCTG TAAAGCACAT TCTGTTTAGG AATCAACTTA 3180
 TCTCAAATTG TAACCTGGGG CCTAACTATA TGAGATGGCT GAAAAAATAC CACATCGTCT 3240
 GTTTTCACTA GGTGATGCCA AAATATTTTG CTTTATGTAT ATTACAGTTC TTTTAAAAAC 3300
 ACTGGAAGAC TCATGTTAAA CTCTAATTG GAAGGCAGAA TCTCTGCTAA TTTTCAGAT 3360
 TAAATCTCT TTTGAAAAAA T

Seq ID NO: 82 Protein sequence:
 Protein Accession #: NP_000777

1 11 21 31 41 51
 MAAAGMLLL GLQAGGSVL GQAMEKVTGG NLLSMLLIAC AFTLSLVYLI RLAAGHLVQL 60
 PAGVKSPPYI FSPFPLGHA IAFGKSPIEF LENAYEKYGP VFSFTMVGKT FTYLLGSDAA 120
 ALLFNSKNED LNAEDVYSRL TTPVFGKGA YDVPNPVFE QKKMLKSLGN IAHFKQHVSI 180
 IEKETKEYFE SWGESGEKNV FEALSELIL TASHCLHGKE IRSQLEKVA QLYADLDGGF 240
 SHAAWLLPGW LPLPSFRRRD RAHREIKDFI YKAIQKRRQS QEKIDDLQ LLDATYKDR 300
 PLTDDDEVAGM LIGLLLAGQH TSSTSAWMG FFLARDKTLQ KCYLEQKTV CGENLPPTY 360
 DQLKDLNLLD RCIKETRLRL PPMIMMRMA RTPQTVAGYT IPFGHQVCVS PTVNQRKDS 420
 WVERLDNPD RYLQDNPASG EKFAVYVFGA GRHRCIGENF AYVQIKTIWS TMLRLYFDL 480
 IDGYFTVNY TTIHTPENP VIRYKRRSK

Seq ID NO: 83 DNA sequence
 Nucleic Acid Accession #: NM_006551.2
 Coding sequence: 64-336 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 5 AATTCTAGAA GTCCAAATCA CTCATTGTTT GTGAAAGCTG AGCTCACAGC AAAACAAGCC 60
 ACCATGAAGC TGTCGGTGTG TCTCCTGCTG GTCACGCTGG CCTCTGCTG CTACCAGGCC 120
 AATGCCGAGT TCTGCCCAGC TCTTGTTTCT GAGCTGTTAG ACTTCTTCTT CATTAGTGAA 180
 CCTCTGTTCA AGTTAAGTCT TGCCAAATTT GATGCCCTC CGGAAAGCTGT TGCAGCCAAAG 240
 TTAGGAGTGA AGAGATGCAC GGATCAGATG TCCCTTCAGA AACGAAGCCT CATTGCGGAA 300
 10 GTCTGCTGTA AAATATTGAA GAAATGTAGT GTGTGACATG TAAAAACTTT CATCCTGGTT 360
 TCCACTGTCT TTCAATGACA CCTGATCTT CACTGCAGAA TGTAAAGGTT TCAACGTCTT 420
 GCTTTAATAA ATCACTTGCT CTAC

Seq ID NO: 84 Protein sequence:

Protein Accession #: NP_006542.1

1 11 21 31 41 51
 | | | | |
 15 MKLSVCLLLV TLALCCYQAN AEFCPALVSE LLDFFFISEF LFKLSLAKFD APPEAVAANKL 60
 20 GVKRCTDQMS LQKRSLIAEV LVKILKKCSV

Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: NM_002317.1

Coding sequence: 231-1484 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 25 GGGCCAGGAC TGAGAAAGGG GAAAGGGAAG GGTGCCACGT CCGAGCAGCC GCCTTGACTG 60
 GGGAAAGGTC TGAATCCAC CCTTGGCATT GCTTGGTGA GACTGAGATA CCCGTGCTCC 120
 30 GCTCGCTCC TGGTTGAAG ATTCTCCTT CCTCACGTG ATTTGAGCCC CGTTTTTATT 180
 TTCTGTGAGC CAGCTCCTCC TCGAGCGGGG TCAATCTGGC AAAAGGAGTG ATGCGCTTGG 240
 CCTGGAACGT GCTCCTGCTC GGGCCTTGC AGCTCTGCGC GCTAGTGCAC TCGGCCCTC 300
 CCGCCGCCGG CCAACAGCAG CCCCAGCGCG AGCGCCGGC GGTCCGGGC GCCTGGCGCC 360
 AGCAGATCCA ATGGGAGAAC AACGGGCAAG TGTTCAAGCTT GCTGAGCCTG GGCTCACAGT 420
 35 ACCAGCCTCA GCGCCGCCGG GACCCGGGGG CCGCCGTCCC TGGTGACGCC AACGCTCCG 480
 CCCAGCAGCC CCGCATCCG ATCCTGTGA TCCGCGACAA CCGCACCGCC GCGGGGCGAA 540
 CGGGACGGC CGGCTCATCT GGAGTCAACG CTGGCCGCC CAGGCCACC GCCCGTCACT 600
 GGTTCCAAGC TGGCTACTCG ACATCTAGAG CCGCGAAGC TGGGCCCTCG CGCGCGGAGA 660
 ACCAGACAGC GCGGGGAGAA GTTCTGCTC TCAGTAACCT GCGGCCGCC AGCGCGTGG 720
 40 ACGGCATGGT GGGCGACGAC CCTTACAACC CCTACAAGTA CTCTGACGAC AACCTTATT 780
 ACAACTACTA CGATACTTAT GAAAGGCCCA GACCTGGGG CAGGTACCG CCCGATACG 840
 GCACCTGGTA CTTCAGTAC GTTCTCCAG ACCTGGTGGC CGACCCCTAC TACATCCAGG 900
 CGTCCACGTA CGTGCAAGAG ATGTCCATGT ACAACCTGAG ATGCGCGGCG GAGGAAAACT 960
 GTCTGGCCAG TACAGCATAC AGGGCAGATG TCAGAGATTA TGATCACAGG GTGCTGCTCA 1020
 45 GATTTCCCA AAGAGTGAAA AACCAAGGGA CATCAGATTT CTTACCCAGC CGACCAAGAT 1080
 ATTCTGGGA ATGGCACAGT TGTCATCAAC ATTACCACAG TATGGATGAG TTTAGCCACT 1140
 TGTAACCTGT TGATGCCAAC ACCAGAGGA GATGGGCTGA AGGCCACAAA GCAAGTTTCT 1200
 GTCTTGAAGA CACATCCTGT GACTATGGCT ACCACAGGCG ATTTGCATGT ACTGCACACA 1260
 CACAGGGATT GAGTCTGGC TGTTATGATA CCTATGGTGC AGACATAGAC TGCCAGTGGA 1320
 50 TTGATATTAC AGATGTAAAA CCTGGAACT ATATCTTAAA GGTCAGTGTA AACCCAGCT 1380
 ACCTGGTTC TGAATCTGAC TATACCAACA ATGTTGTGCG CTGTGACATT CGCTACACAG 1440
 GACATCATGC GTATGCCTCA GGCTGCACAA TTACCCGTA TTAAGGCA AAGCAAACT 1500
 CCAATGGAT AAATCAGTGC CTGGTGTCT GAAGTGGGAA AAAATAGACT AACTTCAGTA 1560
 55 GGATTTATGT ATTTTGA AAAAGACAGA AAACAACAAA AGAATTTTGT TTTGGACTGT 1620
 TTTCAATAAC AAAGCAGATA ACTGGATTTT GAACGCTTAA GTCATCATTA CTGGGAAAT 1680
 TTTTAATGTT TATTATTAC ATCACTTTGT GAATTAACAC AGTGTTTCAA TTCTGTAATT 1740
 ACATATTTGA CTCITTCAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 86 Protein sequence:

Protein Accession #: NP_002308.1

1 11 21 31 41 51
 | | | | |
 60 MRFAWTVLLL GPLQLCALVH CAPPAAGQQQ PPREPPAAPG AWRQIQWEN NGQVFSLLSL 60
 65 GSQYQQRRR DPGAAPVGA NASAQPRTP ILLIRDNRTA AGRTRTAGSS GVTAGRPRPT 120
 ARHWFAQGYS TSRAREAGPS RAENQTAPGE VPALSNLRPP SRVDGMVGDD PYNPYKYSDD 180
 NPYNYVYDTY ERPRGGRYR PGYGTGYFQY GLPDLVADPY YIQAITYVQK MSMPYLRCAA 240
 EENCLASTAY RADVRDYDHR VLLRFPQVRK NQGTSDFLPS RPRYSWEWHS CHQHYHSMDE 300
 70 FSHLYLLDAN TQRRWAEGHK ASFCLEDTSC DYGYHRRFAC TAHTQGLSPG CYDYGADID 360
 CQWIDITDKV PGNVILKVSV NPSYLVPESD YTNVVRCDI RYTGHHAYAS GCTISPY

Seq ID NO: 87 DNA sequence

Nucleic Acid Accession #: NM_006419.1

Coding sequence: 91-420 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 75 TTCGGCACTT GGGAGAAGAT GTTTGAAAAA ACTGACTCTG CTAATGAGCC TGGACTCAGA 60

5 GCTCAAGTCT GAACTCTACC TCCAGACAGA ATGAAGTTCA TCTCGACATC TCTGCTTCTC 120
 ATGCTGCTGG TCAGCAGCCT CTCTCCAGTC CAAGGTGTTT TGGAGGTCTA TTACACAAGC 180
 TTGAGGTGTA GATGTGTCCA AGAGAGCTCA GTCTTTATCC CTAGACGCTT CATTGATCGA 240
 ATTCAAATCT TGCCCGCTGG GAATGGTTGT CCAAGAAAAG AAATCATAGT CTGGAAGAA 300
 AACAAAGTCAA TTGTGTGTGT GGACCCCTCAA GCTGAATGGA TACAAAGAAT GATGGAAGTA 360
 TTGAGAAAAA GAAGTTCTTC AACTCTACCA GTTCCAGTGT TTAAGAGAAA GATTCCTTGA 420
 TGCTGATATT TCACCTAAGA ACACCTGCAT TCTTCCCTTA TCCCTGCTCT GGATTTTAGT 480
 TTTGTGACTTA GTTAAATCTT TTCCAGGGAG AAAGAACTTC CCCATACAAA TAAGGCATGA 540
 GGACTATGTG AAAAATAACC TTGCAGGAGC TGATGGGGCA AACTCAAGCT TCTTCACTCA 600
 10 CAGCACCTTA TATACACTTG GAGTTTGCAT TCTTATTCAT CAGGGAGGAA AGTTTCTTTG 660
 AAAATAGTTA TCTCAGTTATA AGTAATACAG GATTATTTTG ATTATATACT TGTGTTTAA 720
 TGTTTAAAAA TTCTTAGAAA ACAATGGAAT GAGAATTAA GCCTCAAAAT TGAACATGTG 780
 GCTTGAATTA AGAAGAAAAT TATGGCATAT ATTAAGAGCA GGCTTCTATG AAAGACTCAA 840
 15 AAAGCTGCCT GGGAGGCAGA TGGAACTGA GCCTGTCAAG AGGCAAGGA ATCCATGTAG 900
 TAGATATCTT CTGCTAAAAA ACTCACTACG GAGGAGAATT AAGTCTACT TTTAAAGAA 960
 TTCCTTATAA AATTTACTGT CTAAGATTAA TAGCATTGCA AGATCCCCAG ACTTCATAGA 1020
 ATACTCAGGG AAAGCATTTA AAGGGTGATG TACACATGTA TCCTTTTACA CATTTCGCTT 1080
 GACAAACTTC TTCACTCAC ATCTTTTCA CTGACTTTT TTGTGGGGGC GGGGCCGGGG 1140
 20 GGACTCTGGT ATCTAATCTT TTAATGATTC CTATAAATCT AATGACATTC AATAAAGTTG 1200
 AGCAACATTT TACTTT

Seq ID NO: 88 Protein sequence:

Protein Accession #: NP_006410.1

25 1 11 21 31 41 51
 | | | | |
 MKFISTLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNCG 60
 PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

Seq ID NO: 89 DNA sequence

Nucleic Acid Accession #: NM_002652

Coding sequence: 37-477 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 | | | | |
 CTTCTCTGGG ACACATTGCC TTCTGTTTC TCCAGCATGC GCTTGCTCCA GCTCCTGTTT 60
 AGGGCCAGCC CTGCCACCCCT GCTCCTGGTT CTCTGCTGCG AGTTGGGGGC CAACAAAGCT 120
 CAGGACAACA CTGGGAAGAT CATAATAAAG AATTTTGACA TTCCCAAGTC AGTACGTCCA 180
 40 AATGACGAAG TCCTCGCAGT GCTTGCAGTT CAAACAGAAT TGAAGAAGAT CATGGTGGTT 240
 AAAACTTACC TCATTAGCAG CATCCCTCTA CAAGGTGCAT TTAACATAA GTATACTGCC 300
 TGCCTATGTG ACGACAATCC AAAAACCTTC TACTGGGACT TTTACAOCOA CAGAACTGTG 360
 CAAATTGTCAG CCGTCTGTGA TGTATTGCGG GAATTAGGCA TCTGCCCTGA TGATGCTGCT 420
 GTAATCCCCA TCAAAAACAA CCGGTTTAT ACTATTGAAA TCCTAAAGGT AGAATAATGG 480
 45 AAGCOCTGTC TGTTTGCCAC ACCCAGGTGA TTTCTCTAA AGAAACTTGG CTGGAATTTC 540
 TGCTGTGGTC TATAAAATAA ACTTCTTAAC ATGCTT

Seq ID NO: 90 Protein sequence:

Protein Accession #: NP_002643.1

50 1 11 21 31 41 51
 | | | | |
 MRLLQLLFRA SPATLLLVLC LQLGANKAQD NTRKIIKNF DIPKSVRPND EVTAVLAVQT 60
 ELKECMVVKY YLISSIPLOG AFNYKYTACL CDDNPKTFYW DFYTNRTVQI AAVVDVIREL 120
 55 GICPDAAAVI PIKNNRFYTI EILKV

Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: AK000341

Coding sequence: 85-975 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 GATAGCGCGG GGCAGAGGGA CCCGGCTACC CTGGACAGCG CATCGCCGCC CGCCCGGGTC 60
 GCCGCGCCAC AGCGCTGCG GATCATGGAA CATCTAAAGG CCTTTGATGA TGAAATCAAT 120
 65 GCTTTTITGG ACAATATGTT TGGACCGCGA GATCTCTGAG TCAGAGGGTG GTTCACGTTG 180
 GACTCTTACC TTCCTACCTT TTTCTTACT GTCATGTATC TGCTCTCAAT ATGGCTGGGT 240
 AACAAATATA TGAAAGACAG ACCTGCTCTT TCTCTCAGGG GTATCTCTAC CTTGTATAAT 300
 CTTGGAATCA CACTTCTCTC CGGTACATG CTGGCAGAGC TCATTCTCTC CACTTGGGAA 360
 GGAGGCTACA ACTTACAGTG TCAAGATCTT ACCAGCGCAG GGGAAAGCTGA CATCOGGGTA 420
 70 GCCAAGGTGC TTTGGTGGTA CTATTCTCC AAATCAGTAG AGTTCTCTGA CACAAATTTT 480
 TTGCTTTTGC GGAAAAAAC AGTCAGATT ACITTTCTTC ATGTATATCA TCATGCTTCT 540
 ATGTTTAACT TCTGTTGGTG TGTCTTGAAC TGGATACCTT GTGGACAAGG TTTCTTTGGA 600
 CCAACACTGA ACAGTTTGT CCACATCTT ATGTACTCCT ACTATGGACT TTTCTGTGTT 660
 CCATCTATGC ACAAGTATCT TTTGGTGAAG AAATATCTCA CACAGGCTCA GCTGGTGCAG 720
 75 TTGCTGCTCA CCATACGCA CACCATGAGC GCGTCTGTGA AACCGTGTGG CTTCCCTTTC 780
 GGTGTCTCA TCTTCCAGTC ATCTTATATG CTAACGTTAG TCATCTCTCT CTTAAATTTT 840
 TATGTTTACA CATACCGAAA AAAGCCAATG AAGAAAGATA TGCAAGAGCC ACCTGCAGGG 900
 AAAGAAGTGA AGAATGGTTT TTCCAAGGCC TACTTCACTG CAGCAATGG AGTGATGAAC 960

AAGAAAGCAC AATAAAAAATG AGTAACAGAA AAAGCACATA TACTAGCCTA ACAGATTGGC 1020
 TTGTTTTAAA GCAAAGACTG AATTGAAGGT TACATGTTTT AGGATAAACT AATTTCTTTT 1080
 GAGTTCATAA ATCATTTTGA CCCAGAATGT ATTAATATAT TGCTATTAGG TTAATCTGTT 1140
 AACTGAATGC TTGTATCAGC ATTGAGGTGA TGCTCACCTC CGAGGACCTC AGAACTGGTG 1200
 CAGCTTCTCT CTCCTCCCT CCCACAGACT GAACCTTTCG CCAGAAGCTG TCCTTATAAC 1260
 GCCTTATACG CATACACAGC CAGGAAACGT GGAGCATTGT TTCTACAGA GAGTCTCCAA 1320
 ATAAAAAGGG TTTTGTTCAG ATTAATAATGT TTACAACAAA ATGTTAATTA TATTCTAAAT 1380
 ACAGGGTATG TTCTAATCTA TATTAAGCAA TAATGCCAGT GCATAATCAT TCCATTGTGT 1440
 OCTTTAGCAA TCAACCCAG AAAATATTAA AATGGGATCA TACACAGAAG ATAGAAAAAT 1500
 CTAGCAAAAC TTCTCTTCT GTAAGCCAGA GTCTTGCTA TCAGATTCCC ACAACCACTC 1560
 CTGATTCTAA ATTTAGTAT ATGTAATGA AATTGGTATT TATTTTAAAT ATTAGTTATT 1620
 CTAAGGAGAA AAAAATGCTT CTGCAAGATT TTCATAATTC AGGGGCTGTG GATAGGATTG 1680
 TTCCTCTGTT TCCTAATCA TTCATCTGTT CATGCTCCC TCTGTGCCA GTCAGCCTAG 1740
 GTTATACAGA TGCCATGCTC CACACCAGCA GCAGTGATCA AATCTGGCTG CCCGTTTACT 1800
 TTCTGAGCAA GCACCTGGAGT CCACTCCGAC CTTTTCTTT GAACATGCAAT GCTGCTGGAA 1860
 TATGTATAAA TCAGAACTAG CAGAAGTAGC AGAGTGATGG GAGCAAAATA GGCAGTGAAT 1920
 TCGTCAACTC TTTTTGTGA GCTACTTGT GAATATTACC TCAGATACT GTTGTCACCT 1980
 TTCACAGGTT ATTTAAGTTC TTGAAGCTGG GAGGAAAAAG ATGGAGTAGC TTGGAAGAT 2040
 TCCAGCACTG AGCCGTGAGC CGGTCATGAG CCACGATAAA AAATGCCAGT TTGGCAAACT 2100
 CAGCACTCCT GTTCCCTGCT CAGGTATATG CGATCTCTAC TGAGAAAGCAA GCACAAAAGT 2160
 AGACCAAAGT ATTAATGAGT ATTTCTTTC TCCATAAGTG CAGGACTGTT ACTCACTACT 2220
 AAACCTCTACC AAGAATGGAA ACCAAGAATA TTTTCTGAAG ATTTTGTGA AGATTAATTT 2280
 ATACCTATA AATAAAACT TGTTAGCTTC GATGAAGTCA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 92 Protein sequence:
 Protein Accession #: BAA91096.1

1 11 21 31 41 51
 MEHLKAFDDE INAFLDNMFGR PRDSRVRGWF TLDSTLPTFF LTVMYLLSIW LGNKYMKNRP 60
 ALSRLGILT YNLGITLLSA YMLAELIST WEGGYNLQCC DLTSAGEADI RYKVLVWVYY 120
 FSKSVFLDT IPFVLRKKTQ QITFLHYVHH ASMFNIWVCV LNWIPCGQSF FGPTLNSFVH 180
 ILMYSYYGLS VFFSMHXYLW WKYLYTQAL VQFVLTHT MSVAVKPCGF PFGCLIFQSS 240
 YMLTLVILFL NFVYQYTRKK PMKKDMQEP AGKEVKNGFS KAYFTAANGV MNKKAQ

Seq ID NO: 93 DNA sequence
 Nucleic Acid Accession #: NM_000044
 Coding sequence: 1115-3874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGAGATCCCG GGGAGCCAGC TTGCTGGGAG AGCGGGACGG TCCGGAGCAA GCCACAGGC 60
 AGAGGAGGCG ACAGAGGGAA AAAGGGCCGA GCTAGCCGCT CCACTGCTGT ACAGGAGCCG 120
 AAGGGACGCA CCACGCCAGC CCCAGCCCGG CTCAGCGAC AGCCAACGCC TCTTGACGCG 180
 CGGCGGCTTC GAAGCCGCGC CCCGGAGCTG CCCTTCTCTC TTGGGTGAAG TTTTAAAAAG 240
 CTGCTAAAGA CTCGGAGGAA GCAAGGAAAG TGCCTGGTAG GACTGACGGC TGCCCTTGTG 300
 CTCCTCTCTT CCACCCCGCC TCCCCCAACC CTGCTTCCC CCCTCCCCC GTCTTCTCTC 360
 CCGCAGCTGC CTCAGTCGGC TACTCTCAGC CAACCCCTCT CACCACTCTT CTCCCAACCC 420
 GCGCCCGCGC CCGGCTCGG CAGCGCTGC CAGCCCGAGT TTGCAGAGAG GTAACCTCCT 480
 TTGGCTGCGA GCGGGGCGAG TAGCTGCACA TTGCAAGAA GGCTCTTAGG AGCCAGCGGA 540
 CTGGGGAGCG GCTTCAGCAC TGCAGCCACG ACCCGCTGG TTAGAATTCC GCGGAGAGA 600
 ACCCTCTGTT TTCCCACT CTCTCTCCAC CTCTCTCTG CTTCCTCCAC CCGAGTGGCG 660
 AGCAGAGATC AAAAGATGAA AAGGCAGTCA GGTCTTCACT AGCCAAAAA CAAAACAAAC 720
 AAAAAACAAA AAGCCGAAAT AAAAGAAAA GATAATAACT CAGTTCTTAT TTGCACCTAC 780
 TTCAGTGGAC ACTGAATTG GAAGGTGGAG GATTITGTT TTTTCTTTA AGATCTGGGC 840
 ATCTTTTGA TCTACCTTC AAGTATTAA AGACAGACTG TGAGCCTAGC AGGGCAGATC 900
 TTGTCCACCG TGTGCTCTT TCTGCACGAG ACTTTGAGG TGTCAGAGCG CTTTITGCGT 960
 GGTGTCTCCC GCAAGTTTCC TTCTCTGGAG CTTCCTCCAG GTGGGACGCT AGCTGCAGCG 1020
 ACTACCGCAT CATCAGAGCC TGTTGAACCT TTCTGAGCAA GAGAAGGGGA GCGGGGTAA 1080
 GGGAAAGTAG TGAAGATTG AGCCAAGCTC AAGGATGGAA GTGCAGTTAG GGCTGGGAAG 1140
 GGTCTACCTT CGGCCCGCGT CCAAGACCTA CCGAGGAGCT TTCCAGAATC TGTTCAGAG 1200
 CGTGCGCGAA GTGATCCAGA ACCCGGGCCC CAGGCACCCA GAGGCCGGA GCGCAGCACC 1260
 TCCCGGCGCC AGTTTGCTGC TGCTGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA 1320
 GCAGCAGCAG CAGCAGCAGC AGCAGCAAGA GACTAGCCCC AGGCAGCAGC AGCAGCAGCA 1380
 GGGTGAGGAT GGTCTCTCCC AAGCCATCG TAGAGGCCCC ACAGGCTACC TGGTCTGGA 1440
 TGAGGAACAG CAACCTTCAC AGCCGAGTC GGCCTGGAG TGCCACCCCG AGAGAGGTTG 1500
 CGTCCCAGAG CTTGGAGCCG CCGTGGCCGC CAGCAAGGGG CTGCCGAGC AGCTGCCAGC 1560
 AOCCTCGGAC GAGGATGACT CAGTGGCCC ATCCAGCTT TCCCTGCTGG GCCCACTTT 1620
 CCCCCTGTTA AGCAGCTGCT CCGCTGACCT TAAAGACATC CTGAGCGAGG CCAGCACCAT 1680
 GCAACTCTT CAGCAACAGC AGCAGGAAGC AGTATCCGAA GGCAGCAGCA GCGGGAGAGC 1740
 GAGGGAGGCC TCGGGGGCTC CCACTTCTC CAAGGACAAT TACTTAGGGG GCACTTCGAC 1800
 CATTTCTGAC AACGCCAAGG AGTTGTGTAA GGCAGTGTG GTGTCCATGG GCCTGGGTGT 1860
 GGAGGCGTTG GAGCATCTGA GTCCAGGGGA ACAGCTTCGG GGGGATTGCA TGTACGCCCC 1920
 ACTTTTGGGA GTTCCACCCG CTGTGCGTCC CACTCTTGT GCCCAATTGG CCGAATGCAA 1980
 AGGTTCTCTG CTAGACGACA GCGCAGGCAA GAGCACTGAA GATACTGCTG AGTATTCGCC 2040
 TTTCAAGGGA GGTACACCA AAGGGCTAGA AGGGAGAGC CTAGGCTGCT CTGGCAGCGC 2100
 TGCAGCAGGG ATGCTCCGGA CACTTGAAT GCCCTTACC CTGTCTCTC ACAAGTCCGG 2160

AGCACTGGAC GAGGCAGCTG CGTACCAGAG TCGGACTAC TACAATTTC CACTGGCTCT 2220
GGCCGGGACCG CCGCCCCCTC CGCCGCTCC CCATCCCCAC GCTCGCATCA AGCTGGAGAA 2280
CCCGCTGGAC TACGGCAGCG CCTGGGCGGC TCGGCGGCG CAGTGCCGCT ATGGGGACCT 2340
GGCGAGCTG CATTGGCGGG GTGCAGCGGG ACCCGGTTCT GGGTACCCT CAGCCGCCCG 2400
5 TTCTCATCC TGGCACACT TCTTCACAG CGAAGAAGGC CAGTTGTATG GACCGTGTGG 2460
TGTTGGTGGG GGTGGTGGCG GCGGCGGCGG GCGGCGGCGG GCGGCGGCGG 2520
CGGCGGCGG GAGGCGGGAG CTGTAGCCCC CTACGGCTAC ACTCGGCCCC CTCAGGGGCT 2580
GGCGGGCCAG GAAAGCGACT TCAOCCGACC TGATGTGTGG TACCCTGGCG GCATGGTGAG 2640
CAGAGTGGCC TATCCAGTC CCACITGTGT CAAAAGCGAA ATGGGCCCTT GGATGGATAG 2700
10 CTACTCCGA CCTTACGGG ACATGCGTTT GGAGACTGCC AGGAGCCATG TTTGCCCCAT 2760
TGACTATTAC TTCCACCCC AGAAGACCTG CCTGATCTGT GGAGATGAAG CTTCTGGGTG 2820
TCACATGGA GCTCTACAT GTGGAAGCTG CAAGGTCTTC TTCAAAGAG CCGTGAAGG 2880
GAAACAGAAG TACCTGTGG CACGAGAAA TGATTGCACT ATTGATAAAT TCGAAGGAA 2940
AAATTGTCCA TCTTGTCTG TTCGGAATG TTATGAAGCA GGGATGACTC TGGGAGCCCG 3000
15 GAAGCTGAAG AAATCTGGTA ATCTGAAACT ACAGGAGGAA GGAGAGGCTT CCAGCACCAC 3060
CAGCCCCACT GAGGAGACAA CCCAGAAGCT GACAGTGTC CACATTGAAG GCTATGAATG 3120
TCAGCCCATC TTCTGAATG TCCTGGAAGC CATTGAGCCA GGTGTAGTGT GTGCTGGACA 3180
CGACAACAC CAGCCGACT CTTTGCAGC CTTGCTCTT AGCTCAATG AACTGGGAGA 3240
GAGACAGCT GTACACGTGG TCAAGTGGGC CAAGGCCTTG CCTGGCTTCC GCAACTTACA 3300
20 CGTGGACGAC CAGATGGCTG TCATTCACTA CTCCTGGATG GGGCTCATGG TGTTTGCCAT 3360
GGGCTGGCGA TCCTTACCA ATGTCAACTC CAGGATGCTC TACTTCGCC CTGATCTGGT 3420
TTTCAATGAG TACCGCATGC ACAAGTCCCG GATGTACAGC CAGTGTGTCC GAATGAGGCA 3480
CCTCTCTCAA GAGTTTGGAT GGCTCCAAAT CACCCCCAG GAATTCCTGT GCATGAAAGC 3540
25 ACTGCTACTC TTCAGCATTA TTCCAGTGGG TGGGCTGAAA AATCAAAAAA TCTTTGATGA 3600
ACTTCGAATG AACTACATCA AGGAAGCTGA TCGTATCATT GCATGCAAAA GAAAAAATCC 3660
CACATCTGCT TCAAGACGCT TCTACCAGCT CACCAAGCTC CTGGACTCCG TGCAGCCTAT 3720
TGCGAGAGAG CTGCATCAGT TCACTTTTGA CCTGCTAATC AAGTCACACA TGGTGAGCGT 3780
GGACTTTCGG GAAATGATGG CAGAGATCAT CTCTGTGCAA GTGCCCAAGA TCCTTTCTGG 3840
30 GAAAGTCAAG CCGATCTATT TCCACACCCA GTGAAGCATT GGAACCCCTA TTTCCCAACC 3900
CCAGCTCATG CCCCCTTTCA GATGTCTTCT GCCTGTTATA ACTCTGCACT ACTCCTCTGC 3960
AGTGCCCTGG GAAATTCTCT CTATTGATGT ACAGTCTGTC ATGAACATGT TCTGAAATC 4020
TATTGCTGG GCTTTTTTCT TCTCTTCTC TCCTTCTTT TCTTCTTCC CTCCTATCT 4080
AACCCTCCCA TGGCACCTTC AGACTTTGCT TCCCATTTGT GCTCCTATCT GTGTTTGA 4140
35 TGGTGTGTA TGCCTTTAAA TCTGTGATGA TCCTCATATG GCCCAGTGC AAGTTGTGCT 4200
TGTTTACAGC ACTACTCTGT GCCAGCCACA CAAACGTTTA CTTATCTTAT GCCACGGGAA 4260
GTTTAGAGAG CTAAGATTAT CTGGGGAAT CAAAACAAAA AACAAGCAAA CAAAAAATA 4320
A

Seq ID NO: 94 Protein sequence:
Protein Accession #: NP_000035.1

1 11 21 31 41 51
MEVQLGLGRV YPRPFSKTYR GAFQNLFSV REVIONPGPR HPEAASAAPP GASLLLLQQQ 60
45 QQQQQQQQQQ QQQQQQQQET SPRQQQQQQG EDGSPQAHRR GPTGYLVLDE EQQSPQPSA 120
LECHPERGCV PEPGAAVAAS KGLPQQLPAP PDEDDSAAPS TSLGLPTFP GLSSCSADLK 180
DLSEASTMQ LLQQQQQAEV SEGSSSGRAR EASGAPTSSK DNYLGGTSTI SDNAKELCKA 240
VSVSMGLGVE ALEHLSPGEQ LRGDCMYAPL LGVPPAVRPT PCAPLAECKG SLLDSDAGKS 300
50 TEDTAEYSPF KGGYTKLEG ESLGCSGSA AGSSGTLELP STLSTLYKSGA LDEAAAYQSR 360
DYNNFPLALA GPPPPPPPH PHARIKENP LDYGSAAAAA AAQCRYGDLA SLHGAGAAGP 420
GSGSPSAAAS SSWHTLFTAE EQQLYGPCGG GGGGGGGGGG GGGGGGGGGG GGEAGAVAPY 480
GYTRPPQQA QGESDFTAPD VWYPGGMVSR VPYPSPCTVK SEMGPWMDSY SGYPGDMRLE 540
TARDHVLPID YYFPQKTCL ICGDEASGCH YGALTGCSCK VFFKRAEKG KYLCASRND 600
55 CTIDKFRKKN CPSRLRKCY EAGMTLGARK LKKLGNLKLQ EGEASSTTS PTEETTQKLT 660
VSHIEGYEQ PIFNLVLEAI EPGVVCAHND NNQPDFAAL LSSLNELGER QLVHVVKWAK 720
ALPGRNLHV DDQMAVIQYS WMGLMVFAMG WRSFTNVNSR MLYFAPDLVF NEYRMHKSRL 780
YSQCVMRHL SQEFGWLQIT PQEFLCMKAL LFSIIPVDG LKNQKFFDEL RMNYKELDR 840
60 IACKRKNPT SCSRRFYQLT KLDSVQPIA RELHQFTFDL LKSHMVSVD FPEMMAEIS 900
VQVPKILSGK VKPIYFHTQ

Seq ID NO: 95 DNA sequence
Nucleic Acid Accession #: NM_002497
Coding sequence: 135-1472 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GGCACGAGTA GGGGTGGCGG GTCACTGCTG CTCGGGGGCT TCTCCATCCA GGTCCCTGGA 60
65 GTTCTGTGTC CTGGAAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG CGCGACTCTG 120
GCGACTGGCC GGCATGCTCT TCCCGGGCTG AGGACTATGA AGTGTGTAC ACCATTGGCA 180
70 CAGGCTCTTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT 240
GGAAAGAAGT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTCTGAAG 300
TGAATTTGCT TGTGAAGCTG AAACATCCAA ACATCGTTCG TTACTATGAT CGGATTATTG 360
ACCGGACCAA TACAACACTG TACATTGTAA TGGAAATATT TGAAGGAGGG GATCTGGCTA 420
GTGTAATTAC AAAGGGAACC AAGGAAGGCG AATACTTAGA TGAAGAGTTT GTTCTTCGAG 480
75 TGATGACTCA GTTGACTCTG GCCCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA 540
CCGTATTGCA TCGGGATCTT AAACCAGCCA ATGTTTCTCT GGATGGCAAG CAAAACGTCA 600
AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTT TCAAAAAACAT 660

TTGTTGGCAC ACCTTATTAC ATGTCTCCTG AACAAATGAA TCGCATGTCC TACAATGAGA 720
 AATCAGATAT CTGGTCATTG GGCTGCTTGC TGTATGAGTT ATGTGCATTA ATGCCTCCAT 780
 TTACAGCTTT TAGCCAGAAA GAACCTCGCTG GGAAAAATCAG AGAAGGCCAAA TTCAGGCGAA 840
 TTCCATACCG TTACTCTGAT GAATTGAATG AAATTATTAC GAGGATGTTA AACTTAAAGG 900
 ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACC TTTAATAGCA GATTGTGTTG 960
 CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGGCGACA ATTAGGAGAG CCAGAAAAAT 1020
 CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAACCTGAA GGAAATTCAG TTACAGGAGC 1080
 GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG 1140
 TTGCTGAGAG ACTAGCAGAG GACAACTGG CTAGAGCAGA AAATCTGTTG AAGAACTACA 1200
 GCTTGCTAAA GGAACGGAAG TTCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC 1260
 CATCCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA 1320
 GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA 1380
 GGCTTCACGC TGCCCAAGCTG CGGGCTCAAG CCTGTGCAGA TATTGAGAAA AATTACCAAC 1440
 TGAAGAGCAG ACAGATCTCT GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC 1500
 AGGATGTAAT ATTACCAACC TTAAAGACT GATATTCAAA TGCTGTAGTG TTGAATACTT 1560
 GGCCCATGTA GGCATGCGCT TCTGTATAGT ACACATGATA TTTCGGAATT GGTTTACTG 1620
 TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TTCTTCTCTC TTTAAGAAGC 1680
 ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTAATC CTGTGTGTGA TTAAGTAGAG 1740
 GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAAT AATATTAGGA AAAAAATATT 1800
 TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT 1860
 TGTCAATGCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTGAG CTTAGAAAAA 1920
 CCAAGTAGAT GCAATTGGT CATTAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC 1980
 TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT 2040
 TTTTTTCTG TTTAACAGAA TATGAGCTGT CTGTCAATTA CTAATCTCTT TCCCACTAAA 2100
 TAAAAAATT CTTCAGTTA

Seq ID NO: 96 Protein sequence:
 Protein Accession #: NP_002488

1 11 21 31 41 51
 | | | | |
 GIREFNPIM ANEVERINMI TOSIGENEA RELATEDKIN ASEHOMOSAP IENSMPSPRAE 60
 DYEVLYTIGT GSYGRCKQIR RKSDGKILVW KELDYGSMTAE AEKQMLVSEV NLLRELKHPN 120
 IVRYYYDRIID RNTTLTYIVM EYCEGGDLAS VITKGTKERQ YLDEEFVLRV MTQLTLALKE 180
 CHRRSDGGHT VLHRLDKPAN VFLDGKQNVK LGDFGLARIL NHDTSFAKTF VGTPTYMSPE 240
 QMNRMSYNEK SDIWSLGCLL YELCALMPFF TAFSOKELAG KIREGKFRRI PYRYSDELNE 300
 IITRMLNLKD YHRPSVEEIL ENPLIADLVA DEQRRNLERR GRQLGEPEKS QDSSPVLSL 360
 KLKEIQLQER ERALKAREER LEQKEQELCV RERLAEDKLA RAENLLKNYS LLKERKFLSL 420
 ASNPPELLNLP SSVIKKKVHF SGESKENIMR SENSESQLTS KSKCKDLKKR LHAAQLRAQA 480
 LSDIEKNYQL KSRQILGMR

Seq ID NO: 97 DNA sequence
 Nucleic Acid Accession #: NM_007050.2
 Coding sequence: 185-4576 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCTCCCGCCT CAGTTCGCGC CGCGCCTCGG CTGGAACGC AGGAGCGCCG GCTCCGGGAG 60
 CCGGAGCGGA GCCAGCGCGC CGCACAGCCA GCGGCGCGCG CGCGGATGCG GGGCCACCCC 120
 GCGCCCGCCC CAGTCCCGGC CCCGGCCCCC GCGGGAAGGG GCTGAGCTGC CCGCCGCGGC 180
 CCGGATGCGC AGCTCGCGC CGCTCGCCT CAGCCTGCTC CTGAGGCTGC AGCTGCCGCC 240
 ACTGCCGGC GCCCGGGCTC AGAGCGCCCC AGGTGGCTGT TCCTTTGATG AGCACTACAG 300
 CAACTGTGGT TATAGTGTGG CTCTAGGGAC CAATGGGTTT ACCTGGGAGC AGATTAACAC 360
 AACGGAGAAA CCAATGCTGG ACCAGGCAGT GCCACAGGA TCCTTCATGA TGGTGAACAG 420
 CTCTGGGAGA GCCTCTGGCC AGAAGGCCCA CTTCTCCTG CCAACCTGA AGGAGAATGA 480
 CACCCACTGC ATCGACTTCC ATTACTACT CTCCAGCCGT GACAGGTCCA GCCCAGGGGC 540
 CTTGAACGTC TACGTGAAGG TGAATGGTGG CCCCCAAGGG AACCCCTGTG GGAATGTGTC 600
 CGGGGTGCTC ACTGAGGGCT GGGTGAAGGC AGAGCTCGCC ATCAGCACTT TCTGGCCACA 660
 TTCTATCAG GTGATATTG AATCCGCTCT ATTGAAGGGT CATCCTGGCT ACATCGCCGT 720
 GGACGAGGTC CGGGTCTCTG CTCATCCATG CAGAAAAAGCA CCTCATTTTC TGCGACTCCA 780
 AAACGTGGAG GTGAATGTGG GGCAGAAATGC CACATTTTCA TGCAATTGCTG GTGGGGAAGTG 840
 GTCTCAGCAT GACAAGCTTT GGCTCCAGCA ATGGAATGGC AGGGACACGG CCCTGATGGT 900
 CACCGTGTG GTCAACCACA GCGCTTCTC AGCCACAGTC AGTGTGGCAG AACTGCCCCA 960
 GCGGAGCGTC AGCAAGTACC GCTGTGTGAT CCGCTCTGAT GGTGGGTCTG GTGTGTCCAA 1020
 CTACGCGGAG TGTGCTGTGA AAGAGCCTCC CACGCCCATT GCTCCCCAG AGCTGCTGGC 1080
 TGTGGGGGCC ACATACCTGT GGATCAAGCC AAATGCCAAC TCATCATCG GGGATGGGCC 1140
 CATCATCTTG AAGGAAGTGG AATATCGCAC CACCACAGGC ACGTGGGCAG AGACCCACAT 1200
 AGTCGACTCT CCAACTATA AGCTGTGGCA TCTGGACCCC GATGTTGAGT ATGAGATCCG 1260
 AGTGCTCTCT ACACGACCAG GTGAGGGGGG TACGGGACCG CCAGGGGCTC CCCTCAACCAC 1320
 CAGGACCAAG TGTGCTGATC CGGTACATGG CCCACAGAAC GTGGAATTCG TAGACATCAG 1380
 AGCCCGGCAG CTGACCTGCG AGTGGGAGCC CTTCGGCTAC GCGGTGACCC GCTGCCATAG 1440
 CTACAACCTC ACCGTGCACT ACCAGTATGT GTTCAACCAG CAGCAGTACG AGGCCGAGGA 1500
 GGTCACTCCAG ACCTCTCCCG ACTACACCCT GCGAGGCTG CGCCCTTCA TGACCATCCG 1560
 GCTGCGACTC TTGCTGTCTA ACCCCGAGGG CCGAATGGAG AGCGAGGAGC TGGTGGTGCA 1620
 GACTGAGGAA GACGTTCCTG GAGCTGTTCC TCTAGAATCC ATCCAAGGGG GGCCCTTTGA 1680
 GGAGAAGATC TACATCCAGT GGAACCTCC CAATGAGACC AATGGGGTCA TCACGCTCTA 1740
 CGAGATCAAC TACAAGGCTG TGGGCTCGCT GGACCCAGT GCTGACCTCT CGAGCCAGAG 1800

5 GGGGAAAGTG TTCAAGCTCC GGAATGAAAC CCACCACCTC TTTGTGGGTC TGTACCCAGG 1860
 GACCACCTAT TCCTTCACCA TCAAGGCCAG CACAGCAAAG GGCTTTGGGC CCCCTGTCAC 1920
 CACTCGGATT GCCACCAAAA TTTCAGCTCC ATCCATGCCT GAGTACGACA CAGACACCCC 1980
 ATTGAATGAG ACAGACACGA CCATCACAGT GATGCTGAAA CCGGCTCAGT CCCGGGGAGC 2040
 10 TCCTGTGATG GTTTATCAGC TGGTTGTCAA GGAGGAGCGA CTTCAGAAGT CACGGAGGGC 2100
 AGCTGACATT ATTGAGTGCT TTTCCGTGCC CGTGAGCTAT CGGAATGCCT CCAGCCTCGA 2160
 TTCTCTACAC TACTTTGCTG CTGAGTTGAA GCCTGCCAAC CTGCTGTCA CCCAGCCATT 2220
 TACAGTGGGT GACAATAAGA CATACAATGG CTACTGGAAC CCTCTCTCT CTCCCCTGAA 2280
 AAGCTACAGC ATCTACTTCC AGGCACTCAG CAAAGCCAAT GGAGAGACCA AAATCAACTG 2340
 15 TGTTCTGTTG GCTACAAAAG CACCAATGGG CAGCGCCCAG GTGACCCCGG GGACTCCTACT 2400
 CTGCCTCTC ACCACAGGTG CCTCCACCCA GAATTCTAAC ACTGTGGAGC CAGAGAAGCA 2460
 GGTGGACAAC ACCGTGAAGA TGGCTGGCGT GATCGCTGGC CTCCTCATGT TCATCATCAT 2520
 TCTCCTGGGC GTGATGCTCA CCATCAAAAAG GAGAAGAAAT GCTTATTCTT ACTCCTATTA 2580
 20 CTGTGCCCAA AGGAAGCTGG CCAAGAAAGCA GAAGGAGACC CAGAGTGGAG CCCAGAGGGA 2640
 GATGGGGCCT GTGGCTCTG CCGACAACC CACCACCAAG CTCAGCGCCA GCCGCAATGA 2700
 TGAAGGCTTC TCTTCTAGTT CTCAGGACGT CAACGGATTG ACAGATGGCA GCCCGGGGGA 2760
 GCTTTCCAG CCCACCTCA CGATCCAGAC TCATCCCTAC CGCACCTGTG ACCCTGTGGA 2820
 GATGAGGTAC CCCCGGAGC AGTTCCAAT CGCCATCCGG GTGGCTGACT TGCTGCAGCA 2880
 25 CATCACGCAG ATGAAGAGAG GCCAGGGCTA CGGGTTCAAG GAGGAATACG AGGCCTTACC 2940
 AGAGGGGACG ACAGCTTCGT GGGACACAGC CAAGGAGGAT GAAAACCGCA ATAAGAATCG 3000
 ATATGGGAAC ATCATATGCT ACGACCATTC CCGGGTGAGG CTGCTGGTGC TGGATGGAGA 3060
 CCCGCACTCT GACTACATCA ATGCCAACTA CATTGACGGA TACCATCGAC CTCGGCACTA 3120
 CATTGGCCTT CAAGGTCCGA TGCAGGAGAC TGTAAGGAC TTTTGGAGAA TGATCTGGCA 3180
 30 GGAGAATCC GCCAGCATCG TCATGGTCA AAACCTGGTG GAAGTGGGCA GGGTGAAATG 3240
 TGTGCGATAC TGGCCAGATG ACACGGAGGT CTACGGAGAC ATTAAGTCA CCTGATTGA 3300
 AACAGAGCCC CTGGCAGAAT ACGTCATACG CACCTTCACA GTCCAGAAGA AAGGCTACCA 3360
 TGAGATCCGG GAGCTCCGCC TCTTCCAATT CACCACTGGG CCTGACCAAG CGCTTCCCTG 3420
 CTATGCCAAT GGCCTTCTGG GCTTCGTCCG CAGGTCAAG TTTCTCAACC CCCGGAAGC 3480
 35 TGGGCCATA GTGGTCACT GCAGTGCTGG GGCTGGGCGG ACTGGCTGCT TCATTGCCAT 3540
 TGACACCATG CTGACATGG CCGAGAATGA AGGGGTGGTG GACATCTTCA ACTGCGTGGC 3600
 TGAGCTCCGG GCCCAAAGGG TCAACCTGGT ACAGACAGAG GAGCAATATG TGTTTGTGCA 3660
 CGATGCCATC CTGAAGGCTG GCCTCTGTGG CAACACTGCC ATCCCTGTGT GTGAGTTCCG 3720
 TTCTCTTAC TACAATATCA GCAGGCTGGA CCCCAGACA AACTCCAGCC AAATCAAAGA 3780
 TGAATTTAG ACCCTCAACA TTGTGACACC CCGTGTGGCG CCCGAGGACT GCAGCATTTG 3840
 40 GCTCCTGCC CGGAACCATG ATAAGAAATG AAGTATGGAC GTGCTGCCCT TGGACCGCTG 3900
 CCTGCCCTTC CTATCTCTG TGGACGGAGA ATCCAGCAAT TACATCAACG CAGCACTGAT 3960
 GGATAGCCAC AAGCAGCCTG CCGCTTCTGT GGTACCCAG CACCTCTAC CCAACACCGT 4020
 GGCAGACTTC TGGAGGCTGG TGTTGATTA CAACTGCTCC TCTGTGGTGA TGCTGAATGA 4080
 GATGGACACT GCCCAGTTCT GTATGCAGTA CTGGCCTGAG AAGACCTCCG GGTGCTATGG 4140
 45 GCCCATCCAG GTGGAGTTCG TCTCCGAGA CATCGACGAG GACATCATCC ACAGAAATAT 4200
 CCGCATCTGT AACATGGGCC GGCCACAGGA TGGTTATCGT ATAGTCCAGC ACCTCCAGTA 4260
 CATTGGCTGG CTGCCTACC GGGACACGCC CCCCTCCAAG CGCTCTCTGC TCAAAGTGGT 4320
 CCGACGACTG GAGAAGTGGC AGGAGCAGTA TGACGGGAGG GAGGAGCCTA CTGTGGTCCA 4380
 50 TGCTGCTAAT GGGGAGGGCC GTAGTGAAC CTCTGTGCC ATCTGCAGTG TGTGTGAGAT 4440
 GATCCAGCAG CAAACATCA TTGACGTGTT CCACATCGTG AAAACACTGC GTAACAACAA 4500
 ATCCAACATG TTGGAGACCC TGAACAGTA TAAATTTGTA TACGAGGTGG CACTGGAATA 4560
 TTTAAGCTCC TTTAGCTCA ATGGGATGGG GAACTGCCGG AGTCCAGAGG CTGCTGTGAC 4620
 CAAGCCCCCT TTTGTGTGAA TGGCAGTAAC TGGGCTCAGG AGCTCTGAGG TGGCACCCCTG 4680
 55 CCTGACTCCA AGGAGAAGAC TGGTGGCCCT GTGTTCCACG GGGGGCTCTG CACCTTCTGA 4740
 GGGGTCTCCT GTTGCCGTGG GAGATGCTGC TCCAAAAGGC CCAGGCTTCC TTTTCAACCT 4800
 AACCAGCCAC AGCCAAGGGC CCAAGCAGAA GTACACCCAC AAGCAAGGCC TTGGATTCTT 4860
 GGCTCCCGA CCACGTGCTT TTGTTCTGAG TTTGTGGATC TCTTGGCAAG CCAACTGTGG 4920
 AGGTGCTGGG GAGTGGGAGG CTCGCCCTGC CTCCTTCTCC TTAGGAGTGG AGGAGATGTG 4980
 60 TGTTCTGCTC TCTACGTCA TGGAAAAGAT TGAGGCTCTT GGGGGTCACT GCTCTGCTGC 5040
 CCCTGCAAC CTCTTCAGG GGCCTCTGGC ACCAGACATT TGCACTCTGG ACCAGTGTGA 5100
 CCTTACGATG TTCCCTAGGC CACAAGAGAG GCCCCCATC CTCACACCTA ACCTGCATGG 5160
 GGCTTCGCCC ACAACCATTC TGTACCCCTT CCCCAGCCTG GGCCTTGACC GTCCAGCATT 5220
 CACTGGCCCG CCAGCTGTGT CCACAGCAGT TTTTGATAAA GGTGTTCTTT GCTTTTTTGT 5280
 65 GTGGTCAGTG GGAGGGGGTG GAACCTGACG GAACCTTCTT GCTCCTCTT GTCTTTGTAA 5340
 AAAGGGACCA CCTCCCTGGG GCAGGGCTTG GGCTGACCTG TAGGATGTAA CCCCTGTGTT 5400
 TCTTTGGTGG TAGCTTCTT TGGAAAGAGC AAACAAGATA AGATTGTGATT ATTTTCAAAA 5460
 GTGTATGTGA AAAGAAACTT TCTTTTGGAG GGTGTAAAAT CTAGTCTCT TATGTCAAAA 5520
 AGAAGGGGGC GGGGAGTTT GAGTATGTAC CTCTAAGACA AATCTCTCGG GCTTTTATT 5580
 TTTTCTGGC AATGTCTTA AAAGCTCCCA CCTGGGACA GCATGCCACT GAGCAAGGAG 5640
 70 AGATGGGTGA GCTGGAAGAT GGTCCCTTTG GTTCTGGGG CAAATAGAGC ACCAGCTTTG 5700
 TGCAATAATT GGTATGTCAA ATTTGAACCT CTTCCTAAAG AAACCCAGCA GCCACCTTGA 5760
 AAAAGGCCAT TGTGGAGGCC ATTATACTTT GATTAAAAAT AGGCCAAGAG AATCAGGCCCT 5820
 GGAGATCTAG GGTCTGTCC AAAGTGTGAG TGAATCAATG AGAGGGAACC AACATTGCT 5880
 AAGTCTCTAC TGATGCCAG GGATCATGCT TGGCACTTTC CATAGGACAT TTCACACAGT 5940
 75 CCTTAGAACC CCGAGGAGG AGCTACTGAC TTGTTATCAT CTCCATTGTA TCATCTCTC 6000
 CAATGAGGAA ACCCAGCAC CTTCCTTAGT AATGAAATCC TGGGTTCCTA AGGGGAGGCT 6060
 AATGGCAATG AGACTTCTCC GTGCTGTTTT CTTCATCTTC TCTAAGCCAA GCAATTATT 6120
 TATGGAGGGA AAATAAGGCC AGAACTTCT GAGCAGATAA CTCCACAAAT GGAATTATTAG 6180
 TACTTCTCT CTGATGCCAG TTCTTCTGGG AAGCGCAGAA TTTCAGATAT ATTTTGTAA 6240
 CACATCCCA GCTCCCGAG AAAGCCAGTC TCATCTAATT TCTTAGTCAG TAAAAACAAT 6300
 TCCCTGTCC TTCAGGCTAT GAATGGACCA GCCAGGGAAA CTCTCGACCT TGATCTCTAG 6360
 CCAAGTCTTA GGCCCAATAT CTGACAGCCT CAGGTGGGCT GGGACCTAGG AAGCTCCATC 6420

TTGAAGGCTG GTCTAGCCCC AGACAGGGCA TGAGGGGCG AGAATTCAAG AAGGTACAGC 6480
 TTTGGCCCTC AAGAGCCAC TGTATGCTGG GGAAATGGAA CCATGGTGCA GTAGTGTGGA 6540
 GTGGATGAGT GTTCCATGAG CCTAGGAGCA AGAAAGTCTC TTCGGCCTCG GGCTTCTCGG 6600
 AGAAGGGGAC GTCCATTCTT GCTGGGTCTT AACAAAGCATA AAAAGGAAAA AAAGGAAACT 6660
 CAGGCAAGG GATCCATATG TGCAATGGCA AAGAAATGTG AAAAGGCATT GGGAGAAGCA 6720
 GTCTGGGGGA GGGCAGCCCA GTGCGGGCAC AGCACAACAC GGGGAGCAGC AAGAGATGAG 6780
 CCAGGGTCCA GGAGACAGAT GCCCATCGCG AGTACAGACT TTGTCTATT GGCAACAAGG 6840
 AGTOCATGGA GCTTTAGAGA GATGCACTCA GCTTCGTGTT GGCCAAGACT CCTTCTGGGC 6900
 CAATGGGGCT GCCTCTTTTC CTTTCATCAG ACACGTGTGAA AACATTCCCT TAAGCGTGCA 6960
 CTTTTAATA TCACATCTAT TTGTCTGTCT GCTCAITGTT TTGTGTCTGG AACTAAATAT 7020
 GCAATGGATC ATGAGACTCA GATTCTATGA GAAACCCAGG GTCTCTGCTT TACCACGGAG 7080
 CAGGGTCACC AACCCAGATC TCCAGGCCCA TGAGGATGGA ACATGAAAGG AGCCGACAAA 7140
 AGTTGCTTCC ATTGGCATGG GCTCTGGAGC GTGCCAGAAG TCCAGGGACA CCAGACTTGA 7200
 TCAAGGAAGG GCTGTCACTT TAGAGTTTCA AAAGGAAGTG CCTCAAAGCA AAGGCAAGCA 7260
 AAGGAACCCC ACGATGAATC TGCTCTTTTC CTTTGATGAG CCTCTCCCA GGTGTATTTT 7320
 AGCAGACCCC GGGGACCCAC CCCCACTGGG CCTGTGGGC TCCCTCGGT CCAGCCCAAT 7380
 GCCCAGCTG GCCTTCCCA GCCTGCAAGG AGCCTGTAGC ATGGCAAAATC TGCTGTCTGT 7440
 ATGCTATTTT CTTAGATCTT GGTACATCCA GACAGGATGA GGGTGGAGGG AGAGCTATTT 7500
 AACACAAATC CTAAGATTTT TTCTGTCTCA GGAAGGGGTG AAATGCTGG CAGATACAAA 7560
 AGACAGTGGC TTTTATCATT TTAATGGTA GGAATTTAAG GTGTGACTTC AGGGAGAAAC 7620
 AAACCTTGCAA AAAAAAATAA TCTCAGGCCA TGTGGGGTA ACCCAGCAAG GGCCAGTGAT 7680
 GATTTCCCCC AGCTCATCCC CTTATTTTCC CACAACCCAA CCATTCTCTA AAGCAGGACA 7740
 GTGAATAGGT CTTAGGCCAG TGCACACAGG AAGAAATTGA GGCTTATGGA TGGGGATGAC 7800
 TTCCCTAAGA TCCCATGGGA CAAGGATGTG GCAAGGCTTG GATGAGATGG GGCACCATG 7860
 CCCAGGAAT TGAACATTTT CCTTTACCCA GGAAATCTCC GGAGCCAAAC CCACCACCCC 7920
 CAGGGGGTCT CCCCAACCCA CCCCATTAC AGGGTGAGCT CAGCCTGTCA TGAGCAGAGG 7980
 AAAATATTAT TAATGCTCTC TGAGTCTTTA CAACAGGAGC TCTTACCTCA TAGATGTGGG 8040
 CTCTGTTTGG GGAAGATGCA AGGAAGTAAT GAGAAGCCCA GGAAATTTCT CCACCTGTGT 8100
 TTATGGCCTA AATAGCTTCA GGATGTATCT TAGCTGCACT CCAACATTCG ATCCTTTCTG 8160
 GGGTGGAAGAA TCTGGGCCAA CCAGGGGTCC TTGGGCTCT AGAAGGCCAC AGTAGGCCTC 8220
 TCTTTGTGGG AATGGAAGGG GACAGTTTGC TTTTAGTGCT GGCCCTCTCT GTGGGTGTGG 8280
 OCTGCAAGG AACCAACAGA CCTATGCTG GGGACTCTAA CATGTGAGCT CATTAATTC 8340
 TTCCAGCATT CTAAGGAGG GTTTGTGATT GTCACCATTT ACTGATGAGG AAATAAGGC 8400
 TCCTAGGGCA AATAGCTTCT GCCACAGTT CCACAGCTAG TGAGTGAATG AACCAGGATT 8460
 TAAACGGGT TTTTCTCACT ACAGAGACAA TATTTTCCA CCATTGTATC TCACATTTT 8520
 CCCAGGAGT TACCATAAAG AGAAGAGACT AGAGTGAAC AGATACGTCA GTGGATAAAG 8580
 CTCAAAGCAA ACAACAGTAA GCTTAAATTT CCTTCATAGT CTCATGTTTT ACGTTCACAA 8640
 TTATGCAAAA ATTTGCATTC CACTTTCTGA TTTAGCCTTG TTGGTTTAA TATGACTCTA 8700
 TGAATATTTC AAAAAAATAA GTGCTCTGTT CCTCATGTTG TTCTGTTCTG TTCACCCCGC 8760
 TATGACGGAG CCTAGGTGAG CTGCTCTTCA GCTTGACCTC AGAATTGACT CTAGGAGCAG 8820
 TGACCTGCT CCTTCCCA GCGAGTTATA GGCTCAAGAT CAAGACCAAC TGACCTTCTC 8880
 CTAGGAGCT CCTTTGGTGT GTGGGTGCTC TGACCTCACT GTTCATGAGG GGAACCTCAAC 8940
 TAAGGCATCT TCCAGTTGGG TGCTGGAAGG AACCCATTAA CTCACACTAG AATGATGAGG 9000
 ATTTGCTCAT CTGGCCTGGA GAAGGATGAG CCCACAAAAC CCTAAAGGGA AAAGAGAAGC 9060
 TGGACACAGC GTACTCAGC AGATTCTGA ATGCTAGGCT GGAAAGTGGT GCCTGTTGTC 9120
 CAAGTGGAGT CACATGGTTG CTAATGTGGG CAAGTCTGAG GACACACTTC ATGAGCAGCT 9180
 GGGGTCTGGA AGGCTCTCCA CTTTACCCTA GCCACACATA ATTACTGGGT GCCTACAGCA 9240
 CCTAGCACCT TGGAGGGGGC ACTATTAGGA AATCGAGATT ACTATGGCAC AATTAATTCC 9300
 TGGTAAAGC ATGGGGTTGT GGTGGACAGA GCTCAGTCTT TAGITTGAAC GAAACATAC 9360
 ATACATGAAA AACATACATG AAAAAAGGAC CCTCATCAAC ATTAGAAGGG GTAGATTTGG 9420
 AGCACTTATG GCAGGAAAAC AGGAACGCAA GGCCAGGAAA CTGGAACCCA GTGAATACTC 9480
 AGAACCGAGG ATGCAGATGA CTTATTTAGC AAAATGGTCA CTTCTGTGAC ATAGCTGGAG 9540
 AAAGGATGGG TAACAGCTTG CCAGAGCCAC TTGGAACAAG GGCAAAATCTC AGTGTCTGGG 9600
 GCAAAAGATG ATGCATTTCC CTCTGACCCA TCATGTTTAT TCATCTCCA CTCCTTATG 9660
 CCACACTAGC TCTTGCTGTA AGTCTCTACC AGGATCTACA TTCTCTGTC GCTGGTGGGA 9720
 ACCOCTTAGA GTACATAGAG GTATCAGTCC AGTAAGACTG CTCTACACAA CAGAAGTGAG 9780
 GCCCAGGGAG TAGCAGCCAG GCCCTTATCC TGTTACCTCT GCAGGAGTGA CTGCCCAACC 9840
 CAGATCCAGA GACATTGAAG GAAATGATAA TTCCTGGTA CCTCACTGCC TTGGGACAAA 9900
 ATGAAGAAAG CCACCCTTC TTAGGCTGCA GCTTGCCACT CCTGGGCTGG GTAAACAGGT 9960
 CATCAGCACC AGGCTCAACC AGGAGTACA TTCTGGAAGA CATGGGTGAG CCCAAGAGGA 10020
 AGCATGAACA GGACGCTGTT CCTAAGTCAT GTCAACAGGT TGTCTGGGC CAGGATCCCC 10080
 AGGGAAAAAA ATGGTCAACC CAACTGGAGG GTAGGTTAGA AGAAAAAAA CATAAACGTG 10140
 GATAGTCATG TCATCTCAA TCCCTGACTT GGCTTCCCA TTACTTGACA GTCTGAGCTC 10200
 CTCTTAGGCC TGTGACCAGC TTCAAATCAC AGCCAAGTAA AACAAGGAAA TAGGAAAAAGT 10260
 AAATCCAAC AGAAGAGACA AGCTGAGATT CAGATTTGTT TACTCTCCC ATGCAAGTT 10320
 TCCCTGTTGG AGGTTTCCA TGTATACATG TCTAGAAGTG ATAGAATGCA AGGCCTTGGC 10380
 TTTGCTTGG AGGGATCTG CTTTGAAGTC ATAGACTGAA CAGCAGGGAG AGAGGTTAGT 10440
 GGTGGAGTGT GGGGGAGCT GTTCTAGCTC CAGTTTCTC TGACACATTT TTCAGGATCA 10500
 TGGATCTGAT CCTCCGAAGC ACAGCAGAGA TATCTAAGCC ATATTGTGC ACATGAGCAG 10560
 ACTCTTCTAG TTTTATTAGT ACCAGGGATG GGCTTTTGA TGGCACTGAC TATAGAGATG 10620
 TCTGTAGAG ATCAAGCCAG TCCTTTGAT CCCACCTGCC CACCTCCAGA AGAGATGGGA 10680
 AAAGGTCATC AAAGGGCATT CACCAACTGA AATCCACTCA TGAATGTTAG GTCTCTAAAA 10740
 GGAGGCATCA CACTCACTCA TGGTAGCCTC CAAACCTAGC ATCCACCTA TCTAAGAGCT 10800
 CAGGGGTGGT CACTGGGGC AGATACAAGG GAAGTGCAAG GGCTCAGGAT GAAAGAAAAA 10860
 CTATTGGGAA GAGTTTATAG GGCTTGATCA TTATGGGGCT TCCTTCTATA TCTGAGAACT 10920
 GCTCTGGGTG GTGAGATGTG GACTCTGATC CTTAATTGGA ATGTTCCGGAG AATGAGTGTG 10980
 TGGTGGCCTT GAAGTGTGG ACAGAAAAAT ATCAGTATAA AAGCTGGAG CTCAGGGTAA 11040

TTAATGTAGT TCATGGTTCC TTAGTGAGCA GGACTCTTGG ATGTGGAGGA GAAAGGGTCA 11100
 TAGGAAGTAA ACCACCAAAA TTACAAAAATT GAGTCTCTGT ACAATTACTT CAGTGCCTTT 11160
 GGGCTTATGA ATACAAATCA GTGGGCCTTC TCTATGATGG TCCAACAAC TCTCAGTGTG 11220
 CACCCGTGCC CTGTATCTCC CATGGAAGAT GAATAATGTC AGGTGTTCTT TGGGTCAAAG 11280
 GCCCCAGGGC AGTCTGGAGG CTTAGAGGGC AGAGTGGTGT CATTCCATGT AAAGTTAGGC 11340
 TTCTGAGGGG TCAGGCAGAA TATGGTGTCC ATATCTTCCA TAGCTCTGCA GATTCTTGGA 11400
 TGAAGTCAAG CACAGTTTGC TAGACCCAGG TCACTCTCTT GAGTATACT AGGACCCATG 11460
 AGTGAACCTT AATAGCTTGA AGGAAGAACC TGCTGTCTGC CAGAGAGGAT AAGCTGCCCA 11520
 TCTCAGCAGC TGTCTAAAG AAGGCAGGTG TCTCTTTAAA GGGGAAGAGAA GCATTGGTGA 11580
 AATGGATTTC AGGTCACTTC CATTCCAGAT GGGTGAGATC TTGTGGAGCT GGGATCATGT 11640
 TTGAAGTCAT TCATACCTGT AGAGCACGAA TCCAAGTAGA TTGTGTTTGG TCTGTACAGG 11700
 CTGAAGCCCC CTGCTCTCCC ACCCAAGTGC CCCCACTGAG CAGGCCAACA TGCTGTTGTG 11760
 GCCACATATA CTGGGCTGAT CCAGGCTGGT TATCACCAAA CAGCAAAACCA TAGGGAACAG 11820
 CTGCTTTGCC ATAGACCCAA TACCCATGTA GATCTCTCAT GAGAGCAGCC ATAACCTAGA 11880
 CCCACTGACC AACAGGGCCA TGAGTGACAG CCAGAACCAG TGAAGGTCCA AGTAGGACAC 11940
 AGAGCAGGGC TTTTCTTACC ATACACATTA TCTCCAGAGG TTAATTTCTAC CCCACTCCCT 12000
 ATTCAGGGCC TGTGGAGCA CACTGCAAAA GCAAAAGCAC AGTAACCTAA TTACACATG 12060
 ATTATAATCA TTCCAGTGC ACACATTTCA TCACCAGGTG GATCCTGAGC TAGCCCATGT 12120
 AAATCCGGGT TAACCCATAT TGGTAATCAT ACTCAAAGC ACTTTTCACC CTACATTCTA 12180
 CTAGCCAATC AAAGACAAAG AGTTGTGGCC TCTACCATTG CCTTGGCTTC TGGACACCTT 12240
 CACAAGCTAT CCCAAGGTTT CCGCTCAACT CCAGGGAGGC TGACATCTTC ACATCCACTG 12300
 GGCAATATAAT ATTGCATGAG ACCAAAGTCT CCACACTCTT TGCAGCCTCC TCCATGAATC 12360
 CCAATGGCCT GCACCTGTAC AGTTTGGGTG TTTGATAGAT AAAGCACGTA TGAGAAGAGA 12420
 AAACAAATA AATCAACTTT TAAAAAAGC CAGCACTGTG CTGTCAATGT TTTTTTTTTC 12480
 TTTTCAATTC TAGCTCAGAA AAGCAGAAGG TAAATAATGT CAGGTCAATG AATATCAGAT 12540
 ATATTTTTTG ACTGTACATT ACAGTGAAGT GTAATCTTTT TACACCTGCA AGTCCATCTT 12600
 ATTTATTCTT GTAAATGTTT CCTGACAATG TTGTGAATAT GGCTGTGTGA AAAAATCTAT 12660
 ACAATAAGC TGTGACCTG

Seq ID NO: 98 Protein sequence:
 Protein Accession #: NP_008981.1

1 11 21 31 41 51
 | | | | |
 GIREFNPPO TEINTYROSI NEPHOSPHAT ASERECEPTO RTYPETHOMO SAPIENSMAS 60
 LAALALSLLL RLQLPLPGA RAQSAPGGCS FDEHYSNCGY SVALGTNGFT WEQINTTEKP 120
 MLDQAVPTGS FMMVNSSGRA SGQKAHL LLP TLKENDTHCI DFHYFSSRD RSSPGALNVY 180
 VKVNGGPQGN PVWNVSGVVT EGWVKAE LAI STF WPHFYQV IFESVSLKGH PGYIAVDEV 240
 VLAHPCRKAP VFRLQNV EV NVGQNATFQC IAGGKWSQHD KLWLQWNGR DTALMVTRVV 300
 NHRRFSATVS VADTAQRSVS KYRCVIRSDG GSGVSNY AEL IVKEPPTPIA PPELLAVGAT 360
 YLWIKPNANS IIGDGPILK EVEYRTTGT WAETHIVDSP NYKLWHLDPD VEYEURVLLT 420
 RFGEGGTGPP GAPTTRTRKC ADPVHGPQNV EIVDIRARQL TLQWEPFGYA VTRCHSYNLT 480
 VQYQYVFNQ QYEAEEVIQT SSHYTLRGLR PFMTIRLRL LSNPEGRMES EELVVQTEED 540
 VPGA VPLESI QGGPFEEKIY IQWKPPNETN GVITLYEINY KAVGSLDPSA DLSSQRGKVF 600
 KLRNETHHLF VGLYPGTYS FTIKASTAKG FGPPVTIRIA TKISAPSMPE YDTDIPLNET 660
 DTTITVMLKP AQSRGAPVSV YQLVVKERL QKSRRADII ECFVSVPSYR NASSLDSLHY 720
 FAAELKPANL PVTPPTVGD NKTNYGYWNP PLSPLKSYSI YFQALSKANG ETKINCVR LA 780
 TKAPMGSAQV TPGTPLCLLT TGASTQNSNT VEPEKQVDNT VKMAGVIAGL LMFIIILLGV 840
 MLTIKRRRNA YSYSYLSQR KLAKKQKETQ SGAQREMGPV ASADKPTTKL SASRNDEGFS 900
 SSSQDVNGFT DSGRGLSQP TLTIQTHPYR TCDPVEMSYP RDQQLAIRV ADLLQHTQM 960
 KRGGYGFKE EYEALPEGQT ASWDTAKEDE NRNKNRYGNI ISYDHSVRRL LVLGDGPHSD 1020
 YINANYIDGY HRPRIHYIA TQ GPMQETVKDF WRMIWQENSA SIMVMTNLVE VGRVKCVRYW 1080
 PDDTEVYGD I KVTLIETEPL AEYVIRTFV QKKG YHEIRE LRLFHTSWP DHGVPCYATG 1140
 LLGFVRQVKF LNPPEAGPIV VHCSAGAGRT GCFIAIDTML DMAENEGVVD IFNCVRELRA 1200
 QRVNLVQTEE QYVVFVDAIL EACLCGNTAI PVCEFRSLYY NISRLDPQTN SSQIKDEFQT 1260
 LNI VTPRV RP EDCSIGLLPR NHDKNRSM DV LPLDRCLPFL ISVDGESSNY INAALMDSHK 1320
 QPAAFVVTQH PLPNTVADF W RL VFDYNCSS VVMLNEMDTA QFCMQYWEK TSGCYGPIQV 1380
 EFVSADIDED IHRIFRICN MARPQDGYR I VQHLQYIGWP AYRDTPPSKR SLLKVVRRL 1440
 KWQEYDGRE GR TVVHCLNG GGRSGTFC AI CSVCEMIQQQ NIHDVFHIVK TLRNKNKNMV 1500
 ETLEQYKFVY EVALEYLSSF

Seq ID NO: 99 DNA sequence
 Nucleic Acid Accession #: NM_002988.1
 Coding sequence: 71-340 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCGGCACGAG AGGAGTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCCT 60
 GCCCAGCATC ATGAAGGGCC TTGACGCTGC CCTCTTGTG CTGCTCTGCA CCATGGCCCT 120
 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCCTCGTCT ATACCTCTG 180
 GCAGATTCCA CAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCCAGT GCCCCAAGCC 240
 AGGTGTCA TCCTCTAACCA AGAGAGGCCG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300
 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCCTGGA AGCTGCGAGG 360
 GCCCAGTGAA CTGGTGGGCG CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
 CCACCTGGA GGCCACCTCT TCTAAGAGTC CCATCTGCTA TGCCACGCCA CATTAACATA 480
 CTTTAATCTT AGTTTATGCA TCATATTCA TTTTGAAATT GATTTCATT GTTGAGCTGC 540
 ATTATGAAAT TAGTATTTTC TGTGACATCT CATGACATTG TCTTTATCAT CCTTCCCCT 600

TTCOCTTCAA CTCTTCGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTTCTCAG 660
 CAGACATTGT GCCATATGTA TCAATGACA AATCTTTATT GAATGGTTTT GCTCAGCACC 720
 ACCTTTAAAT ATATTGGCAG TACTTATTAT ATAAAAGGTA AACCCAGCATT CTCACTGTGA 780
 AAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 100 Protein sequence:
 Protein Accession #: NP_002979.1

1 11 21 31 41 51
 | | | | |
 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI 60
 LLTKRGRQIC ADPNKKWVQK YISDLKLNA

Seq ID NO: 101 DNA sequence
 Nucleic Acid Accession #: NM_015507.2
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGGCCCCCA GCCCTCCCC AGGCCGCGAG 60
 CGCCCTGCC GCGGTGCTG GCCTCCCTC CCAGACTGCA GGGACAGCAC CCGGTAAC TG 120
 CGAGTGGAGC GGAGGACCGC AGCGGCTGAG GAGAGAGGAG GCGGCGCTT AGCTGCTACG 180
 GGGTCCGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTCCGAGA 240
ATGCTCTGC CTGAGCCT TCGCTCCC CTGCTGCTCT CTTGGGTGGC AGGTGGTTTC 300
 GGGAACGCGG CCGTGGCAAG GCATCACGGG TTGTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAATAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCCAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAATGTC 480
 AGATGCTTTC CAGGATACAC CGGGAACACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
 GGTAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
 AAATGTCACA TTGGTTTGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
 GGGTCCTTCA AGTGTAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
 ATCCCTGAAA ATTCTGTGAA GGAAGTCTCT AGAGCACCTG GTACCATCAA AGACAGAAATC 1080
 AAGAAGTTGC TTGCTACAAA AAACAGCATG AAAAAGAAGG CAAAATTA AAATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGGCGGGA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCTGA AGAATGACAT AGAGGAGCGA 1320
 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
 CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAA TATCTCGGTT 1440
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAACTCTG CTGATCGAGA TAACTGCTAT GGCCTTCTATA TGGCAGITCC GGCCTTGGCA 1560
 GGTACAAAGA AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACTGCA ACCCAAAGC 1620
 AACTTCTGTT TGCTCTTGA TTACCGGCTG GCCGAGACA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
 TGGGAAGCAG GGAATAATCA GTTGTATCAA GGAAGTATG CTACCAAAG CATCATTTT 1800
 GAAGCAGAAC GTGGCAGGG CAAACCGGC GAAATGCGAG TGGATGGCGT CTTGCTTGT 1860
 TCAGGCTTAT GTCCAGATAG CTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 TTGACTTTGT ATGTCAGTTC CTTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
 TCTTGATATA GATATGCCAA TATTGCTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
 TTTCTGAATC TTTCCACATT ATATTATAAA ATATGAAAT GTCACTTTAT CTCCCTCT 2160
 CAGTATATCT GATTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
 TAGAAAAAAA AGCACAGAGA AATGTTTAACT TGTGACTC TTATGATACT TCTGGAAAC 2280
 TATGACATCA AAGATAGACT TTTGCTAAG TGGCTTAGCT GGGTCTTCA TAGCCAAACT 2340
 TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAA AAAAAAAA

Seq ID NO: 102 Protein sequence:
 Protein Accession #: NP_056322.2

1 11 21 31 41 51
 | | | | |
 MPLPWSLALP LLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
 CEATCEPGCK FGECVGNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFCF 120
 LSGHMLMPDA TCVNSRTCAM INCOYSCEDT EEPQCLCP SGLRLAPNGR DCLDIDECA 180
 GKVICPYNRR CVNTFGSYQY KCHGFELQY ISGRYDCIDI NECTMDSHTC SHHANCNTQ 240
 GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLALHKNM KKKAKIKNVT 300
 PEPTRTPTPK VNLQPFNYEE IVSRGNSHSG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
 SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPS NFCLLDYRL AGDKVGKLRV 480
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSHF EAERGKGTGT EIAVDGVLLV 540
 SGLCPDSLVS VDD

Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67-363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 5 | | | | |
 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCAGTCTC 60
 AGCACCATGA ATCAAACCTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
 ATTCAGGGAG TACCTCTCTC TAGAACCCTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 10 CGTGTGTAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 TCGAAGGCCA TCAAGAAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAAATCAGC TGCTACTACT CCTGTAGGAA 540
 15 GGTTAATGTT CATCATCTTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCCTACTGGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAAA TATTTCCCTC 660
 ACCTTTCCCA TCTTCAAGG GTACTAAGGA ATCTTCTGCT TTTGGGGTTT ATCAGAATTC 720
 TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTAAAG AATGCTCTT 780
 ACTTCATGGA CTTCACCTGC CATCTCCCA AGGGGCCAA ATCTTTCAG TGGCTACCTA 840
 20 CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAATATT 900
 CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
 TTTCAAGTGA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAATAA AAAATGAGGT ACTCTCTGG AAATATTAAG

Seq ID NO: 104 Protein sequence:
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
 30 | | | | |
 MNQTAILICC LIFLTLGIQ GVPLSRVRC TCISISNPV NPSLEKLEI IPASQFCPRV 60
 EIIATMKKKG EKRCCLNPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 105 DNA sequence
 Nucleic Acid Accession #: NM_015068.1
 Coding sequence: 1170-2243 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 | | | | |
 GTAACAACCG TCACCTGGG TCCCGACTGC CCACCTCTC CTCTCCCCC TCCGCCAAC 60
 AACACAACA ACAACAATC CAAGCACACC GGCCATAAGA GTGCGTGTGT CCCCACATG 120
 ACCGAACGAA GAAGGGACGA GCTCTCTGAA GAGATCAACA ACTTAAGAGA GAAGGTGATG 180
 AAGCAGTCGG AGGAGAACA CAACCTGCAG AGCCAGGTGC AGAAGCTCAC AGAGGAGAAC 240
 45 ACCACCCTC GAGAGCAAGT GGAACCCACC CCTGAGGATG AGGATGATGA CATCGAGCTC 300
 CGCGGTGTGT CAGCAGCTGC TGCCCCACCC CCTCCAATAG AGGAAGAGTG CCCAGAAGAC 360
 CTCCAGAGA AGTTCGATGG CAACCCAGAC ATGCTGGCTC CTTTCATGGC CCAAGTGCAG 420
 ATCTTCTAGG AAAAGAGCAC CAGGGATTTC TCAGTTGATC GTGTCCGTGT CTGCTTCGTG 480
 ACAAGCATGA TGACCGGCGG TGCTGCCCGT TGGGCCTCAG CAAAGCTGGA GCGCTCCAC 540
 50 TACCTGATGC ACAACTACCC AGCTTTCATG ATGGAATGA AGCATGTCTT TGAAGACCTC 600
 CAGAGGCGAG AGGTTGGCAA ACGCAAGATC AGACGCTGC GCCAAGGCAT GGGGTCTGTG 660
 ATCGACTACT CCAATGCTTT CCAGATGATT GCCCAGGACC TGGATTGGAA CGAGCCTGCG 720
 CTGATTGACC AGTACCAGA GGGCCTCAGC GACCACATTC AGGAGGAGCT CTCCACCTC 780
 GAGGTGCGCA AGTCGCTGTC TGCTCTGATT GGGCAGTGCA TTCACATTGA GAGAAGGCTG 840
 55 GCCAGGGCTG CTGCAGCTGC CAAGCCACGC TCGCCACCC GGGCGCTGGT GTTGCTCAC 900
 ATTGCAAGCC ACCACAGGT AGATCCAACC GAGCGGTGG GAGGTGCCCG CATGCGCTG 960
 ACGCAGGAAG AAAAAGAAAG ACGCAGAAAG CTGAACCTGT GCCTCTACTG TGAACAGGA 1020
 GGTCACTACG CTGACAATTG TCCTGCCAAG GCCTCAAAGT CTTGCGCGGC GGAACCTCC 1080
 CCGGCCCGCG TGTAGAGGGA CCTTCAGCGA CCGGGCCAGA AATAATAAGG TCCCCACAAG 1140
 60 ATGATGCTCT ATCTCCACAC TTGCAAGTGA TGCTCCAGAT TCATCTTCCG GGCAGACACA 1200
 CCTGTTTCTG CCGAGCCATG ATCGATTCTG GTGCTTCTGG CAACTTCATT GATCAOGAAT 1260
 ATGTTGTCTA AAATGGAATT CCTCTAAGAA TCAAGGACTG GCCAATACCT GTGGAAGCAA 1320
 TTGATGGGCG CCCATAGCA TCGGGCCAG TTGTCCACGA AACTCACGAC CTGATAGTTG 1380
 ACCTGGGAGA TCACCGAGAG GTGCTGTCAT TTGATGTGAC TCAGTCTCCA TTCTCCCTG 1440
 65 TCGTCTTAGG GGTTCGCTGG CTGAGCACAC ATGATCCCAA TATCATATGG AGCACTCGAT 1500
 CATCTGCTTT TGATTCTGAA TACTGCCGCT ACCACTGCCG GATGTATTCT CCAATACCAC 1560
 CATCGCTCCC ACCACCAGA CCACAACCGC CACTCTATTA TCCAGTAGAT GGATACAGAG 1620
 TTTACCAACC AGTGAGGTAT TACTATGTCC AGAATGTGTA CACTCCAGTA GATGAGCAGG 1680
 TCTACCCAGA TCACCGCTG GTTGACCTC ACATAGAAAT GATACCTGGA GCACACAGTA 1740
 TTCCAGTGG ACATGTGTAT TCACTGTCCG AACCTGAAAT GGCAGCTCTT CGAGATTITG 1800
 70 TTGCAAGAAA TGTAAAAAT GGGCTAATTA CTCCAACGAT TGACCTAAT GGAGCCCAAG 1860
 TTCTCCAGGT GAAGAGGGGG TGGAACTGC AAGTTTCTTA TGATTGCCGA GCTCCAACA 1920
 ATTTTACTAT CCAGAATCAG TATCTCGCC TATCTATCC AAATTTAGAA GACCAAGCAC 1980
 ACCTGGCAAC TCACCGCTG TTGTAACCTC AAATACCTGG ATACCAACA TACCCACAT 2040
 75 ATGCCGCGTA CCGGACCTAC CCAGTAGGAT TCGCTGGTA CCCAGTGGGA CGAGACGGAC 2100
 AAGGAAGATC ACTATATGTA CTTGTGATGA TCACTTGGAA TCCACTGG TACCAGGAC 2160
 CTCGGTACC ACAGTACCCG CCGCCACAGC CGCGGCTCC ACCACCACA CCGCGCGCGC 2220
 CTCCATCTTA CAGTACCCTG TAAATACCTG TCATGCTCT CAGGATCTCT GCCCTCAAAA 2280

TTTATTCTG TTCAGTCTCT CAATCAGTGA CTGTGTGCTA AATTTTAGGC TACTGTATCT 2340
 TCAGGCCACC TGAGGCACAT CCTCTCTGAA ACGGCTATGG AAGGTTAGGG CCACCTCTGGA 2400
 CTGGCACACA TCCTAAAGCA CCAAAAGACC TTCACATTT TCTGAGAGCA ACAGAGTATT 2460
 TGCCAATAAA TGATCTCTCA TTTTCCACC TTGACTGCCA ATCTAACTAA AATAATTAAT 2520
 5 AAGTTTACTT TCCAGCAGCT CCTGGAAGTC TGGGTTTAC CTGCCAAAAC CTCCATCACC 2580
 ATCTAAATTA TAGGCTGCCA AATTTGCTGT TTAACATTTA CAGAGAAGCT GATACAAAACG 2640
 CAGGAAATGC TGATTTCTTT ATGGAGGGGG AGACGAGGAG GAGGAGGACA TGACTTTTCT 2700
 TGCGGTTTCG GTACCCCTCT TTTAAATCAC TGGAGGACTG AGGCCTTATT AAGGAAAGCCA 2760
 AAATTATCGG TGCAGTGTGG AAAGGCTTCC GTGATCCTCT CGCTGCACCC TTAGAAACTT 2820
 10 CACCGTCTTC AAATCCATT TCCATGGTTC TGTTAATCT CAAGGAGCAG CAACTCGACT 2880
 GGTTCCTCCA GGAGCTGGA AAACCCCTGT GACATGAAAC ATCTCAGGCC TGAAAAGAAA 2940
 GTGCTCTCTC AGATGGACTT TTGCATGTTA AGACTATGTC TTCACATCAT GGTGCAAAATC 3000
 ACATGTACCC AATGACTCCG GCTTTGACAC AACACCTTAC CATCATCATG CCATGATGGC 3060
 15 TTCCACAAAG CATTAAACCT GGTAACCAGA GATTACTGGT GGCTCCAGCG TTGTAGATG 3120
 TTCATGAAAT GTGACCACT CTCAATCACC TTGAGGGGCT AAAGAGTAGC ACATCAAAAG 3180
 GACTCCAAAA TCCCATTACC AACTCTTAAG AGATTGTCC TGGTACTTCA GAAAGAAATTT 3240
 TCATGAGTGT TCTTAATGG CTGGAAGAGC ACCAGCTGAC GTTTTGAAG AATCTATCCA 3300
 TGTGTCTGCC TCCATATGCA TCTGGGCATT TCATCTTCA TCCCTCATT AGACTGTAGC 3360
 20 ATTAGGATGT GTGGAGAGAG GAGAAATGAT TTAGCACCCA GATTACACT CCTATGCCTG 3420
 GAAGGGGGAC ATCTTTGAAG AAGAGGAATT AGGGCTGTGG ACACCTGTCT GAGGATGTGG 3480
 ACTTCCTTAG TGAGCTCCAC ATTACTTGAT GGTAACCACT TCAAAAGGAT CAGAATCCAC 3540
 GTAATGAAAA AGGTCCTCT AGAGGATGGA GCTGATGTGA AGCTGCCAAT GGATGAAAA 3600
 CCTCAGAAAG CAACTCAAAG GACTCAAAGC AACGGACAAC ACAAGAGTTG TCTTCAGCCC 3660
 25 AGTGACACCT CTGATGTCCC CTGGAAGCTT TGTGTAACC TGGGACTGCC TGACTTCCTT 3720
 TAGCCTGGTC CCTTGCTACT ACCTTGAAC GTTTTATCTA ACCTCTCTT TCTGTTTAA 3780
 TTCTTGCTA CTGCCATTGA CCTGCTGCA GGATTGTGT CATTTTCTG CCTGGTTGCT 3840
 GAGACTCCAT TTTGCTGCCA CACACAGAGA TGTAAGAGGC AGGCTTTAAT TGCCAAAGCA 3900
 CAGTTTGAGC AGTAGAAAC AACATGGGT ATATCTCAA TTGCCTGACA TGAAGAGGAG 3960
 30 TCTAACGGTG AAGTTTCACT TTTATCAGC ATCATCTTTC ACATGTTTAT TATCATCCGC 4020
 TCTTATCTT GCATGTTTAA ACACITAAAA TTTTAGTAT AATTTTAGT GTGTTTTGAA 4080
 GTGGTGACTA GGCTTTCAA AACTTCCATT GAATTACAAA GCACTATCCA GTTCTATTG 4140
 TTAATAAAG TAAAAATGAT AAGTAACATA GTGTAAAAA TTCCTTACT GTGAACCTCT 4200
 TACAATGCTG TGAATGAGAG GCTCCTCAGA ACTGGAGCAT TTGTATAATA ATTCATCCTG 4260
 35 TTCACTTCA ATTTTAACT CATATATAAT TTCAATTCTA TCAATTGGGC CTTTAAAAAT 4320
 CATATAAAG GATATAAAT TTGAAAGAG AAACCTAAT GGCTATTAA TCCAAACAA 4380
 CTTTTTTTT TCCTCAATG GAATCAGAAA GCTTGTCAAT CACTCATGTG TTTTAGAGTA 4440
 ATTACTTTA AAATGTGCA TTTGTGCTT TGAACATTT TGAAGAGTCA CTCTGTITA 4500
 CCTCAAGTAT CAATTCATCC TCCATACATT TGAATTCAG TTGTTTTTG TCAAAATTAC 4560
 40 AGTTGTCAAT TGAATTTCAA GCTGCAGGT GCCTAGAAAT GGGCCGTGT CTGTAGCCCT 4620
 GGCATGTGCA CACGGACATT TGCCACCACT GCAAGCAAAA GTCTGGAGAA GTTCACCAAC 4680
 GACAAGAACG ATTAGGGAAA ATATGCTGCT GTGGGTTAAC AACTCAGAAA GTCCCTGATC 4740
 CACATTTGGC TGTTTACTAA AGCTTGTGAT TAACTTTTG CAGTGTGTA CTATGCTCTA 4800
 TTGCTATATA TGCTATCTAT AAATGTAGAT GTTAAGGATA AGTAATCTA AATTTATTAT 4860
 45 TCTATAGTTT TGAAGTTTGG TTAAGTTTCC TTCACTCAA TTGATTATT TTGTTGTAA 4920
 TCAAATTAT GTTAATTGGA TCCTTTAAAT TTTTGTGGC ATTTTCCAAC AAAAATGGCT 4980
 TTATTCATAA GAAAGGAAAA AAATCAATGG AATTGTATAT CTAAAGAGT TAGAAAGGGA 5040
 GCAAAATAAA AAACATAAAG GAGATAGATG AATTAGTAAG CAAATCAGTA GTCGAGTTT 5100
 TCAAACCTGGC AAAATTAAT AATTGACTTT TAGCCCAAA TTACATTGTT AATTAATCA 5160
 50 AGAAGGAAGA AGATCTAAGA GCTCCCATTT ATAGGCAAGC CTAGAGAGAA CTAGCTAAAT 5220
 TTATCATGCT AGGATATTGA AACACAGAAA GTTTACATAC ATTTAGTAAG GGTCAATTTA 5280
 GTTTGGACAG TGAGGTATT GTCTTAGTGG AAAAAAGGAG AATTAGTCTG ATCAAAATCGT 5340
 GAAGTAATAC AGTGAACCTG CAGGTGCACA AAATAAGAGG GCCACATCTA TATGGTGAG 5400
 TCTGGAATTC TGTTAAGTT TGTAGGTACC TCTTGGACTT CTGAATTGAT CCAAGTTGTA 5460
 55 TCCACACAG ACATCTACA TCAGATACAG ACAGTTCCAA GATTGACAAC AGAGAACAAC 5520
 CTGCTGGAAG GACCTGGGCA GAAATGGAGA GCCCTGCGGG AACCATGCTA CATTTTCATC 5580
 TAAAGAGAGA ATGCATCTCT GATGAGACTG AAAGTCTTT GTTGTGTTAG ATTGTAGAAT 5640
 GGTATTGAAT TGGTCTGTGG AAAATTGCAT TGCTTTTATT TCITTTGTGA ATCAAGTTTA 5700
 AGTAATAGGG GATATATAAT CATAAGCATT TTAGGGTGGG AGGGAATATT AAGTAATTTT 5760
 AAGTGGGTGG GGTATTATT AATGTTAGAA TAATATTATG TATTAGATAT CGCTATAAGT 5820
 60 GGACATGCGT ACTTACTTGT AACCTTTTAC CCTATAATTG CTATCCTTAA AGATTTCAAA 5880
 TAACTCGGA GGGAACTGCA GGGAGACCAA CTATTATTGA GCGAATTGGA CATGGATAAA 5940
 AACCCAGTG GGAGAAAGTT CAAAGGTGAT TAGATTAATA ATTAAATAGA GGATGAGTGA 6000
 CCTCTGATAA ATTACTGCTA GAATGAACCT GTCAATGATG GATGGTAAAT TTTTCATGGA 6060
 65 GTTATAAAG TGATAAATAA AAACCTTGC TTTTACCCCT GTCAGTAGCC CTCCTCTAC 6120
 CACTGAACCC CATTGCCCT ACCCTCCTT CTAACCTTAT TGCTGTATTC TCTTCACTCT 6180
 ATATTCTCT CTATTGCTA ATATTGCATT GCTGTTACAA TAAAAATCA ATAAAGATT 6240
 AGTGTTAAG TGC

Seq ID NO: 106 Protein sequence:

Protein Accession #: NP_055883.1

| | | | | | |
|---|----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
| | | | | | |

MTERRRDELSEINNLREKVMKQSENNNLQSQVQKLTEE NTLREQVEP TPEDEDDIE 60
 75 LRGAATAAAP PPIIEECPE DLPEKFDGNP DMLAPFMAQC QFMKSTRD FSDVRVRVCF 120
 VTSMMTGRAA RWASAKLERS HYLHNYPAF MMEMKHVFEQ PQRREVAKRK IRLRQGMGS 180
 VIDYNAFQM IAQDLWNPE ALIDQYHEGL SDHIQEELSH LEVAKLSAL IGQCIIHRR 240

LARAAAARKP RSPPRALVLP HIAASHQVDP TEPVGGARMR LTQEEKERRR KLNLCLYCGT 300
GGHYADNCPA KASKSPAGN SPAPL

Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_003679.1
Coding sequence: 47-1507 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
10 GGCACGAGCA GAAGCAACAA TAATTGTGAA AAATACTTCA GCAGTTATGG ACTCATCTGT 60
CATTCAAAGG AAAAAAGTAG CTGTCAATTGG TGGTGGCTTG GTTGGCTCAT TACAAGCATG 120
CTTTCTTGCA AAGAGGAATT TCCAGATTGA TGTATATGAA GCTAGGGGAAG ATACTCGAGT 180
GGCTACCTTG ACACGTGGAA GAAGCATTAA CTTAGCCCTT TCTCATAGAG GACGACAAGC 240
CTTGAAAGCT GTTGGCCTGG AAGATCAGAT TGTATCCCAA GGTATTCCCA TGAGAGCAAG 300
15 AATGATCCAC TCTCTTTCAG GAAAAAAGTC TGCAATTCCC TATGGGACAA AGTCTCAGTA 360
TATTCTTTCT GTAAGCAGAG AAAATCTAAA CAAGGATCTA TTGACTGCTG CTGAGAAAATA 420
CCCCAATGTG AAAATGCACT TTAACCACAG GCTGTTGAAA TGTAAATCCAG AGGAAGGAAT 480
GATCACAGTG CTTGATCTG ACAAAGTTCC CAAAGATGTC ACTTGTGACC TCATTGTAGG 540
ATGTGATGGA GCCTATTCAA CTGTGAGATC TCACCTGATG AAGAAACCTC GCTTTGATTA 600
20 CAGTCAGCAG TACATTCTCT ATGGGTACAT GGAGTTGACT ATTCCACCTA AGAACGGAGA 660
TTATGCCATG GAACCTAATT ATCTGCATAT TTGGCCTAGA AATACCTTIA TGTGATTGCT 720
ACTTCTTAAC ATGAACAAAT CATTCACATG TACTTTGTTT ATGCCCTTTC AAGAGTTTGA 780
AAAACTTCTA ACCAGTAATG ATGTGGTAGA TTTCTTCCAG AAATACTTTT CGGATGCCAT 840
CCCTCTAATT GGAGAGAAAC TCCTAGTGCA AGATTCTTTC CTGTGTCCTG CCCAGCCCAT 900
25 GATATCTGTA AAGTGCTCTT CATTTCACTT TAAATCTCAC TGTGTACTGC TGGGAGATGC 960
AGCTCATGCT ATATGCGCGT TTTTGGGCA AGGAATGAAT GCGGGCTTTG AAGACTGCTT 1020
GGTATTTGAT GAGTTAATGG ATAAATTCAG TAACGACCTT AGTTTGTGTC TTCTGTGTTT 1080
CTCAAGATTG AGAATCCAG ATGATCACGC GATTTCAGAC CTATCCATGT ACAATTACAT 1140
AGAGATGCGA GCACATGTCA ACTCAAGCTG GTTCATTTTT CAGAAGAACA TGGAGAGATT 1200
30 TCTTCATGCG ATTATGCCAT CGACCTTTAT CCCTCTCTAT ACAATGGTCA CTTTTTCCAG 1260
AATAAGATAC ATATGCGCGT TGCAGCGTTG GCATTGGCAA AAAAAGGTGA TAAACAAAGG 1320
ACTCTTTTTC TTGGGATCAC TGATAGCCAT CAGCAGTACC TACCTACTTA TACACTACAT 1380
GTCACACGCA TCTTCTCTCT GCTTGAGAAG ACCATGGAAC TGGATAGCTC ACTTCCGGAA 1440
35 TACAACATGT TTCCCGGCAA AGGCCGTGGA CTCCTAGAA CAAATTTCCA ATCTCATTAG 1500
CAGGTTATAG AAAGGTTTTC TGGTAGCAAA TGCATGATT CTCTGTGACC AAAATTAAGC 1560
ATGAAAAAAA TGTTCCTATT GCCATATTTG ATTCACCTAGT GGAAGATAGT GTTCTGCTTA 1620
TAATTAACCT GAATGTAGAG TATCTCTGTA TGTAAATGCA AATTACTGGT TGGGGGGTGC 1680
ATTTTAAAG ATGAACATG CAGCTTCCCT ACATTACACA CACTCAGGTT GAGTCATTCT 1740
40 AACTATAAAA GTGCAATGAC TAAGATCCTT CACTTCTCTG AAAGTAAGGC CTTAGATGCC 1800
TCAGGGAAGA CAGTAATCAT GCCTTTTCTT TAAAGACAC AATAGGACTC GCAACAGCAT 1860
TGACTCAACA CCTAGGACTA AAAATCACAA CTTAACTAGC ATGTTAATG CACTTTTCAT 1920
TACGTGAATG GAACCTACCT AACACAGGG CTCAGACTTA CTAGATAAAA CCAGAAATGG 1980
AAATAAGGAA TTCAGGGGAG TTCCAGAGAC TTACAAAAAT AACTCATTTT ATTTTCCCAC 2040
45 CTCAAAATAT AAGTATTATC ATCTATCTGT TTATCGTCTA TCTATCTATC ATCTATCTAT 2100
CTATCTATCA TCTATCTATC TATCTATCTA TCTATCTATC TATCTATCTA TCTATCTATC 2160
TCTATTTATT TATGTATTAT GAGATCAGGT CTCACTCTGT TGACCGGCT GGAGTGCAGT 2220
GGTGAGATCT GGGTTCAGT CAACCTCTGC CTCCTGGGCT CAAGCAATCC TCCCACTTCA 2280
GCCTCCCAAA TAGCTGGGGC TACCATTGTA TTTTTCAGTA GAGACCGGGT CTTGCCATGC 2340
50 TGCCCAGGCC AGTCTCAAA CTTCTGGCTC ATGTGATCTG CCCACCTCAG CCTCCCAAAG 2400
TACAGGGATT AGAGTTGTGA GCCACCGCTG CCAGCCGAGA GTTACCCTCT AAAGATAAGA 2460
AAAAGGCTAT TAATATCAT CTAAGTGAAG GACAGGAAAG GGTTTTATTC ATAAATTAAG 2520
TGCTCATGAT TGCCAGAATG GAAAGGAAAC AAGGGGAGAC AACTTTTATA GAAATACAAA 2580
GCCATTACTT TATTCAAATT CAGACCTTCA GAAGCAATT ACTAATTTAT TCTTCGACTA 2640
55 CATACTGCAG CAGAACCAGC AATACACTTG ATTTTAAAA GCACATTTAG TGAAATGTTT 2700
TCTTTGGTTC ATCCTTCTTT AACAGGCTGC TGAGTCACTC AGAAATCCTT CAAACATGAT 2760
TAATTATGAA GATGAAACAC TAGAGTCATA TAAGAAATAA AAATTGGGCA ATAAAAATAA 2820
ATGATTCAGT GTTCTTTTTC TATATTGTCA ATGAAAACCT TGAGTTCTAA TAATCCATGT 2880
TCAGTTTGTG GGGAAAGAAA AAATAATTTT TCCTTCTACC CACTTTAGGT TCCTTGGCTG 2940
60 GGGCCCTTAT AACAAAAGAC AGATTGACAA GAGAAAAACA AACATAAATT TATTAGCGGG 3000
TATATGTAAT ATATATGTGG GAAATACAGG GGAATGAGCA AATCTCAAAG AGCTGGCGTC 3060
TTAGAACTCC CTGGCTTATA TAGCATCGAC AAAGAACAGT AAATTTTATG AGAAACAACA 3120
AAACAAAGAA AAAGAGCTTT GAGTCTGTAG GGGCAGCAAT TTGGGGGAAG CAAATATATG 3180
GGAGTTTGCC TTGTAGATTG CTCTGGTGGT GGTCTOCAGG CTGACAAGGA TTCAAAGTTG 3240
65 TCTCTGAAAC TCCTCTTGT CATACTGCAC ATATAAACG TCCTTTGTTT CCAACAAGAG 3300
GATTTCCTTT TCATTCTAGA ATATCTCTCT TGATAACTTG ATCAGATATA GGACATGACA 3360
CTGAATAGAG TCCAACAGTA CAAAAAATAT TCAGTATGTT CTAGCTACTT CACACATGTG 3420
TACGCGACAG TTATTTTAC AGTAAGGTAT TTTGAGAGAA AATGCATTAC GTGTTTGGGA 3480
AAATAGAGTA ATTTAAAAA TATATTGAA ATGAAATCT CCAACACATT AGAAGATGAT 3540
70 GATGTTAGAT GCCCATCGTG TGCCACAAGT GGTTTTTTCA TTATGTAAG CACCCGTTGA 3600
ATTAAAAAGG TTGTTTGTG TTCAACCTCT TCCTGAGGCC CAAGAGCATA TGGGCAATTC 3660
GGATTTCCTG CTGGACCACA AGGTTCTGTT GATATTACAT AGAAACGGGT ATTCCAGACA 3720
CTTCTTATG TGAAAGTCCA AAGTGGCAT CCAATTAAAG GCCCATCTT TCGTTGCCAT 3780
TCTTCATTCC TACAAAGGAC GAACCTGGAT TACATCAACT TTGGACCAT TGGTTTTGTC 3840
GCTGTCGTCA ACTGACAGTG ATTCACCCT GGTGATGATA AAAATGATGG AAGAAGAGTT 3900
75 GAAAGTCACT TTTTCTTCTG GCTGTCCCTT ATCTTCTGT GACATCACAA TGGGTCTGAT 3960
CTGCATTTCA CTTCAGCTG CTGGTAGGTC TTAGCAGGC CTCTGGCACC TCAGCAGTCG 4020
GAGGCACAGA AGCTGCAAAA GGGATCTTCG AAAGTGGCA GAGAAAAAT AAAGTGAAT 4080

5 ATTAAGTAAA AGTTGGGCAC TAATCTGGAT TAACATTCGA GGAAATCAGT TGAGCTGATT 4140
 TAAGTGTGTT TTTGTTTGT AGCAGGTGTG GATGTGGGGT TATGTGGTCA TGCTCAGATC 4200
 TACCTAAATC ACCCCAGAGC TTTATGTCTT TTATTCATT TAAATCTTAT TAACCGGAAT 4260
 ATGTAGGACC ATTTCAATAC CTGTGAATCC TCCAAGCTTC AATCTGCACA CACTTTCTAT 4320
 10 GAGGGCAGGT ACAACTATTA AGAGATTTTG AACATTAAGT TAGTCCACAA ATATTCAGTG 4380
 GGCATCTACT AGGTGACAGC CACTGTGCTA TAATTAGAGA CTTTTACTA TAAGCATCAA 4440
 AAACAGATAA GGCTCTTCTT GGCAGAGTTT ACAGCCTGGT GTACTTGCTA ATGTCTCTTT 4500
 AATTAGGTGA AGAATTTTTT TTTTCTATCG AAATTACTAA TCAGTTGGGG AAAAAAATAC 4560
 TATAGCAGAC AGCACTAATG TCATCAACAA ACATTGTTCT TCTCCGTGTC CTGGGTACAA 4620
 15 CATCGAATAA TATTCTTGG CCTCCTTTCC GCTTCTCCTC TCTGCTGTC CTCTCTACAA 4680
 GAACCTGGGA GGCCACGCC TAAAGATCAT AATATCACA TGAAGGAAC CTAGATTCCT 4740
 AAATGACTGC ATAGGACAGA TCCCATCTCC TCCACCCAAT ACATTATTAG ACTGAACTGT 4800
 GACCTGAAAT GAGCAATAAA CTCTGTATTA ATTCAGTCAA ATGTTGGGGT TGCTTGTTAT 4860
 AGTAGTCGGT CCATCATGAC CAGTAAACAA TAAATCAAAA GTTAATGTAA TTGTTATCCC 4920
 20 ATTTATTAGA GCGAAATAAA TGTGGAATAT ATGGACTTTC TCAGATTAGG AAATACCAAT 4980
 TAAAAATATA ATAAATAGCT

Seq ID NO: 108 Protein sequence:

Protein Accession #: NP_003670.1

20 1 11 21 31 41 51
 MDSSVIQRKK VAVIGGGLVG SLQACFLAKR NFQIDVYEAR EDTRVATFTR GRSINLALSH 60
 25 RGRQALKAVG LEDQIVSQGI PMRARMIHSL SGKKSAIPYG TKSQYILSVS RENLNKDLLT 120
 AAEKYPNVKM HFNRHLKCN PEEGMITVLG SDKVPKDVTC DLIVGCDGAY STVRSHLMKK 180
 PRFDYSQQYI PHGYMELTIP PKNGDYAMEP NYLHIWPRNT FMMIALPNMN KSFTCTLFMP 240
 FEEFEKLLTS NDVVDFQKY FPDAILIGE KLLVQDFLL PAQPMISVKC SSFHFKSHCV 300
 30 LLGDAHAIV PFFGQGMNAG FEDCLVDEL MDKFSNDLSL CLPVFSRLRI PDDHAISDLS 360
 MYNYIEMRAH VNSSWFIFQK NMERFLHAIM PSTFIPLYTM VTFSRIRYHE AVQRWHWQKK 420
 35 VINKGLFFLG SLAISSTYL LIHYMSPRSF LCLRRPWNWI AHFRNTTCFP AKAVDSLEQI 480
 SNLISR

Seq ID NO: 109 DNA sequence

Nucleic Acid Accession #: NM_006115.1

Coding sequence: 236-1765 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 40 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCGCT GCAGCCCCTC AGCACCCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGCCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 45 CCCACGGAGA CTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCGCCCA CTCTTCATGG CAGCCTTTGA 420
 CCGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAGC TTCAAGTGCT 600
 50 GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGAAGTGA TGGTCTGGAA ACAGGGCCAG 660
 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGGCCATG ACAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCGC AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGTG GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
 55 TATCAAGATG ATCTGAAAA TGGTGACGT GGAAGTCTAT GAAGATTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 GCGTAGACTC CTCTCTCCC ACATCCATGC ATCTCTCTAC ATTCCCCGG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGITCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TGTGGAAGCT TATTTTCC TTAGAGGCCG CTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
 60 CCCCTTGGAA ACCCTCTCAA TAACTAACTG CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260
 GTCCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCCAGAGCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTGCGCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCACAGCTTA CAACCTTAAG CTCTACGGG AATTCCATCT CCATATCTGC 1500
 65 CTGTCAGAGT CTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCAGG TGCTGTATCC 1560
 TGTCCCTCTG GAGAGTTATG AGGACATCCA TGGTACCTC CACTGGAGA GGCTTGCTTA 1620
 TCTGATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCAGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCT ACTGTGGGA CAGAACCCTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTAGTGCCTA ACTAGCTGGG TGCACATATC AATGCTTCA TTCTGCATAC 1800
 70 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTGGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAAATGTT AGTGAGTGTG AGGAAAAACAT GTTCAAGTGA GAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTTGACTTG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGA 2040
 75 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGAAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 110 Protein sequence:

Protein Accession #: NP_006106.1

1 11 21 31 41 51
 | | | | |
 5 MERRRLWGSQ QSRYISMVSW TSPRRLVELA QSLLKDEAL AIAALELLPR ELFPPLFMAA 60
 FDGRHSQTLK AMVQAWPFTC LPLGVLMKGQ HLHLETFAV LDGLDVLLAQ EVRPRRWKLQ 120
 VLDLRKNSHQ DFWTVWSGNR ASLYSFEPE AAQPMTKKRK VDGLSTAEQ PPIPVLEVLD 180
 LFLKEGACDE LFSYLIEKVK RKKNVLRLLCC KKLKIFAMPM QDIKMILKMV QLDSIEDLEV 240
 TCTWKLPTLA KFSPYLGQMI NLRRLLSHI HASSYISPEK EEQYIAQFTS QFLSLQCLQA 300
 10 LYVDSLFLR GRLDQLLRHV MNPLETSLT NCRLESGDVM HLSQSPVSQ LSVLSLSGVM 360
 LTDVSPLEPL ALLERASATL QDLVFDECGI TDDQLLALLP SLSHCSQLTT LSFYGNISIS 420
 SALQSLQLHL IGLSNLTHVL YPVPLESYED IHGTLHLERL AYLHARLREL LCELGRPSMV 480
 WLSANPCPHC GDRTFYDPEP ILCPCFMPN

15 Seq ID NO: 111 DNA sequence
 Nucleic Acid Accession #: NM_003815
 Coding sequence: 8-2452 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 CGTGCCATG CGGCTGGCGC TGCTCTGGGC CTGGGGGCTC CTGGGCGCGG GCAGCCCTCT 60
 GCCTTCCTGG CGGCTCCCAA ATATAGGTGG CACTGAGGAG CAGCAGGCAG AGTCAGAGAA 120
 GGCCCGGAGG GAGCCCTTGG AGCCCCAGGT CCTCAGGAC GATCTCCAA TTAGCCTCAA 180
 25 AAAGGTGCTT CAGACCAGTC TGCCTGAGCC CCGTGGGATC AAGTTGGAGC TGGACGGTGA 240
 CAGTCATATC CTGGAGCTGC TACAGAATAG GGAGTTGGTC CCAGGCCGCC CAACCCCTGGT 300
 GTGGTACCAAG CCCGATGGCA CTCGGGTGGT CAGTGAGGGA CACACTTTGG AGAACTGCTG 360
 CTACCAGGGA AGAGTGCGGG GATATGCAGG CTCTGGGTG TCCATCTGCA CTGCTCTGG 420
 GCTCAGAGGC TTGGTGGTCC TGACCCCA GAGAAGCTAT ACCTGGAGC AGGGGCTGG 480
 GGACCTTCAG GGTCTCCCA TTATTCGCG AATCCAAGAT CTCACCTGC CAGGCCACAC 540
 30 CTGTGCCCTG AGCTGGCGGG AATCTGTACA CACTCAGACG CCACCAGAGC ACCCCCTGGG 600
 ACAGCGCCAC ATTCGCGGGA GCGGGGATGT GGTAAACAGAG ACCAAGACTG TGGAGTTGGT 660
 GATTGTGGCT GATCACTCGG AGGCCAGAA ATACCGGAC TCCAGCACC TGCTAAACCG 720
 CACACTGGAA GTGGCCCTCT TGCTGGACAC ATCTTCCGG CCCCTGAATG TACGAGTGGC 780
 35 ACTAGTGGCG CTGGAGGCGT GGACCCAGCG TGACCTGGTG GAGATCAGCC CAAACCCAGC 840
 TGTCACCTC GAAACTTCC TCACTGGCG CAGGGACAT TTGCTGCCTC GATTGCCCA 900
 TGACAGTCC CAGCTGGTA CTGTACTTC ATTCTCTGG CCTACGGTGG GCATGGCCAT 960
 TCAGAACTCC ATCTGTTCTC CTGACTTCTC AGGAGGTGTG AACATGGACC ACTCCACCAG 1020
 CATCTGGGA GTGCGCTCCT CCATAGCCCA TGAGTTGGGC CACAGCCTGG GCCTGGACCA 1080
 40 TGATTTGCC CTGGAAATAGT GCCCTGTCC AGGTCCAGCC CCAGCCAAGA CTGTCATCAT 1140
 GGAGGCTCC ACAGACTTCC TACCAGGCTC GAACTTCAGC AACTGCAGCC GACGGGCCCT 1200
 GGAGAAAGCC CTCTGGATG GAATGGGCG CTGCTCTTC GAACGGCTGC CTAGCCTACC 1260
 CCCTATGGCT GCTTCTCGG GAAATATGTT TGTGGAGCCG GCGAGCAGT GTGACTGTGG 1320
 CTCTCTGGAT GACTGCGTG ATCCCTGCTG TGATTCCTTG ACCTGCCAGC TGAGGCCAGG 1380
 45 TGACAGTGT GTGATGAGG GACCCTGTTG TCAAAATTGC CAGCTGCGCC CGTCTGGCTG 1440
 GCAGTGTCTG CTACCCAGAG GGGATTGTGA CTGCGCTGAA TTCTGCCAG GAGACAGCTC 1500
 CCAGTGTCCC CCGTATGTCA GCCTAGGGGA TGGCGAGCCC TGCGTGGCG GGCAAGCTGT 1560
 GTGCATGCAC GGGCGTTGTG CCTCCTATGC CCAGCAGTGC CAGTCACTTT GGGGACCTGG 1620
 AGCCAGGCC GCTGCGCCAC TTTCCTCCA GACAGCTAAT ACTCGGGGAA ATGCTTTTGG 1680
 50 GAGCTGTGG CGCAACCCCA GTGGCAGTTA TGTGTCTGC ACCCTAGAG ATGCCATTG 1740
 TGGGCACTC CAGTGCCAGA CAGGTAGGAC CCAGCCTCTG CTGGGCTCCA TCCGGGATCT 1800
 ACTCTGGAG ACAATAGATG TGAATGGGAG TGAGCTGAAC TGCACTGGG TGCACTGGA 1860
 CCTGGGAGT GATGTGGCC AGCCCTCCT GACTCTGCCT GGCACAGCCT GTGGCCCTGG 1920
 CCTGGTGTG ATAGACCATG GATGCCAGCG TGTGATCTC CTGGGGCCAC AGGAATGTGG 1980
 55 AAGCAATGC CATGGACATG GGGTCTGTGA CAGCAACAGG CACTGCTACT GTGAGGAGG 2040
 CTGGGCACCC CCGTACTGCA CCACTCAGCT CAAAGCAACC AGCTCCCTGA CCACAGGGCT 2100
 GCTCTCAGC CTCTGGTCT TATTGTCTCT GGTGATGCTT GGTGCCGGCT ACTGGTACCG 2160
 TGCCCGCTG CACCAGCGAC TCTGCCAGCT CAAGGGACCC ACCTGCCAGT ACAGGGCAGC 2220
 CCAATCTGGT CCTCTGAAC GGCCAGGACC TCCGACAGAG GCCTGCTGG CACGAGGCAC 2280
 60 TAAGTCTCAG GGGCCAGCCA AGCCCCACC CCCAAGGAAG CCACTGCCTG CGACCCCCA 2340
 GGGCCGGTG CCATCGGGTG ACCTGCCGG CCCAGGGGCT GGAATCCCGC CCTAGTGGT 2400
 ACCCTCCAGA CCAGCGCCAC CGCCTCCGAC AGTGTCTCG CTCTACCTCT GACCTCTCCG 2460
 GAGGTTCCGC TGCCTCAAG CCGGACTTAG GGCTTCAAGA GCGGGGCGTG CCTCTGGAG 2520
 TCCCTACCA TGACTGAAG CGCCAGAGAC TGGCGGTGTC TTAAGACTCC GGGCAOCCG 2580
 65 ACGGCTGTC AAGCAACACT CTGGGAGCT GCCTGGCTAG TTGCAGCGGG GGCTTGGGA 2640
 GGGGCTGGG GTTGGACGGG ATTGAAGGAAG GTCCGCACAG CCTGTCTCTG CTCAGTTGCA 2700
 ATAAACGTGA CATCTTGGGA GCGTTAAAA AAAAAAAAAA

Seq ID NO: 112 Protein sequence:
 Protein Accession #: NP_003806.2

1 11 21 31 41 51
 | | | | |
 70 MRLALLWALG LLGAGSPLPS WPLNIGGTE EQAESEKAP REPLEQVLQ DDLPLSLKKV 60
 LQTSLEPLR IKLELDGDSH ILELLQNREL VPGRPTLVVY QPDGTRVVSE GHLENCCYQ 120
 75 GRVRYAGSW VSLCTCSLR GLVVLTPERS YLEQGPGLD QGPIISRIQ DLHLPHTCA 180
 LSWRESVHTQ TPPEHLQQR HIRRRDVT ETKTVELVIV ADHSEAKYR DFOHLLNRTL 240
 EVALLDTEF RPLNVRVALV GLEAWTORDL VEISNPAPT LENFLHWRR HLLPRLPHDS 300

AQLVTGTSFS GPTVGMAIQN SICSPDFSOG VNMDHSTSIL GVASSIAHEL GHSGLDHDH 360
 PGNSCPGPGP APAKT CIMEA STDPLGLNF SNCSRRALEK ALLDGMGSCF FERLPSPPM 420
 AAFCGNMFVE PGEQDCDGL DDVDPCCDS LTCQLRPGAQ CASDGPCCQN CQLRPSGWQC 480
 RPTRGDCDLP EFPCGDSQSC PFDVSLGDGE PCAGGQAVCM HGRCASYAQ CQLRWGPGAQ 540
 PAAPLCLQTA NTRGNAFGSC GRNPSGSYVS CTPRDAICGQ LQCQTGRTQP LLSIRDLLW 600
 ETIDVNGTEL NCSWVHLDLG SDVAQPLL TL PGTACGPGLV CIDHRCQRVD LLGAQECSRK 660
 CHGHGVCDNS RHCYCEEGWA PFDCTTLQKA TSSLTTGLLL SLLVLLVLM LGAGYWYRAR 720
 LHQRLCQLKG PTCQYRAAQSPSERPGPPQ RALLARGTKS QGPAKPPPPR KPLPADPQGR 780
 CPSGDLPGPG AGIPLVVPSPAPPPPTVS SLYL

Seq ID NO: 113 DNA sequence
 Nucleic Acid Accession #: NM_002416
 Coding sequence: 40-417 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATCCAATACA GGAGTGACTT GGAAGTCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTT 60
 TTCTCTTGG GCATCATCTT GCTGGTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120
 AAGGGTCGCT GTTCTGTCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA 180
 GACCTTAAAC AATTGTGCCC AAGCCCTTCC TGCAGAGAAA TGAATCAT TGCTACACTG 240
 AAGAATGGAG TTCAAAACATG TCAAAACCA GATTAGCAG ATGTGAAGGA ACTGATTAAA 300
 AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
 AAGAAAGTTC TGAAGATTCG AAAATCTCAA CGTCTCTGTC AAAAGAAGAC TACATAAGAG 420
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTCTCA TTTAATTAT ACCGCTATCA 480
 TTCAAAGGA GGATGGCATA TAATACAAG GCTTATTAAT TTGACTAGAA AATTAAAAAC 540
 ATTACTCTGA AATTGTAAC TAAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600
 TTGTTAAAGG CTATGATTGT CTTGTGTTCT TAACACCCCA CCAGTTGAAT TTCATCATGC 660
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATOCCA 720
 CTCACAAACG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCACAGAGAG 780
 TATCTGAGGC ACATGTCAGC AAGTCTAAG CCTGTAGCA TGCTGGTGAG CCAAGCAGTT 840
 TGAAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
 CTACAGGCTT CACACACAAT GTGTCTGAGA GATTATGCT GATTGTTAT GGGTATCACC 960
 ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020
 TTCCATCTTG CCCGCTCAGG CTGAACCACT TATTCTTTT TGTCCCTT TGCTTCATT 1080
 AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTCTCTCCA GTGCACCTGT 1140
 CATATGCTCT GATTATCTG AGTCAACTCC TTCTCATCT TGTCCCAAC ACCCCACAGA 1200
 AGTGCTTTCT TCTCCCAAT CATCTCACT CAGTCCAGCT TAGTTCAAGT CTGCGCTCTT 1260
 AAATAAACCT TTTTGGACAC ACAAATTATC TTAATACTCC TGTTTCACTT GGTTCAGTAC 1320
 CACATGGGTG AACACTCAAT GGTAACTAA TTCTTGGGTG TTAATCTAT CTCTCCAACC 1380
 AGATTGTGAG CTCTTGAGG GCAAGAGCCA CAGTATATTT CCTGTGTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACCA GGTTTAAATA ATTTTAAAT TGATGTGTT ATGGGCAAGG 1500
 TGGCAACCCG ACCATGTGCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCAATGTTG 1560
 CTAGCCTCTG GTAACTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAAATCTT TTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAAGATAG CCACCGAGAT CCTATCGAA ACTCATTITA GGCAAAATATG 1920
 AGTTTATATG TCCGTTTACT TGTTCAGAG TTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGGAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAGC TCCTTCCAGG 2100
 GGAGGTTGAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTAAA OCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATT AGAGTGCTGT CCGGTGGAGA 2220
 TCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAACTCAA GTGTTTCATA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
 TCATTTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAATT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTGTAAAT TGAAATATTT TCTTTGTAA AATAGAATGG 2520
 TATCAATAAA TAGACCATA ATCAG

Seq ID NO: 114 Protein sequence:
 Protein Accession #: NP_002407

1 11 21 31 41 51
 | | | | |
 MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIATLKNQ VQTCLNPDSA DVKELKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQSR 120
 QKKTT

Seq ID NO: 115 DNA sequence
 Nucleic Acid Accession #: NM_003238.1
 Coding sequence: 182-1426 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CAAGCAGGAT ACGTTTCTT GTTGGGCATT GACTAGATTG TTGCAAAAG TTTCGCATCA 60
 AAAACAAACA ACAACAACAA AAAACCAAC AACTCTCCTT GATCTACT TTGAGAATTG 120

TTGATTTCTT TTTTITTTATT CTGACTTTTA AAAACAACCT TTTTITCCAC TTTTITAAAA 180
 AATGCACTAC TGTGTGCTGA GCGCTTTTCT GATCCTGCAT CTGGTCAACGG TCGCGCTCAG 240
 CCTGTCTACC TGCAGCACAC TCGATATGGA CCAGTTTCATG CGCAAGAGGA TCGAGGCGAT 300
 CCGCGGGCAG ATCCTGAGCA AGCTGAAGCT CACCAGTCCC CCAGAAGACT ATCCTGAGCC 360
 CGAGGAAGTC CCCCCGGAGG TGATTTCAT CTACAACAGC ACCAGGGACT TGCTCCAGGA 420
 GAAGGCGAGC CGGAGGGCGG CCGCTGCGA GCGCGAGAGG AGCGACGAAG AGTACTACGC 480
 CAAGGAGGTT TACAAAATAG ACATGCGGCC CTCTTCCCC TCCGAAAATG CCATCCCGCC 540
 CACTTTCTAC AGACCTACT TCAGAATTGT TCGATTGAC GTCTCAGCAA TGGAGAAGAA 600
 TGCTTCCAAT TTGGTGAAGG CAGAGTTCAG AGTCTTTCGT TTGCAGAACCC CAAAAGCCAG 660
 AGTGCTGAA CAACGGATTG AGCTATATCA GATTCTCAAG TCCAAAGATT TAACATCTCC 720
 AATCCAGCGC TACATCGACA GCAAAGTTGT GAAAACAAGA GCAGAAGGCG AATGGCTCTC 780
 CTTCGATGTA ACTGATGCTG TTCATGAATG GCTTCACCAT AAAGACAGGA ACCTGGGATT 840
 TAAAAAAGC TTACTGTGC CCTGTGCAC TTTGTACCA TCTAATAATT ACATCATCCC 900
 AAATAAAGT GAAGAACTAG AAGCAAGATT TGCAGGTATT GATGGCACTT CCACATATAC 960
 CAGTGGTGAT CAGAAAACTA TAAAGTCCAC TAGGAAAAAA AACAGTGGGA AGACCCACCA 1020
 TCTCTGTCTA ATGTTATTGC CCTCTACAG ACTTGAGTCA CAACAGACCA ACCGGCGGAA 1080
 GAAGCGTGCT TTGGATGCGG CTTATTGCTT TAGAAATGTG CAGGATAATT GCTGCCTACG 1140
 TCCACTTAC ATTGATTCA AGAGGGATCT AGGGTGGAAA TGGATACACG AACCCAAAGG 1200
 GTACAATGCC AACTTCTGTG CTGGAGCATG CCGGTATTTA TGGAGTTCAG ACACTCAGCA 1260
 CAGCAGGGCT CTGAGCTTAT ATAATACCAT AAATCCAGAA GCATCTGCTT CTCTTGCTG 1320
 CGTGTCCCAA GATTTGAAC CTCTAACCAT TCTCTACTAC ATTGGCAAAA CACCCAAGAT 1380
 TGAACAGCTT TCTAATATGA TTGTAAAGTC TTGCAAAATG AGCTAAATTT CTGGGAAAAG 1440
 TGGCAAGACC AAAATGACAA TGATGATGAT AATGATGATG ACGACGACAA CGATGATGCT 1500
 TGTAACAAGA AAACATAAGA GAGCCTTGGT TCATCAGTGT TAAAAAATTT TTGAAAAGGC 1560
 GGTACTAGTT CAGACACTTT GGAAGTTTGT GTTCTGTTG TTAACACTGG CATCTGACAC 1620
 AAAAAAAGTT GAAGGCCCTA TTCTACATTT CACCTACTTT GTAAGTGAGA GAGACAAGAA 1680
 GCAAATTTTT TAAAA

Seq ID NO: 116 Protein sequence:
 Protein Accession #: NP_003229.1

1 11 21 31 41 51
 | | | | |
 MHYCVLSAFL ILHLVTVALS LSTCSTLMD QFMRKRIEAI RGQILSKLKL TSPPEDYPEP 60
 EEVPPVISI YNSTRDLLQE KASRRAACE RERSDEEYIA KEVYKIDMPP FFPSENAIPP 120
 TFYRPPYFRV RFDVSAMEKN ASNLVKAER VRLQNPKEAR VPEQRIELYQ ILKSKDLTSP 180
 TRYIDSKVY KTRAEGEWLS FDTVDAVHEW LHHKDRNLGF KISLHCPCT FVPSNNYIIP 240
 NKSEELERAF AGIDGTSTYT SGDQKTKST RKKNSTGKTPH LLLMLLPYR LESQQTNRKK 300
 KRALDAAYCF RNVQDNCCRL PLYIDFKRDL GWKWIHEPKG YNANFCAGAC PYLWSSDTQH 360
 SRVLSLYNTI NPEASAPCC VSQDLEPLTI LYYIGKTPKI EQLSNMIVKS CKCS

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26-2299 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCGGACACCC GCCTGCGTTC TTCTGCTCAC 60
 CCTGGCTGCC CTGGCGCGGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGGCC 120
 GCAGATGCTT CGGGAACCTG AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCAGGGAGA TCACGTTCTT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
 CGGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCTGC TOCACTGCGC 300
 GCGCGGCTTC TGCTTCCCGC GCGTGGCGTG CATCCAGACG GAGAGCGGCG GCGCTGCGG 360
 CCCCTGCCCG GCGGGCTTCA CGGGCAACCG CTCGCACTGC ACCGACGTCA ACGAGTGCAA 420
 CGCCCAACCC TGCTTCCCGC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
 GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAAGGGC GTGGGGCTGG CTTTCGCCAA 540
 GGCCAAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGT 600
 CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCTTCCAG TCGGGCCCGT GCCAGCCCGG 660
 CTTGCTGGGC GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCCGACGG 720
 CTCGCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
 GTGCGTGTGT CGCGTTGGCT GGGCCGGCAA CGGGATCCTC TGTGTGCGCG ACACGTACCT 840
 AGACGGCTTC CCGGACGAGA AGCTGGGCTG CCGGAGCCCG CAGTGCCGTA AGGACAACCTG 900
 CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCCG GATGGCATCG GAGACGCGTG 960
 CGATCCGGAT GCCAGCGGGG ACGGGGTCCC CAATGAAAAG GACAACCTGC CGCTGGTGCG 1020
 GAACCCAGCG CAGGCGAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAAAGTCCG 1080
 GTCCGAGAAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCTGGGGC ATGGCTGCGA 1140
 CGACGACATC GACGCGGACC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGTACCCCAA 1200
 CTCAGACCAAG AAGGACGATG ATGGCGATGG TATAGGGGAT GCTGTGTACA ACTGTCCCAA 1260
 GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACGTGC CCACGTTGCC 1380
 TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCTGCG ACGACGACGA 1440
 CGACAATGAC GGATGCCCTG ACAGTCGGGA CAACTGCCCG CTGGTGCTTA ACCCCGGCCA 1500
 GGAGGACGCG GACAGGGAAG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
 GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
 GGCCTTCCAG ACAGTCGTGC TGGACCGGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG CCGTGGCTGT 1740
 GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAAC 1800

GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
 CATGTGGAAG CAGATGGAGC AAAAGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
 CGCTCTGTGG CACACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
 AAAAGTGGGT TGGGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCAAGT 2100
 GGGCTACATC AGGGTGCAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
 CTGGACACA ACCATGCGGG GTGGCCGCTT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
 CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
 TCAGCTGCGG CAAGCTAGG GACCAGGGT AGGACCCGCC GGATGACAGC CACCCTACCC 2340
 CGGGCTGGAT GGGGGCTCTG CACCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAAGTGAG 2400
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

Seq ID NO: 118 Protein sequence:
 Protein Accession #: NP_000086.1

1 11 21 31 41 51
 | | | | |
 M V P D T A C V L L L T L A A L G A S G Q G Q S P L G S D L G P Q M L R E L Q E T N A A L Q D V R D W L R Q Q V R E I T 60
 F L K N T V M E C D A C G M Q Q S V R T G L P S V R P L L H C A P G F C F P G V A C I Q T E S G G R C G P C P A G F T G 120
 N G S H C T D V N E C N A H P C F P R V R C I N T S P G F R C E A C P P G Y S G P T H Q G V G L A F A K A N K Q V C T D 180
 I N E C E T G Q H N C V P N S V C I N T R G S F Q C G P C Q P G F V G D Q A S G C Q R G A Q R F C P D G S P S E C H E H 240
 A D C V L E R D G S R S C V C R V G W A G N G I L C G R D T D L D G F P D E K L R C P E P Q C R K D N C V T V P N S Q Q 300
 E D V D R D G I G D A C D P D A D G D G V P N E K D N C P L V R N P D Q R N T D E D K W G D A C D N C R S Q K N D D Q K 360
 D T D Q D G R G D A C D D D I D G D R I R N Q A D N C P R V P N S D Q K D S D G D G I G D A C D N C P K S N P D Q A D 420
 V D H D F V G D A C D S D Q D Q G D G H Q D S R D N C P T V P N S A Q E D S D H D G Q G D A C D D D D D N D G V P D S 480
 R D N C R L V P N P Q E D A D R D G V G D V C Q D D F D A D K V V D K I D V C P E N A E V T L T D F R A F Q T V V L D 540
 P E G D A Q I D P N W V V L N Q G R E I V Q T M N S D P G L A V G Y T A F N G V D F E G T F H V N T V T D D D Y A G F I 600
 F G Y Q D S S S F Y V V M W K Q M E Q T Y W Q A N P F R A V A E P G I Q L K A V K S S T G P G E Q L R N A L W H T G D T 660
 E S Q V R L L W K D P R N V G W K D K K S Y R W F L Q H R P Q V G Y I R V R F Y E G P E L V A D S N V L D T T M R G G 720
 R L G V F C F S Q E N I I W A N L R Y R C N D T I P E D Y E T H Q L R Q A

Seq ID NO: 119 DNA sequence
 Nucleic Acid Accession #: NM_014211
 Coding sequence: 157-1479 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 G G G A C A G G G C T G A G G A T G A G G A G A A C C C T G G G A C C C A G A A G A C C G T G C C T T G C C C G G A A 60
 G T C C T G C C T G T A G G C C T G A A G G A C T T G C C C T A C A G A G C C T C A A C A A C T A C T G G T G A T T 120
 C C T A C T T C A G C C C T T G G T G T G A C A G C C T T C T A A C A T G A A C T A C A G C C T C A C T T G G C C 180
 T T C G T G T G T C T G A G T C T C T C A C T G A G A G G A T G T G C A T C C A G G G A G T C A G T T C A A C G T C 240
 G A G G T C G G C A G A A G T G A C A A G C T T C C C T G C T G G C T T T G A A C C T C A C A G C A G A T A T 300
 A A C A A A T T T C T A G G C C C A A T T T T G T G G A G A A C C G T A C A G A T A G C G C T G A C T C T G G A C 360
 A T T G C A A G T A T C T C T A G C A T T T C A G A G A G T A A C A T G G A C T A C A G C C C A C A T A T A C C T C 420
 C G A C A G C C G C T G G A T G G A C C A G C G G C T G G T G T T G A A G G C A A C A A G A G C T T C A C T C T G G A T 480
 G C C C G C C T C G T G G A G T T C C T C T G G T G C C A G A T A C T A C A T T G G A G T C C A A G A A G T C C 540
 T T C T C C A T G A A G T A C T G T G G A A A C A G G C T C A T C C G C C T C T T C T C C A A T G C A C G G T C 600
 C T G T A T G C C C T C A G A A T C A C A C A A C T G T T G C A T G T A A C A T G G A T C T G T C T A A T A C C C C 660
 A T G G A C A C A C A G C A T G A C A A G T T G C A G C T G G A A A G C T G G G C T A T G A T G G A A A T G A T G T G 720
 G A G T T C A C C T G C T G A G A G G G A A C A C G A C T C T G T G C T G G A C T G G A A C A C C T G C G G C T T G C T 780
 C A G T A C A C C A T A G A G C C G T A T T C A C C T T A G T C A C C A G A T C G C A G C A G G A G A C A G G A A A T 840
 T A C A T A G A T T G G T C T T A C A G T T G A G C T T C G G A G G A A T G T T C T G A T T T C A T T T T G G A A 900
 A C C T A C G T T C C T T C A C T T T C T G G T G G T G T T G T C C T G G G T T T C A T T T T G G A T C T C T C 960
 G A T T C A G T C C C T G C A A G A A C C T G C A T T G G A G T G A C G A C C G T G T T A T C A A T G A C C A C A C T G 1020
 A T G A T C G G G T C C G C A C T T C T C T C C A A C A C C A A C T G C T T C A T C A A G G C C A T C G A T G T G 1080
 T A C T G G G G A T C T G C T T A G C T T G T G T T G G G C C T T G C T A G A A T A T G C A G T T G C T C A C 1140
 T A C A G T T C C T T A C A G C A G A T G G C A G C C A A A G A T A G G G G A C A A C A A A G G A A G T A G A A G A A 1200
 G T C A G T A T T A C T A A T A T C A T C A A C A G C T C C A T C C A G C T T T A A A C G G A A G A T C A G C T T T 1260
 G C C A G C A T T G A A A T T T C C A G C G A C A A C G T T G A C T A C A G T G A C T T G A C A A T G A A A A C C A G C 1320
 G A C A A G T T C A A G T T G T C T T C C G A G A A A A G A T G G G C A G G A T T G T T G A T T T T C A C A A T T 1380
 C A A A A C C C C A G T A A T G T T G A T C A C T A T T C C A A C T A C T G T T T C T T T G A T T T T A T G T C A 1440
 G C C A A T G T A T T T A C T G G G C A T A C T A C A T G T A T T T T T G A G T C A A T G T T A A A T T T C T T G C A 1500
 T G C C A T A G G T C T T C A A C A G G A C A A G A T A A T G A T G T A A A T G T A T T T T A G G C C A A G T G T G C 1560
 A C C C A C A T C C A A T G G T G C T A C A A G T A C T G A A A T A T T T G A G T C T T T C T G C T A A A G A 1620
 A T G A A G C T C C A A C C A T T G T T C T A A G C T G T G T A G A A G T C C T A G C A T T A T A G A T C T T G T A A 1680
 T A G A A A C A T C A G T C C A T T C C T C T T T C A T C T T A A T C A A G G A C A T T C C C A T G A G C C C A A G A 1740
 T T A C A A A T G T A C T C A G G G C T G T T A T T O G G T G G C T C C C T G T T T G C A T T T A C C T C A T A T 1800
 A A G A A T G G G A A G G A G A C C A T T G G G T A A C C C T C A A G T G T C A G A A G T T G T T C T A A A A G T A A C 1860
 T A T A C A T G T T T T T A C T A A A T C T C T G C A G T G C T T A T A A A A T A C A T T G T T G C C T A T T T A G G 1920
 G A G T A A C A T T T C T A G T T T T T G T T C T G T T A A A A T G A A A T A T G G G C T T A T G T C A A T T C A 1980
 T T G G A A G T C A T G C A C T A A C T C A A T A C C A A G A T G A G T T T T A A A T A A T G A A T A T T A T T T A 2040
 A T A C C A C A A C A G A A T T A T C C C A A T T T C C A A T A A G T C C T A T T T G A A A A T T C A A A T A T A 2100
 A T G A A G A A A A A A T T A G T A G A T C A A C A A T C T A A C A A A T C C C T G G T T C T A A G A T A C A A T 2160
 G G A T T C C C C A T A C T G G A A G G A C T C T G A G G C T T T A T T C C C C A C T A T G C A T A T C T A T C A T 2220
 T T T A T T A T T A T A C A C A C A T C A T C C T A A A C T A T A C T A A A G C C C T T T T C C C A T G C A T G G A T 2280
 G G A A A T G G A A G A T T T T T T G T A A C T T G T C T A G A A G T C T T A A T A T G G G C T G T T G C C A T G A 2340
 A G G C T T G C A G A A T T G A G T C C A T T T C T A G C T G C C T T A T T C A C A T A G T G A T G G G G T A C T A 2400

5 AAAGTACTGG GTTGACTCAG AGAGTCGCTG TCATTCTGTC ATTGCTGCTA CTCTAACACT 2460
 GAGCAACACT CTCCAGTGG CAGATCCCCT GTATCATTCC AAGAGGAGCA TTATCCCTT 2520
 TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAAACAAAC TGCTTGACCC AGGAACAAAGT 2580
 GGCTTAGCTT AAGTAAACCTT GGCTTTGCTC AGATCCCTGA TCCTTCCAGC TGGTCTGCTC 2640
 TGAGTGGCTT ATCCCGCATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT 2700
 AACAAATGAGA CACGTTACAG AACCTATGTT CAGGTTGCGG GTGAGCTGCC CTCTCCAAAT 2760
 CCAGCCAGAG ATGCACATTC CTCGGCCAGT CTCAGCCAAC AGTACCAAAA GTGATTTTTG 2820
 AGTGTGCCAG GGTAAAGGCT TCCAGTTCAG CCTCAGTTAT TTAGACAAT CTGOCATCT 2880
 10 TTAATTTCTT AGCTTCTGT TCTAATAAAT GCACGGCTTT ACCTTCTCTG TCAGAAATAA 2940
 ACCAAGGCTC TAAAAGATGA TTTCCCTTCT GTAACCTCCT AGAGCCACAG GTTCTCATT 3000
 CTTTCCCAT TATACTTCT ACAATTCACT TTCTATGAGT TTGATCACCT GATTTTTT 3060
 ACAAATATT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGT 3120
 TATGAGCCAA TCATATTGT GATTTTTTAA AAAAGTTTAA AAAGGAATA TCTGTTCTGA 3180
 15 AACCCACTT AAGCATGTT TTTATATAAA AACATGATA AAGATGTGAA CTGTGAAATA 3240
 AATATACCAT ATTAGCTACC CACC

Seq ID NO: 120 Protein sequence:
 Protein Accession #: NP_055026.1

20 1 11 21 31 41 51
 | | | | |
 MNYSLHLAFV CLSLFTRMCI IQSQFNVFV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP 60
 VQIALTLIDIA SISSISESNM DYATATYLRQ RWMDQRLVFE GNKSFTLDAR LVEFLWVDPDT 120
 25 YIVESKKSFL HEVTVGNRLI RLFSNGTVLY ALRITTVAC NMDLSKYPMD TQTKLQLES 180
 WGYDGNDFEF TWLRGNDVSR GLEHLRLAQY TIERYFTLV TSQQTGNYT RLVLQFELRR 240
 NVLYFILETY VPSTFLVLS WVSFWISLDS VPARTICGVT TVLSMTTLMG GSRTSLFNTN 300
 CFKADIVYL GICFSFVFGA LLEYAVAHYS SLQQMAAKDR GTTKEVEVS ITNINSSIS 360
 SFKRKISFAS IEISSDNVDY SDLTMTKTSK FKFVFREKMG RIVDYFTQN PSNVHDHYSKL 420
 30 LFPLIFMLAN VFYWAYMYF

Seq ID NO: 121 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 163-5582 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 | | | | |
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTCC CCCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 40 TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTA 180
 GGTGGAAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTAGCCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTAATAAAA GCACTAGATT 300
 TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAAAT 360
 CTAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACACTCAGT GCCCAACAA 420
 45 AACAGTTATT TCCAGGTGGA ACTTCCAG AAGACTTTTC AATACTATT ACAGTAAAA 480
 CAAAAAAGG AATTCACTCT TTCTTTTAT CTATATATA TGAGCATGGT ATTCAGCAA 540
 TTGGTGTGA GGTGGGAGA TCACCTGTTT TTCTGTTGA AGACCACACT GGAACACCTG 600
 CCCCAGAAGA CTATCCCTC TTCAGAACTG TTAACATGCG TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 50 CGAAACCACT TGATGAGAAGT GAGAGAGCAA TTGTTGATAC CAATGGAATC ACGGTTTTG 780
 GAACAAGGTT TTGGATGAA GAAGTTTTG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
 CACCAAGGC TGCTCAAGT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATA 960
 TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 55 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGGAACA ATGGAAAGTT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
 GGACAAATGA GCCAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGGAGAGG 1200
 ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAACAAA GAAATAGACG 1260
 GCAGGGATTC TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
 60 AAGAATATGA AGATAAACCA ACAAGCCCCC CTAATGAAGA ATTTGGTCCA GGTGTACCAG 1380
 CAGAAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCATATGGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCAG 1500
 CAGGACCTGC AGGTATTATG GGTCTCCAG GTCTACAAG CCCCACTGGA CCCCTGGTG 1560
 ACCCTGGCGA TAGGGGCCCC CCAGGACGTC CTGGCTTACC AGGGGTGAT GGTCTACCTG 1620
 65 GTCTCTCTGG TACTATGTTG ATGTTACCGT TCCGTTATGG TGGTGATGGT TCCAAAGGAC 1680
 CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC 1740
 TGAGAGGCCC ACCTGGCCCA ATGGGTCTAA CTGGAAGACC AGGTCTGTG GGGGGGCTG 1800
 GTTCATCTGG GGCCAAAGGT GAGAGTGGTG ATCCAGGTCC TCAGGCCCCC CGAGGCGTCC 1860
 AGGGTCCCC TGATCCAACG GGAAACCTG GAAAGGGGG TCGTCCAGGT GCAGATGGAG 1920
 70 GAAAGGAAT GCCAGGAGAA CTTGGGGCAA AGGGAGATCG AGGGTTTGT GGAATCCCG 1980
 GTCTGCCAGG TGACAAAGGT CACAGGGGTG AACGAGGTCC TCAAGTCTCT CCAGGTCTCT 2040
 CTGGTGATGA TGGAATGAGG GGAGAAGATG GAGAAATTGG ACCAAGAGGT CTTCAGGTG 2100
 AAGCTGGCCC ACGAGGTTTG CTGGGTCCAA GGGGAACCTC AGGAGCTCCA GGGCAGCCTG 2160
 GTATGGCAGG TGTAGGTTGC CCCCAGGAC CAAAAGGGA CATGGGTCCC CAAGGGGAGC 2220
 75 CTGGGCTCC AGGTCAACAA GGAATCCAG GACCTCAGGG TCTTCTGCT CCACAAGGTC 2280
 CAATTGGTCC TCCTGGTGAA AAAGGACCAC AAGGAAAACC AGGACTTGCT GGAATCTCTG 2340
 GTGCTGATGG GCCTCTGGT CATCCTGGGA AAGAAGGCCA GTCTGGAGAA AAGGGGGCTC 2400
 TGGGTCCCCC TGGTCCACAA GGTCTATTG GATNNCCGGG CCCCAGGGGA GTAAAGGGAG 2460

CAGATGGTGT CAGAGGTCTC AAGGGATCTA AAGGTGAAAA GGGTGAAGAT GGTITTTCCAG 2520
 GATTCAAAGG TGACATGGGT CTAAGAGGTG ACAGAGGAGA AGTTGGTCAA ATTGGCCCAA 2580
 GAGGNAAGA TGGCCCTGAA GGACCCAAAG GTCGAGCAGG OCCAACTGGA GACCCAGGTC 2640
 5 CTTACAGGTCA AGCAGGAGAA AAGGGAAAAAC TTGGAGTTCC AGGATTACCA GGATATCCAG 2700
 GAAGACAAGG TCCAAAGGGT TCCACTGGAT TCCTGGGTT TCCAGGTGCC AATGGAGAGA 2760
 AAGGTGCACG GGGAGTAGCT GGCAAAACCA GCOCTCGGGG TCAGCGTGGT CCAACGGGTC 2820
 CTCGAGGTTC AAGAGGTGCA AGAGGTCCCA CTGGGAAACC TGGGCCAAAG GGCACCTTCA 2880
 GTGGCGATGG CCTCCTGGC CCTCCAGGTG AAAGAGGTCC TCAAGGACCT CAGGGTCCAG 2940
 10 TTGGATTCCC TGGACCAAAA GGCCCTCCTG GACCACCAGG AAGGATGGGC TGCCACGGAC 3000
 ACCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCCT GGGCCAGGGG 3060
 GAGTGGTTGG ACCACAGGGA CCAACCGGTG AGACTGGTCC AATAGGGGAA CGTGGGTATC 3120
 CTGGTCTCCT TGGCCCTCCT GGTGAGCAAG GTCTTCTGG TGCTGCAGGA AAAGAAGGTG 3180
 CAAAGGGTGA TCCAGGTCTT CAAGGTATCT CAGGGAAGA TGGACCAGCA GGATTACGTG 3240
 15 GTTTCACAGG GAAAAGAGGT CTCTCTGGAG CTCAGGGTGC ACCTGGACTG AAAGGAGGGG 3300
 AAGGTCCCCA GGGCCACCA GGTCCAGTTG GTCACACAGG AGAACGTGGG TCAGCAGGTA 3360
 CAGCTGGCCC AATTGTTTGA CGAGGGCGCC CGGACCTCA GGTCTCCTCT GGTCCAGCTG 3420
 GAGAGAAAGG TGCTCTGGA GAAAAAGGTG CCAAGGGGCC TGCAGGGAGA GATGGAGTTC 3480
 AAGGTCTCTG TGGTCTCCCA GGGCCAGCTG GTCTGCGG CTCCCTGGG GAAGACGGAG 3540
 20 ACAAGGGTGA AATTGGTGAG CCGGGACAAA AAGGCAGCAA GGGTGGCAAG GGAGAAAAATG 3600
 GCCTCCCGC AGGTCCCAAT GGAGCTGATG GACCACAAGG ACCCCAGGT TCTGTTGGTT 3660
 ATGGTGAACC AGGTCTCTAG GACAGCAGG GGATGTTTGG GCAAAAAGGT GATGAGGGTG 3720
 CCAGAGGCTT CCCTGGACCT CCTGGTCCAA TAGGTCTTCA GGTCTGCCA GGCCACCTG 3780
 GTGAAAAAGG TGAATATGGG GATGTTGGTC CATGGGGGCC ACCTGGTCTT CCAGGCCCAA 3840
 25 GAGGCCCTCA AGGTCCCAAT GGAGCTGATG GACCACAAGG ACCCCAGGT TCTGTTGGTT 3900
 CAGTTGGTGG TGTGGAGAA AAGGGTGAAC CTGGAGAAGC AGGAACCCA GGGCCTCCTG 3960
 GGAAGCAGG TGTAGGCGT CCAAGAGGAG AAAGAGGAGA GAAAGGGGAA GCTGGTCCAC 4020
 CTGAGCTGC TGGACCTCCA GGTGCCAAGG GGCCGCCAGG TGATGATGGC CTAAGGGTA 4080
 ACCCGGTGCC TGTGTTGTTT CTTGGAGATC CTGGTCTCC TGGGAACTT GGCCCTGCAG 4140
 30 GTCAAGATGG TGTGTTGGT GACAAGGGTG AAGATGGAGA TCTGGTCAA CGGGTCTCT 4200
 CTGGCCATC TGGTGAAGCT GGCCACCAAG GTCTCTCTG AAAACGAGGT CCTCTGGAG 4260
 CTGAGGTGC AGAGGGAAGA CAAGGTGAAA AAGGTGCTAA GGGGAAGCA GGTGCAGAA 4320
 GTCTCTCTG AAAAAACCGC CCAGTCGGTC CTCAGGGACC TGCAGGAAAG CTTGGTCCAG 4380
 AAGGTCTTCG GGCATCTCCT GGTCTCTGG GAGAACAAGG TCTCCTGGA GCTGCAGGCC 4440
 35 AAGATGGACC ACCTGGTCTT ATGGGACCTC CTGGCTTACC TGGTCTCAA GGTGACCTG 4500
 GCTCCAAGGG TGAAGAGGGA CATCTGGT TAATGGCTT GATTGCTCT CCAGGAGAAC 4560
 AAGGGGAAAA AGGTGACCGA GGGTCTCCTG GAATCAAGG ATCTCCAGGA GCAAAAGGGG 4620
 ATGGGGGAAT TCTTGGTCTT GCTGGTCTT TAGGTCCACC TGGTCTCCA GGCTTACCAG 4680
 GTCTCAAGG CCAAAAGGGT AACAAAGGCT CTACTGGACC CGCTGGCCAG AAAGGTGACA 4740
 40 GTGGTCTTCC AGGGCTCTCT GGGCTCCAG GTCCACCTGG TGAAGTCATT CAGCCTTAC 4800
 CAATCTTGTG CTCAAAAAAA ACGAGAAGAC ATACTGAAGG CATGCAAGCA GATGCAGATG 4860
 ATAATATTCT TGATTACTCG GATGGAATGG AAGAAATATT TGGTTCCTC AATTCCCTGA 4920
 AACAGACAT CGAGCATATG AAATTTCCAA TGGGTACTCA GACCAATCCA GCCCGAAGTT 4980
 GTAAAGACCT GCAACTCAGC CATCTGACT TCCAGATGG TGAATATTGG ATTGATCTA 5040
 45 ACCAAGGTTG CTCAGGAGAT TCCTCAAAG TTTACTGTA TTTACATCT GGTGGTGAGA 5100
 CTTGCATTTA TCCAGACAAA AAATCTGAGG GAGTAAGAA TTTATCATGG CCAAAGGAGA 5160
 AACCAGGAAG TTGGTTTATG GAATTTAAGA GGGGAAAACT GCTTCATAC TTAGATGTTG 5220
 AAGGAAATTC CATCAATATG GTGCAATGA CATCTCTGAA ACTTCTGACT GCCTCTGCTC 5280
 GGCAAAATTT CACCTACCAC TGTCATCAGT CAGCAGCCTG GTATGATGTG TCATCAGGAA 5340
 GTTATGACAA AGCACTTCGC TTCTGGGAT CAAATGATGA GGAGATGTCC TATGACAATA 5400
 50 ATCTTTTAT CAAAACACTG TATGATGGT GTACGTCCAG AAAAGGCTAT GAAAAAAGCTG 5460
 TCATTGAAAT CAATACACCA AAAATTGATC AAGTACCTAT TGTGATGTG ATGATCAGTG 5520
 ACTTTGGTGA TCAGATGAG AAGTTCGGAT TTGAAGTTGG TCTGTTTGT TTTCTTGCT 5580
 AAGATTAAAG CAAAGAACAT ATCAAAATCA CAGAAAATGT ACCTTGGTGC CACCAACCCA 5640
 TTTTGTGCA CATGCAAGTT TTGAATAAGG ATGATGGAA AACACGCTG CATATACAGG 5700
 55 TACCATTAG GAAATACCGA TGCCTTTGTG GGGGCAGAA CACAGACAAA AGCTTTGAAA 5760
 ATCATAAAGA TATAAGTTGG TGTGGCTAAG ATGGAAACAG GGCTGATTCT TGATCCCAA 5820
 TTCTCAACTC TCCTTTTCTT ATTTGAATTT CTTTGGTGTG GTAGAAAACA AAAAAAGAAA 5880
 AATATATATT CATAAAAAAT ATGGTGCTCA TTCTCATCCA TCCAGGATGT ACTAAAAACAG 5940
 60 TGTGTTAAT AAATTTGTAAT TATTTTGTG ACAGTTCTAT ACTGTTATCT GTGTCCATT 6000
 CCAAAACTTG CACGTGTCCC YGAATCCGC TGAATCTAAT TTATGAGGAT GCCGAAGTCT 6060
 GATGGCAATA ATATATGAT TATGAAAAATG AAGTTATGAT TTCCGATGAC CCTAAGTCCC 6120
 TTTCTTGGT TAATGATGAA ATTCCTTTGT GTGTGTTT

Seq ID NO: 122 Protein sequence:
 Protein Accession #: NP_001845

1 11 21 31 41 51
 70 MEPWSSRWKT KRWLWDFVT TLALTFLQA REVRGAAPVD VLKALDFHNS PEGISKTTGF 60
 CTNRKNSKGS DTAYRVSKQA QLSAPTKQLF PGFTFPEDFS ILFTVKPKKG IQSFLLSIYN 120
 EHGIQIQIVE VGRSPVFLFE DHTGKPAED YPLFRTVNIA DGKWHRV AIS VEKKTVMIV 180
 DCKKTKTKPL DRSERAIVD NGITVFGTRI LDEEVFEGDI QQFLITGDPK AAYDYCEHS 240
 75 PDCDDSAFKA AQAQEPQIDE YAPEDIEYD YEYGEAEYKE AESVTEGPTV TEETIAQTEA 300
 NIVDDFQEYN YGTMESYQTE APRHVSQTNE PNPVEEIFTE EYLTGEDYDS QRKNSIEDTLY 360
 ENKEIDGRDS DLVDGDLGE YDFYKEYE DKPTSPNNEE FGPVPAETD ITETSINGHG 420
 AYGEKGQKGE PAVVEPGMLV EGPPGPAGPA GIMPPGLQG PTGPPGPDGD RGPPGRPLP 480

5 GADGLPGPPG TMLMLPFRYG GDGSKGPTIS AQEAQAQAIL QQARIALRGP PGPMLTGRP 540
 GPDGLPLPG DKGHRGERGP QGPPGPGDD GMRGEDGEIG PRGLPGEAGP RLLGLPRGTP 600
 GARGQPGMAG VDGPPGPKGN MGPPGEPGP GQQGNPQPQ LPPGQGP!GP PGEKGPQGKP 720
 10 GLAGLPGADG PPGHPGKEGQ SGEKGALEPP GPQGP!GXPG PRGVKAGDGV RGLKGSKGEK 780
 GEDGFPFGFK DMGLKGDGRGE VQIGPRGXG GPEGPKGRAG PTGDPQPSGQ AGEKGLGV 840
 GLPGYPGRQG PKGSTGPFPG FANGEK GAR GVAGKPGPRG QRGP!TGPGRS RGARGPTGKP 900
 GPKGTSGGDG PPGPPGERGP QGPQGPVGFP GPKGPPGPPG RMGCPGHPGQ RGETGFQGKT 960
 GPPGPGGVVG PQGPTGETP IGERGYPGP GPPGEQGLPG AAGKEGAKGD PGPQISGKD 1020
 GPAGLRGFP ERGLPGAQGA PGLKGGEGPQ GPPGVPSPG ERGSA GTAGP IGLRGRPGPQ 1080
 GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPGQKGSK 1140
 GKGGENGPPG PPLGQGPVGA PGLAGGDGEP GPRGQGMFG QKGDEGARGF PGPPGPIGLQ 1200
 GLPGPPGEKG ENGDVGPWGP PGP!GPRGP GPNADGPPQ PPGSVGVSVG VGEKGEPEA 1260
 15 GNP!GPEAG VGGPKGERGE KGEAGPPGAA GPPGAKGPPG DDGPKGNPGP VGFP!GPGP 1320
 GELGPAGQDG VGGDKGEDGD PGQGP!GPGS GEAGPPGPPG KRGP!GAAGA EGRQGEKGA 1380
 GEAGAEGPGG KTGVPVGPQGP AGKPGPEGLR GIPGPVGEQG LPGAAGQDGP PGP!GPPGLP 1440
 GLKGDPGSKG EKGHPGLIGL IGPPGEQGEK GDRGLPGTQG SPGAKGDGGI PG!GAGPLGP 1500
 GPPGLPGPQG PKGNKGSTGP AGQKGDGSLP GPPGPPGPPG EVIQLPILS SKKTRRHTG 1560
 20 MQADADDN!L DYS!GME!F GSLNSLKQDI EHM!K!F!MTGT TNPARTCKDL QLSHPDFPDG 1620
 EYWD!PNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPK!K!PGS W!SEFKRGKL 1680
 LSYLDVEGNS INMVQMTFLK LLTASARQNF TYHCHQSAW YDVSSGSYDK ALRFLGSNDE 1740
 EMSYDN!NPF! KTYLDGCTSR KGYEKT!VIE! NTPKIDQVPI VDMISDFGD QNQK!GF!EVG 1800
 PVCFLG

25 Seq ID NO: 123 DNA sequence
 Nucleic Acid Accession #: NM_015886
 Coding sequence: 485-1261 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 | | | | |
 GAATTCCTCTGTTGTTACTCTGT GATTCAATTTT TCTTCACCTC TCCAGGTGAA TTTCAATTGC 60
 CATTCTCTGT TGTACTCTGT GATTCAATTTT TCTTCACCTC TCCAGGTGAA TTTCAATTGC 120
 TGAAAAATTTT CCACTGAAAAA TATGCAGTAA TATATTTTGT GGTTCAGACA TTTGGGGCAA 180
 35 ATGGTTTACA TCAATTTTAG GGTTAGTGGT CATGCTGTTT ATTTTCTCT GCTATACAAA 240
 GTTCCTCTTA GGGGTCTGCC TCATGACACT AAAAAATGAA TAGAGATTCT ACTGTAGGTT 300
 ATCTCTAGG CTTGAGTTCA ACATTTGTTT GGTATTTTGA AGAAAGTCAA ATCAAGCAAT 360
 GCTCCCAAT TCAATTTTGA TAAATTCATA CCTCTGGCC CATTTTCTTT TCATAGACCC 420
 TAACTCTACC TTCTGCTTTT AAAGCAAAAT AAACCTCGGT GCCTCTCTTT CTCCACCCCT 480
 CAAAATGATA GCAATCTCTG CCGTCAGCAG TGCACCTCTG TTCTCCCTTC TCTGTGAAGC 540
 40 AAGTACCGTC GTCCTACTCA ATTCCACTGA CTCATCCCG CCAACCAATA ATTTCACTGA 600
 TATTGAAGCA GCTCTGAAG CACAATTAGA TTCAGCGGAT ATCCCCAAAG CCAGGCGGAA 660
 GCGCTACATT TCAGCAAAATG ACATGATCGC CATTCTTGAT TATCATAATC AAGTTCGGGG 720
 CAAAGTGTTT CCACCGGCAG CAAATATGGA ATATATGGTT TGGGATGAAA ATCTTGCAAA 780
 45 ATCGGCAGAG GCTTGGGCGG CTACTTGCA TTTGGGACCA GGACCTTCTT ACTTACTGAG 840
 ATTTTGGGC CAAAATCTAT CTGTACGCAC TGGAAAGATAT CGCTCTATTC TCCAGTTGGT 900
 CAAGCCATGG TATGATGAAG TGAAGATTAT TGCTTTTCCA TATCCCCAGG ATTGCAACCC 960
 CAGATGCTCT ATGAGATGTT TTGGTCCCAT GTGCACACAT TATACGCAGA TGGTTTGGGC 1020
 CACTTCCAAT CGGATAGGAT GCGCAATTCA TGCITGCCAA AACATGAATG TTTGGGGATC 1080
 50 TGTGTGGCGA CGTCAGATT ACTTGGTATG CAACATATGCC CCAAAGGGCA ATTGGATTGG 1140
 AGAAGCACCA TATAAAGTAG GGGTACCATG TTCATCTGTT CCTCCAAGTT ATGGGGGATC 1200
 TTGTAAGTAC AATCTGTGTT TTCCAGGAGT TACGTCAAAC TACCTGTACT GGTTTAAATA 1260
 AGTTTACCTT TTCTCCAGG AATATAATG ATTTCTGGGA ACATGGGCAT GTATATATAT 1320
 ATATGGAGAG AGAATTTTGC ACATATTATA CATATTTTGT GCTAATCTTG TTTCTCTT 1380
 55 AGTATTCCTT TGATAAAAT AGTGTITGTC TAGCATGTTT GTTAACTCT TGGGAATTC

Seq ID NO: 124 Protein sequence:
 Protein Accession #: NP_056970.1

60 1 11 21 31 41 51
 | | | | |
 MIAISAVSSA LLFSLCEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR 60
 YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS AEAWAATCIW DHQPSYLLRF 120
 LGQNL!SVRTG RYRSILQV LK PWYDEVKDYA FPYPQDCNPR CPMRCFGPMC THYTQMVWAT 180
 65 SNRIGCAIHA CQNMNVWGSV WRRVAVYLCN YAPKGNWIGE APYKVGVP!SCS PP!SYGGSC 240
 TDNLCFPGVT SNLYLWFK

70 Seq ID NO: 125 DNA sequence
 Nucleic Acid Accession #: NM_001793
 Coding sequence: 54-2543 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTCTGGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGC!GCG 120
 CCTCCGAGCC GTGCGGCGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CGGAGCAGGA TCCCGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240

CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACCGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGGA 720
 GTGTCTTAGA GGGAGTCCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGAOCCACA CGACCTCATG TTCACAATC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAC CCCAGAAAT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG 1080
 GCCATGAGGT GCAGAGGCTG ACGTCACTG ATCTGGACGC CCCCACCTCA CCAGCGTGGC 1140
 GTGCCACCTA CCTTATCATG GGGGGTGAGC ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTT TGTGCTGAAG CTCCCAACCT 1320
 CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAGA CCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA CGAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCAACATCTG CAACCAAAGC CCTGTGCGCC 1740
 ACGTGTCTGA CATACGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCACG 1800
 CTCAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTGTGCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGAAAC CTGCGCTGGA CCTGGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCTGGCTCT GCTGTTCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGG GACCAGGACT ATGACATCAC CCAGTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT TCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCCTGA 2340
 AGGCGGCTAA CATACAGGCC ACAGCCCCG CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCTCAC CTCCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGGCGGCCCT GCCTGCAAGG CTGGGGACCA AACGTCAGGC 2580
 CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTAC TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGCTCTGG GCTGGGCCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGT CTCAAAAGT GCAGCCAGA GCTGCTGGG CCACTGGCCG 3000
 TCTGCACTT CTGGTTTCCA GACCCCAATG CCTCCATTC GATGGATCT CTGCTTTTT 3060
 ATACTGAGT TGCCTAGTT GCCCTTATT TTTTATTTT CCTGTTGCGT TGCTATAGAT 3120
 GAAGGTGAG ACAATCGTG TATATGTACT AGAATTTTT TATTAAGAA A

Seq ID NO: 126 Protein sequence
 Protein Accession #: NP_001784

1 11 21 31 41 51
 MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN ISHVTQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDGDGDSST TAVAVVEILD ANDNAPMFDQ QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMDP DSGQVTA VGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTTTTLLID 540
 VNDHGPVPEP RQITICNQP RVHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETPCGP WKGGFILPVL 660
 GAVLALLFLL LVLLLVRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 127 DNA sequence
 Nucleic Acid Accession #: NM_003256.1
 Coding sequence: 60-734 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCTGCTGGGG CCGTCCAGTC CCCCAGACCT CACAGGCTCA GTCGCGGATC TGCAGTGTCA 60

5
10
15
20

TCCTGGGAG CCCTCGGCC GCGCCAAGCT GGGTGTCTG GCTGCGGCTG CTGGCGTTGC 120
TGCGGCCCC GGGGCTGGT GAGGCATGCA GCTGCGGCC GCGCACCCCT CAGCAGCACA 180
TCTGCCACTC GGCACCTGTG ATTCGGGCCA AAATCTCCAG TGAGAAGGTA GTTCCGGCCA 240
GTGCAGACCC TGCTGACACT GAAAAATGC TCCGGTATGA AATCAAACAG ATAAAGATGT 300
TCAAAGGGTT TGAGAAAGTC AAGGATGTTC AGTATATCTA TACGCCTTTT GACTCTTCCC 360
TCTGTGGTGT GAAACTAGAA GCCAACAGCC AGAAGCAGTA TCTCTTGACT GGTCAAGTCC 420
TCAGTGTGG AAAAGTCTTC ATCCATCTGT GCAACTACAT CGAGCCCTGG GAGGACCTGT 480
CCTTGGTGCA GAGGAAAAGT CTGAATCATC ACTACCATCT GAACTGTGGC TGCCAAATCA 540
CCACCTGCTA CACAGTACCC TGTACCATCT CGGCCCTAA CGAGTGCCTC TGGACAGACT 600
GGCTGTGGA ACGAAAGTC TATGGTTACC AGGCTCAGCA TTATGTCTGT ATGAAGCATG 660
TTGAOGGCAC CTGACGCTGG TACCGGGCC ACCTGCCTCT CAGGAAGGAG TTTGTTGACA 720
TGTTCAGCC CTAGTAGGGA CCAAGTACCA TCACATCCCT TCAAGAGTCC TGAAGATCAA 780
GCCAGTTCTC CTCCCTGCA GAGCTTTGGC CATTACCAAC TGACCTTTG CTGCCAGCTA 840
ATAAGAAGTG CCAAGTGGAC AGTCTGGCCA CTGTCAAGGC AGGGAAGGGG CCATGACTTT 900
TCTGCCCTG CCTCAGCTG TTGCCCTGCC TCCAAACCC CATTAGTCTA GCCTTGTAGC 960
TGTACTGCA AGTGTTCCT CTGGCTTAGT CTGTTTCTA AAGCCAGGAC TATTCCTTT 1020
CCTCCCCAGG AATATGTGTT TTCTTTGTC TTAATCGATC TGGTAGGGGA GAAATGGCGA 1080
ATGTATACA CATGAGATGG TATATCCTG CGATGTACAG AATCAGAAGG TGGTTTGACA 1140
GCATCATAAA CAGGCTGACT GGCAGGAATG AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_003247.1

25

1 11 21 31 41 51
| | | | |
MPGSPRPAPS WVLLRLALL LRPPGLGEAC SCAPAHPPQH ICHSALVIRA KISSEKVVPA 60
SADPADTEKM LRYEIKQIKM FKGFVKDV QYITPFDSS LCGVKLEANS QKQVLLTGQV 120
LSDGKVFHIL CNYIEPWEDL SLVQRESLNH HYHLNCGCQI TTCYTVPTI SAPNECLWTD 180
WLLERKLYGY QAQHYVCMKH VDGTCWYRG HPLRKEFVD IVQP

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_007207.2
Coding sequence: 143-1591 (underlined sequences correspond to start and stop codons)

35
40
45
50
55
60
65
70

1 11 21 31 41 51
| | | | |
CCACGGGTCC GCAATGAAGC CGAGTGAAT GGGGCTGAAT GTGCGAGTCC ATAGCTGAAG 60
AGGAGCGCCA GATGGTGGAG GAATACACTT ATTTATGAAA CTGTCTTGAG TTCTTCTTGA 120
ATTGCCAGTT TTCAGCTCC TCATGCCCTCC GTCTCCTTTA GACGACAGGG TAGTAGTGGC 180
ACTATCTAGG CCGTCCGAC CTCAGGATCT CAACCTTTGT TTAGACTCTA GTTACCTTGG 240
CTGTGCCAAC CCAGGAGTA ACAGCCACCC TCCTGTCTATC GCCACCAACG TTGTGTCCT 300
CAAGGCTGCG AATCTGACGT ATATGCCCTC ATCCAGCGGC TCTGCCGCT CGTGAATTG 360
TGGATGCAGC AGTGCCAGCT GCTGCACTGT GGCAACCTAC GACAAGGACA ATCAGGCCCA 420
AACCCAAGCC ATTGCCGCTG GCACCAACCC CACTGCCATC GGAACCTCTA CCACTGCCCC 480
TGCTAACAG ATGTTCAACA ATAATGAGAA TACAGGCTCT CTAAGTCCAT CAAGTGGGGT 540
GGGAGGCCCT GTGTCAAGGA CCCCCAAGCA GCTAGCCAGC ATCAAAATAA TCTACCCCAA 600
TGACTTGCCA AAGAAGATGA CCAATGCAG CAAGAGTCAC CTGCCGAGTC AGGGCCCTGT 660
CATCATTGAC TGCAAGGCCCT TCATGGAGTA CAACAAGAGT CACATCCAAG GAGCTGTCCA 720
CATTAACTGT GCCGATAAGA TCAGCCGGCG GAGACTGCAG CAGGGCAAGA TCACTGTCT 780
AGACTTGATT TCCTGTAGGG AAGGCAAGGA CTCTTCAAG AGGATCTTTT CCAAAGAAAT 840
TATAGTTAT GATGAGAATA CCAATGAACC AAGCCGAGTG ATGCCCTCCC AGCCACTTCA 900
CATAGTCTCT GAGTCCCTGA AGAGAGAAGG CAAAGAACCT CTGGTGTGTA AAGGTGGACT 960
TAGTAGTTT AAGCAGAAC ATGAAAACCT CTGTGACAAC TCCTCCAGC TCCAAGAGTG 1020
COGGGAGGTG GGGGCGGGC CATCCGCGGC CTGAGCTTG CTACCTCAGC CCATCCCCAC 1080
CACCCTGAC ATCGAGAAGC CTGAGCTCAC CCCATCTTG CCTTCTGT TCCTTGCCA 1140
TGAGCAGGAT GCTCAGGACC TGGACACCAT GCAGCGGCTG AACATCGGCT ACGTCATCAA 1200
CGTCACCACT CATCTTCCCC TCTACCACTA TGAGAAAGGC CTGTTCAACT ACAAGCGGCT 1260
GCCAGCCACT GACAGCAACA AGCAGAAOCT GCGGCAGTAC TTTGAAGAGG CTTTGTAGTT 1320
CATTGAGGAA GCTCACCAGT GTGGGAAGGG GCTTCTCATC CACTGCCAGG CTGGGGTGTG 1380
COGCTCGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA CCATGACTGA 1440
TGCTTATAAA TTGTCAAAG GCAAACGACC AATTATCTCC CCAAACCTTA ACTTCATGGG 1500
GCAGTTGCTA GAGTTCGAGG AAGACCTAAA CAACGGTGTG ACACCGAGAA TCCTTACACC 1560
AAAGCTGATG GCGGTGGAGA CGGTTGTGTG ACAATGGTCT GGATGGAAAG GATTGCTGCT 1620
CTCCATTAGG AGACAATGAG GAAGGAGGAT GGATTCTGGT TTTTCTTCT TCTTTTTT 1680
TGTAGTTGG GAGTAAAGTT TGTGAATGGA AACAAACCTG GTTAAACACT TTATTTTAA 1740
CAAGTGTAA AAGACTATAC TTTGTATGCC ATTGAGATTC ACCTTCCACA AACTGGCCAA 1800
ATTAAGGAGG TTAAGAAAGT AATTTTTTTT AAGCCCAACC ATTAATAAT TAATACAAC 1860
TGGTTTCTCC CCCTTTTCCC TTTAAAGCTA NTTGTAAAA GTTTATGAG

Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_009138.1

75

1 11 21 31 41 51
| | | | |
MPPSPLDLDRV VVALSRPVRP QDLNLCLDSS YLGSANPGSN SHPPVIATT VSLKAANLTY 60
MPSSSGSARS LNCGSSASC CTVATYDKDN QAQTQALAA TTTAIGTST TCPANQM VNN 120
NENTGSLSPS SGVGSFVSGT PKQLASIKII YPNDLAKKMT KCSKSHLSPQ GPVILDCRPF 180

MEYNKSHIQG AVHINCADKI SRRRLQQGKI TVLDLISCRE GKDSFKRIFS KEIIVYDENT 240
 NEPSRVMP SQ PLHIVLES LK REGKEPLVLK GGLSSFKQNH ENLCDNSLQL QECREVG GGA 300
 SAASSLLPQ IPITPD IENA ELTPILPFLF LGNEQDAQDL DTMQRLNIGY VINVTTHLPL 360
 YHYEKL FNY KRLPATDSNK QNLRQYFEEA FEFIEEAHQ GKGLLIHCQA GVSRSATIVI 420
 5 AYLKMHTRMT MTDAYKFVKG KRPIISP NLN FMGQLEFEE DLNNGVTPRI LTPKLMGVET 480
 VV

Seq ID NO: 131 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 10 Coding sequence: 94-378 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 15 TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACCC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTTGA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 20 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 AAAGGACAAC GATGCCTAAA TCOCAAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAGA ATTTTIAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACITTTCT ATGGTTTTGT GACITTTCAAC TTTGTACAG TTATGTGAAG GATGAAAAGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
 25 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAAGCT 660
 GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGAGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTCAT GCAAATACAC ACTTCTTTCC 960
 30 CCAAATATCA TGTAGCACA CAATATGTAG GGAACATTC TTATGCATCA TTGGTTTGT 1020
 TTTATAACCA ATTCATTAAT TGAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTTC TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 35 TGTACTTTTT GTTTGATCC GTTTGTATA ATGATAGCAA TATCTGGAC ACATTTGAAA 1260
 TACAAATGT TTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTG ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTCAATG CTATATACCT TAAAATTTAG GTACTACTCA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCITTT TAAAAAAA AAA

40 Seq ID NO: 132 Protein sequence:
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 | | | | |
 45 MSVKGMAIAL AVILCATVVQ GPFPMFKRGR LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 133 DNA sequence
 Nucleic Acid Accession #: NM_012342
 50 Coding sequence: 373-1155 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 55 CTGGCGCGGG CGGGAGCTGC GCGGATACC CTGCGTGCT GTGGAGACCC TACTCTCTTC 60
 GCTGAGAACG GCCGCTAGCG GGGACTGAAG GCCGGGAGCC CACTCCGAC CCGGGCTAG 120
 CGTGCGTCCC TAGAGTCGAG CGGGGCAAGG GAGCCAGTGG CCGCCGACGG GGGACCGGGA 180
 AACTTTTCTG GGCTCCTGGA GAGCCCTGTA GCCGCGCTCC ATGCTCCGGC AGCGGCGCGA 240
 AACCCAGCCC CGCCGCTGAC GGAGCCCGCC GCTCCGGCA GGGCCCATGC CCTGCGCGCT 300
 60 CCGGGGGTGG TAGCTGCGCG CGAGCCGGGG CTCGGGAAGC CGGCGGGGGC GCCGCGCGCG 360
 TGCGGGGCGT CAATGATCG CCACTCCAGC TACATCTTCA TCTGGCTGCA GCTGGAGCTC 420
 TGCGCCATGG CCGTGCTGCT CACCAAAAGT GAAATTOGAT GCTACTGTGA TGCTGCCAC 480
 TGTGTAGCCA CTGGTTATAT GTGTAAATCT GAGCTCAGCG CTTGCTTCTC TAGACTTCTT 540
 GATCCTCAGA ACTCAAATTC CCACTCACC CATGGCTGCC TGGACTCTCT TGCAAGCAGC 600
 ACAGACATCT GCCAAGCCAA ACAGGCCCGA AACCACCTCT GCACCAACCAT ACCACATTG 660
 65 GAATGCTGTC ATGAAGACAT GTGCAATTAC AGAGGGCTGC ACGATGTTCT CTCTCTCTCC 720
 AGGGGTGAGG CCTCAGGACA AGGAAACAGG TATCAGCATG ATGGTAGCAG AAACCTTATC 780
 ACCAAGGTGC AGGAGCTGAC TTCTTCCAAA GAGTTGTGGT TCCGGGAGC GGTATTGCC 840
 GTGCCCATTT CTGGAGGGCT GATTTAGTG TTGCTTATTA TGTGGCCCT GAGGATGCTT 900
 CGAAGTGAAA ATAAGAGGCT GCAGGATCAG CGGCAACAGA TGCTCTCCCG TTGCACTAC 960
 70 AGCTTTCACG GACACCATTC CAAAAAGGG CAGGTTGCAA AGTTAGACTT GGAATGCATG 1020
 GTGCCGGTCA GTGGGCACGA GAACCTGCTGT CTGACCTGTG ATAAATAGAG ACAAGCAGAC 1080
 CTCAGCAACT ATAAGATCTCT CTGCTTGT CACTGGGGCA TGTACAGTGG GCACGGGAAG 1140
 CTGGAATTGG TATGACGGAG TCTTATCTGA ACTACACTTA CTGAACAGCT TGAAGGCCCT 1200
 TTGAGTCTCT CTGGACAGGA GCATTTTATC TGAAGACAAA CTCATTTAAT CATCTTTGAG 1260
 75 AGACAAAATG ACCTCTGCAA ACAGAACTCT GGATATTCT TCTGAAAGAT TATTGCACA 1320
 GACTTAAATA CAGTTAAATG TGTTATTTCG TTTTAAATTT ATAAAAAGCA AAGAGAAGAC 1380
 TTTGTACACA CTGTACACAG GGTATTTCG ATCCAAGGGA GCTGGAATTG AGTACCTAAA 1440

TAAACAAAAA TGTGCCCTAT GTAAGCTTCT ACATCTTGAT TTATTGTAAA GATTTAAAAAG 1500
AAATATATAT ATTTTGTCTG A

Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_036474.1

1 11 21 31 41 51
MDRHSSYIFI WLQLELCAMA VLLTKGEIRC YCDAAHCVAT GYMCKSELSE CFSRLLDPOQ 60
SNSPLTHGCL DSLASTTDIC QAKQARNHSG TTIPTLEOCH EDMCNYRGLH DVLSPPRGEA 120
SGQGNRYQHD GSRNLITKVQ ELTSSKELWF RAAVIAVPIA GGLLVLLIM LALRMLRSEN 180
KRLQDQRQOM LSRLHYSFHG HHSKKGQVAK LDLECMVPVS GHENCLCTCD KMRQADLSND 240
KILSLVHWGM YSGHGKLEFV

Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_001627.1
Coding sequence: 64-1815 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGGGACGAAG CCCCTCTG CGGCGTGGAC TCCGTCAGTG GCCACCAAG AAGGAGGAGG 60
AATATGGAAT CCAAGGGGGC CAGTTCCTGC CGTCTGCTCT TCTGCCTCTT GATCTCCGCC 120
ACCGTCTTCA GGCCAGGCCT TGGATGGTAT ACTGTAAATT CAGCATATGG AGATACCATT 180
ATCATACCTT GCCGACTTGA CGTACCTCAG AATCTCATGT TTGGCAAATG GAAATATGAA 240
AAGCCCGATG GCTCCCCAGT ATTTATTGCC TTCAGATCCT CTACAAAGAA AAGTGTGCAG 300
TACGACGATG TACCAGAATA CAAAGACAGA TTGAACCTCT CAGAAACTA CACTTTGTCT 360
ATCAGTAATG CAAGGATCAG TGATGAAAAG AGATTGTGT GCATGCTAGT AACTGAGGAC 420
AAGGTGTTTG AGGCACCTAC AATAGTCAAG GTGTTCAAGC AACCATCTAA ACCTGAAATT 480
GTAAGCAAAG CACTGTTTCT CGAAACAGAG CAGCTAAAAA AGTTGGGTGA CTGCATTTC 540
GAAGACAGTT ATCCAGATGG CAATATCACA TGGTACAGGA ATGGAAAAGT GCTACATCCC 600
CTTGAAGGAG CGGTGGTCAT AATTTTAAAA AAGGAAAATGG ACCCAGTGAC TCAGCTCTAT 660
ACCATGACTT CCACCTCGGA GTACAAGACA ACCAAGGCTG ACATACAAAT GCCATTACCC 720
TGCTCGGTGA CATATTATGG ACCATCTGGC CAGAAAAACA TTCTATTCTG ACAGGCAGTA 780
TTTGATATTT ACTATCCTAC AGAGCAGGTG ACAATACAAG TGCTGCCACC AAAAAATGCC 840
ATCAAGAAGG GGGATAACAT CACTCTTAAA TGCTTAGGGA ATGGCAACCC TCCCCCAGAG 900
GAATTTTGTG TTTACTTACC AGGACAGCCC GAAGGAATAA GAAGCTCAAA TACTTACACA 960
CTGATGGAATG AGAGGCGCAA GTCAACAGGA GACTACAAGT GTTCCCTGAT AGACAAAAAA 1020
AGCATGATG CTTCACAGC CATCAGATT CACTATTGGG ATTTGTCTCT AAACCCAAAGT 1080
GGAGAAGTGA CTAGACAGAT TGGTGATGCC CTACCGTGT CATGCACAAT ATCTGCTAGC 1140
AGGAATGCAA CTGTGGTATG GATGAAAGAT AACATCAGGC TTGATCTAG CCCGTCATT 1200
TCTAGTCTTC ATATCAGGA TGCTGGAAAC TATGTCTGGG AAATGCTCT GCAGGAGGTT 1260
GAAGGACTAA AGAAAAGAGA GTCAATTGACT CTCATTGTAG AAGGCAAACC TCAAAATAAA 1320
ATGACAAAGA AAATCTATCC CAGTGGACTA TCTAAACAA TAATCTGCCA TGTGGAAGGT 1380
TTTCAAAGC CAGCCATTCA GTGGACAATT ACTGGCAGTG GAAGCGTCAT AAACCAAACA 1440
GAGGAATCTC CTATTATTAA TGGCAGGTAT TATAGTAAAA TTATCATTTT CCCTGAAGAG 1500
AATGTTACAT TAACCTGCAC AGCAGAAAAA CAACTGGAGA GAACAGTAAA CTCCTTGAAT 1560
GTCTCTGCTA TAAGTATCCC AGAACACGAT GAGGCAGACG AGATAAGTGA TGAACACAGA 1620
GAAAAGGTGA ATGACACGGC AAAACTAATT GTGGGAATCG TTGTTGGTCT CCTCTTGCT 1680
GCCCTTGTTG CTGGTGTCTG CTACTGGCTG TACATGAAGA AGTCAAAGAC TGCATCAAAA 1740
CATGTAACA AGGACCTCGG TAATATGGAA GAAAACAAAA AGTTAGAAGA AAACAATCAC 1800
AAAACCTGAAG CCTAAGAGAG AAATGTCTCT AGTTGTCCAG AGATAAAAA CATATAGACC 1860
AATTGAAGCA TGAACGTGGA TTGATTAA GACATAACA AAGACATTGA CAGCAATTCA 1920
TGGTTCAAGT ATTAAGCAGT TCATTCTACC AAGCTGTCAC AGGTTTTCAG AGAATTATCT 1980
CAAGTAAAAA AATGAAATT TAATTACAAA CAATAAGAAC AAGTTTGGC AGCCATGATA 2040
ATAGGTCATA TGTGTGTTT GGTTCATTT TTTTCCGTA AATGTCTGCA CTGAGGATTT 2100
CTTTTGGTT TGCCTTTTAT GTAAATTTT TACGTAGCTA TTTTATACA CTGTAAGCTT 2160
TGTTCTGGGA GTTGTGTTA ATCTGATGTA TAATGTAATG TTTTATTTT AATTGTTTAT 2220
ATGGATAATC TGAGCAGGTA CATTCTGAT TCTGATTGCT ATCAGCAATG CCCCCAACTT 2280
TCTCATAAGC ACCTAAAACC CAAAGGTGGC AGCTTGTGAA GATTGGGGAC ACTCATATTG 2340
CCCTAATTAA AAACGTGTAT TTTTATCACA AGGGAGGGGA GGCCGAGAGT CAGACTGATA 2400
GACACCATAG GAGCCGACTC TTTGATATGC CACCAGCGAA CTCTCAGAAA TAAATCACAG 2460
ATGCATATAG ACACACATAC ATAATGGTAC TCCCAAACCTG ACAATTTTAC CTATTCTGAA 2520
AAAGACATAA AACAGAATT

Seq ID NO: 136 Protein sequence:
Protein Accession #: NP_001618.1

1 11 21 31 41 51
MESKGASSCR LLFCLLSAT VFRPGLWY VNSAYGDTH IPCRLDVPQN LMFGKWYK 60
PDGSPVFI AF RSSTKKSQVY DDVPEYKDR L NLSNYTL SI SNARISDEKR FVCMLVTE DN 120
VFEAPTIVKV FKQPSKPEIV SKALFLETEQ LKKLGD CISE DSYPDGNITW YRNGKVLHPL 180
EGAVVIFKQ EMDPVTQLYT MTSTLEYKTT KADIQMPFTC SVTYGPGSQ KTHSEQAVF 240
DIYPTQEVY IQVLPKNAI KEGDNITLKC LGNGNPPPEE FLFYLPQPE GIRSSNTYTL 300
MDVRRNATGD YKCSLIDKKS MIASTAITVH YLDLSLNP SG EVTRQIGDAL PVSCTISASR 360
NATVVWMKDN IRLRSSPSFS SLHYQDAGNY VCETALQEVE GLKKRESLTL IVEGKPOIKM 420
TKKTDPSGLS KTIICHVEGF PKPAIQWTTT GSGSVINQTE ESPYINGRY Y SKIHSPEEN 480

VTLTCTAENQ LERTVNSLV SAISIPEHDE ADEISDENRE KVNDQAKLIV GIVVGLLLAA 540
LVAGVVYWLWY MKKSKTASKH VNKDLGNMEE NKKLEENNHK TEA

5 Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: XM_030559
Coding sequence: 1-119 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
| | | | |
ATGAACCGCA GCCACCGGCA CGGGGCGGGC AGCGGCTGCC TGGGCACTAT GGAGGTGAAG 60
AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT 120
GAGGAGTTTI ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTTGGTA 180
15 GGCTATGCAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCACAAA 240
GCTGTTTCAA CGGCCAATCC ACTGCTTAGG ATATTATAC AAAAGAAGGA AGAAGCAGAC 300
TACAGTGCC TTTGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTAAAC CAAGGTATTG 360
CGTCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCA AGACTTTAGA 420
CCTGTGTCTT CTATTATAGA CGTGGATATT CTCCAGAAA CGCATCGTAG GGTACGCTT 480
20 TACAAATACG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGGCTC CAGTGTCAAG 540
GTAACACCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCCAGGA 600
GGTCTGGCTC AAAGTACAGG ACTATTAGCT GTTAATGATG AAGTTTGA AGTTAATGGC 660
ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGATGATTGC AAATAGCCGT 720
AACCTCATCA TAACAGTGAG ACCGGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG 780
25 ACTTCTGGCA GTTCCGGTCA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT 840
GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC 900
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCCTAATA CTGAGAGCCT GGAGTCATTA 960
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATCCCTC TAATGAAGTG 1020
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTG AAACACATGC TCCAGATCAA 1080
30 AACTCTTAG AAGAAGATGG AACAATCATA ACATTATGA

Seq ID NO: 138 Protein sequence:
Protein Accession #: XP_030559

35 1 11 21 31 41 51
| | | | |
MNRSHRHGAG SGCLGTMEVK SKFGAEFRRF SLERSKPGKF EEFYGLLQHV HKIPNVDVLV 60
GYADIHGDL PINNDNYHK AVSTANPLL IFIQKKEAD YSAFGDTLI KKNVLTNVL 120
RPDNRKPKH IVISMPODFR PVSSHDVDI LPETHRRVRL YKYGTEKPLG FYIRDGSSVR 180
40 VTPHGLEKVP GIFISRLVPG GLAQSTGLLA VNDEVLEVNG IEVSGKSLDQ VTDMMIANSR 240
NLIITVRPAN QRNNVVRNSR TSGSSGQSTD NSLLGYPQI EPSFEPEDED SEEDDIIIED 300
NGVPQQIFKA VPNTESLESL TQIELSFESG QNGFIPSNEV SLAAIASSN TEFETHAPDQ 360
KLEEDGTII TL

45

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All
5 publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a breast cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-25.
- 1 2. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 3. The method of claim 2, wherein the nucleic acids are mRNA.
- 1 4. The method of claim 2, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 5. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-25.
- 1 6. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 7. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat breast cancer.
- 1 8. The method of claim 1, wherein the patient is suspected of having
2 breast cancer.
- 1 9. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-25.
- 1 10. The nucleic acid molecule of claim 9, which is labeled.
- 1 11. An expression vector comprising the nucleic acid of claim 9.
- 1 12. A host cell comprising the expression vector of claim 11.

- 1 13. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-25.
- 1 14. An antibody that specifically binds a polypeptide of claim 13.
- 1 15. The antibody of claim 14, further conjugated to an effector component.
- 1 16. The antibody of claim 15, wherein the effector component is a
2 fluorescent label.
- 1 17. The antibody of claim 15, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 18. The antibody of claim 15, which is an antibody fragment.
- 1 19. The antibody of claim 15, which is a humanized antibody
- 1 20. A method of detecting a breast cancer cell in a biological sample from
2 a patient, the method comprising contacting the biological sample with an antibody of claim
3 14.
- 1 21. The method of claim 20, wherein the antibody is further conjugated to
2 an effector component.
- 1 22. The method of claim 21, wherein the effector component is a
2 fluorescent label.
- 1 23. A method for identifying a compound that modulates a breast cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a breast cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-25; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 24. A drug screening assay comprising the steps of

- 2 (i) administering a test compound to a mammal having breast cancer or a cell
3 isolated therefrom;
- 4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of breast cancer.